

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:35:04 ; Search time 7.28571 Seconds
(without alignments)
672.941 Million cell updates/sec

Title: US-09-855-158-6

Perfect score: 284

Sequence: 1 MAGQCSQNEYFDSLHACIP.....LTCQRYCNASVTNSVKGTNA 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	284	100.0	184	2	S43486
2	74.5	26.2	1101	2	T16840
3	70.5	24.8	1548	2	S34503
4	69.5	24.5	5376	2	T42215
5	66	23.2	63	2	S07127
6	66	23.2	330	2	T25169
7	65.5	23.1	1299	2	T43251
8	62.5	22.0	999	2	T19275
9	62.5	22.0	1513	2	T23691
10	61.5	21.7	483	2	S60231
11	61.5	21.7	483	2	T24856
12	61.5	21.7	520	2	G88846
13	60.5	21.3	1574	2	T13954
14	60.5	21.3	3034	2	T14119
15	59	20.8	758	2	T15577
16	59	20.8	1717	2	T45558
17	58.5	20.6	2533	2	T28675
18	58.5	20.6	2533	2	T28675
19	58	20.4	1816	1	S68960
20	57.5	20.2	1680	2	T43434
21	57	20.1	802	2	T20130
22	57	20.1	838	2	T36675
23	57	20.1	838	2	T20125
24	56.5	19.9	701	2	S62460
25	56	19.7	447	2	A96639
26	56	19.7	2476	2	T34022
27	56	19.7	2824	2	T22759
28	55.5	19.5	339	1	KHRTB
29	55.5	19.5	388	2	T31887

30	55.5	19.5	388	2	T31888
31	55.5	19.5	438	2	T31889
32	55.5	19.5	445	2	T31898
33	55.5	19.5	815	1	T05754
34	55.5	19.5	989	2	T01519
35	55	19.4	294	2	T23682
36	55	19.4	339	1	KHMSB
37	55	19.4	474	2	T27297
38	55	19.4	552	2	T27424
39	55	19.4	758	2	S46625
40	55	19.4	1620	2	T27283
41	54.5	19.2	392	2	T27303
42	54.5	19.2	419	2	S69207
43	54.5	19.2	493	2	JC5486
44	54.5	19.2	592	1	JC1480
45	54.5	19.2	2155	2	T30197

ALIGNMENTS

RESULT 1

S43486 B-cell maturation factor - human
 A:Species: Homo sapiens (man)
 C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 21-Jul-2000
 C:Accession: S43486; S31208; S36661
 R:Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Teapis, A.
 Nucleic Acids Res. 22, 1147-1154, 1994
 A:Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bidirectional.
 A:Reference number: S43486; MUID:94218235; PMID:8165126
 A:Accession: S43486
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-184 <LAA>
 A:Cross-references: EMBL:Z29574; NID:9471244; PIDN:CAA82690.1; PID:9471245
 R:Laabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Teapis, A.
 EMBO J. 11, 3897-3904, 1992
 A:Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16) translocation.
 A:Reference number: S31208; MUID:93010984; PMID:1396583
 A:Accession: S31208
 A:Molecule type: mRNA
 A:Residues: 1-184 <LAA>
 A:Cross-references: EMBL:Z14954; NID:929407; PIDN:CAA78679.1; PID:929408
 A:Accession: S36661
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 4-184 <LAA>
 A:Cross-references: EMBL:Z14955
 C:Genetics:
 A:Gene: GDB:BCMA
 A:Cross-references: GDB:135977; OMIM:109545
 A:Map position: 16p13.1-16p13.1
 A:Introns: 44/1; 93/1
 C:Superfamily: human B-cell maturation factor

Query Match 100.0%; Score 284; DB 2; Length 184;
 Best Local Similarity 100.0%; Pred. No. 8.3e-25;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGQCSQNEYFDSLHACIPCOLRCSSNTPLTCORYCNASVTNSVKGTNA 51
 DB 4 MAGQCSQNEYFDSLHACIPCOLRCSSNTPLTCORYCNASVTNSVKGTNA 54

RESULT 2

T16840
 A:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T16840
 R:Geisel, C.

submitted to the EMBL Data Library, October 1995
A:Description: The sequence of C. elegans cosmid T10E10.

A:Reference number: Z18598

A:Accession: T16840

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1101 <GB1>

A:Cross-references: EMBL:U39644; NID:G1049339; PID:G1049343; PIDN:AAA80360.1; CESP:T10E1

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:T10E10.4

A:introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7

Query Match

Best Local Similarity 26.2%; Score 74.5; DB 2; Length 1101;

Matches 18; Conservative 11; Mismatches 15; Indels 5; Gaps 3;

OY 4 OCSONEYFDSLHACIPQOLR--CSSNTPPLTCORVCNASTNSVKGTN 50

DB 350 OCSQSTVFNSDLNVCPLAIQNSCHDSITQPVCS--C-SQVSSSCPGTS 395

RESULT 3

S34583
serine proteinase (EC 3.4.21.-) PCGB - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999

C:Accession: S34583

R:Nakagawa, T.; Murakami, K.; Nakayama, K.

FEBS Lett. 327, 165-171, 1993

A:Title: Identification of an isoform with an extremely large Cys-rich region of PCG, a

A:Reference number: S34583; MUID:93327934; PMID:8335106

A:Accession: S34583

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1548 <NAK>

A:Cross-references: GB:D17583; NID:G407344; PIDN:BA04507.1; PID:G440374

C:Keywords: hydrolase; serine proteinase

Query Match

Best Local Similarity 24.8%; Score 70.5; DB 2; Length 1548;

Matches 17; Conservative 5; Mismatches 22; Indels 5; Gaps 1;

OY 4 OCSONEYFDSLHACIPQOLR--CSSNTP--LTCORVCNASTNSVK 47

DB 1151 ECAAYEVNDEGSHRCQCHKRCSCGSEDCYCTCPREPLNLTTCVK 1199

RESULT 4

T42215
zonadhesin - mouse

N:Alternate names: sperm-specific membrane protein

C:Species: Mus musculus (house mouse)

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T42215

J:Gao, Z.; Garbers, D.L.

J:Biochem. J. 341S-342S, 1998

A:Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane pro

A:Reference number: Z22080; MUID:98123114; PMID:9452463

A:Accession: T42215

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-5376 <GAO>

A:Cross-references: EMBL:U97068; NID:G3327420; PID:G3327421; PIDN:AAC26680.1

C:Genetics:

A:Gene: Zan

A:Map position: 5

C:Function: functions in multiple cell adhesion processes

A:Note: found exclusively on the apical region of the sperm head

C:Keywords: cell adhesion

Query Match

24.5%; Score 69.5; DB 2; Length 5376;

Best Local Similarity 36.8%; Pred. No. 16;

Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

OY 4 OCSONEYFDSLHACIP--COLRCSNTP--PLTCORVC 38

DB 3299 QCPTNSQFTDCLPSCVPCSCNSNCEVTSFSPVSSCRGCG 3336

RESULT 5

S07127
chymotrypsin/elastase inhibitor - common roundworm

C:Species: Ascaris lumbricoles (common roundworm)

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C:Accession: S07127

R:Babin, D.R.; Peanasky, R.J.; Goos, S.M.

Arch. Biochem. Biophys. 232, 143-161, 1984

A:Title: The isoforms of chymotrypsin/elastase from Ascaris lumbricoles: the prim

A:Reference number: S07127; MUID:84255715; PMID:6564898

A:Accession: S07127

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-63 <BAB>

C:Superfamily: roundworm trypsin inhibitor

Query Match

Best Local Similarity 23.2%; Score 66; DB 2; Length 63;

Matches 17; Conservative 7; Mismatches 18; Indels 8; Gaps 4;

OY 5 CSONEYFDSLHACIPQOLR--SSNTP--PLTCORVCNASTNSVKGTN 50

DB 5 CGNEVWTE---CTCGEMKCGPDENTPCPLMCRPSCSCSGRGWRRTN 50

RESULT 6

T25169
hypothetical protein T23F1.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000

C:Accession: T25169

R:Milkinson, J.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z19990

A:Accession: T25169

A:Status: preliminary

A:Experimental source: clone T23F1

A:Cross-references: EMBL:T81129; PIDN:CAB03405.1; GSPDB:GN00023; CESP:T23F1.6

A:Molecule type: DNA

A:Residues: 1-330 <WIL>

A:Gene: CESP:T23F1.6

A:Map position: 5

A:Superfamily: gliadin

Query Match

Best Local Similarity 23.2%; Score 66; DB 2; Length 330;

Matches 15; Conservative 8; Mismatches 22; Indels 8; Gaps 2;

OY 5 CSONEYFDSLHACIP--COLRCSNTPPL--TCORVCNASTNSVKGT 49

DB 59 CASSQOYQLOTSCWPCACCOOSQOCCOSNTNTQOCPCCOOSCTSCNPMST 111

RESULT 7

T43251

furin (EC 3.4.21.75) - fall armyworm

N:Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; seri

C:Species: Spodoptera frugiperda (fall armyworm)

C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000

C:Accession: T43251

R:Cieplik, M.; Klenk, H.

submitted to the EMBL Data Library, January 1996

A:Description: Cloning and functional characterization of FURIN from Spodoptera frugipe

Query Match

A:Reference number: Z2368
 A:Accession: T43251
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1299 <CIE>
 A:Cross-references: EMBL:Z68888; NID:gl167859; PID:e219690; PIDN:CAA93116.1
 A:Experimental source: Clone Sfrun 6; ovary
 C:Function:
 C:Description: responsible for the endoproteolytic processing of proproteins with specific keywords: hydrolase; serine proteinase

Query Match 23.1%; Score 65.5; DB 2; Length 1299;
 Best Local Similarity 34.0%; Pred. No. 14;
 Matches 18; Conservative 8; Mismatches 14; Indels 13; Gaps 4;

QY 5 CSQNEYFDSLHACIPQLRCS-----SNTPLTCQRYCNAS----VTNSVKG 48
 DB 1150 CSRPLRLDLNNOCVFC---CSRGVTNSTPTDC-CHCNPENGCINSSVAG 1198

RESULT 8
 T19275
 hypothetical protein F34D10.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T19275; T21723
 R:Haris, B.
 submitted to the EMBL Data Library, September 1994
 A:Reference number: Z19099
 A:Accession: T19275
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-999 <WIL>
 A:Cross-references: EMBL:Z37139; PIDN:CAA85494.1; GSPDB:GN00021; CESP:F34D10.2
 A:Experimental source: clone C1481
 R:Kershaw, J.
 submitted to the EMBL Data Library, June 1994
 A:Reference number: Z19464
 A:Accession: T21723
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-999 <W12>
 A:Cross-references: EMBL:Z34799; PIDN:CAA84320.1; GSPDB:GN00021; CESP:F34D10.2
 A:Experimental source: clone F34D10
 C:Genetics:
 A:Gene: CESP:F34D10.2
 A:Map position: 3
 A:Introns: 20/3; 40/3; 72/1; 234/3; 387/3; 457/1; 523/2; 541/3; 682/1; 784/2; 822/2; 870

Query Match 22.0%; Score 62.5; DB 2; Length 999;
 Best Local Similarity 42.5%; Pred. No. 24;
 Matches 17; Conservative 2; Mismatches 20; Indels 1; Gaps 1;

QY 10 YFSLHACIPQLRCSNTPLTCQRYCNASVTNSVKG 48
 DB 516 YEDSLKTCIGRAFRVKKMTPLRIQYFVSSTPGLDG 555

RESULT 9
 T23681
 hypothetical protein M02G9.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T23681
 R:Matthews, L.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19781
 A:Accession: T23681
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1513 <WIL>
 A:Cross-references: EMBL:Z81573; PIDN:CAB04625.1; GSPDB:GN00020; CESP:M02G9.1
 A:Experimental source: clone M02G9

C:Genetics:
 A:Gene: CESP:M02G9.1
 A:Map position: 2
 A:Introns: 23/3; 71/3; 121/3; 183/1; 1083/3; 1141/3; 1408/1; 1449/1

Query Match 22.0%; Score 62.5; DB 2; Length 1513;
 Best Local Similarity 35.8%; Pred. No. 34;
 Matches 19; Conservative 3; Mismatches 18; Indels 13; Gaps 3;

QY 12 DSLHAC-IPCQLRCS-SNTPLTCQRYCNASV-----TNSVKG 51
 DB 141 DSCNVQNVQACVSONSPPAVCQTCRQSCQFCATNEQLPTTSSSTNA 193

RESULT 10
 S60231
 gibberellin-regulated protein GAS3 precursor - Arabidopsis thaliana
 N:Alternate names: GAST1 protein homolog
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 09-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 24-Sep-1999
 C:Accession: S60231
 R:Herzog, M.; Dorne, A.M.; Grellet, F.
 Plant Mol. Biol. 27: 743-752, 1995
 A:Title: GAS3, a gibberellin-regulated gene family from Arabidopsis thaliana related to F1-18/Domain: signal sequence #status predicted <SIG>
 A:Reference number: S60229; MUID:95244835; PMID:7727751
 A:Accession: S60231
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-99 <HER>
 A:Cross-references: EMBL:U11764; NID:G887934; PIDN:AAB06308.1; PID:G887935
 C:Genetics:
 A:Gene: GAS3
 C:Superfamily: gibberellin-regulated protein GAS2
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-99/Product: gibberellin-regulated protein GAS3 #status predicted <MAT>

Query Match 21.7%; Score 61.5; DB 2; Length 99;
 Best Local Similarity 35.6%; Pred. No. 4.4;
 Matches 16; Conservative 7; Mismatches 17; Indels 5; Gaps 2;

QY 3 GQCSNEYFDSLHACIPQLRCSNTPLTCQRY---CNASVT 43
 DB 47 GRCSKSRPNLCRLACNSCCYRCNC-VPECTAGNHLCPYASIT 90

RESULT 11
 T24856
 hypothetical protein T12A7.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T24856
 R:Lennard, N.
 submitted to the EMBL Data Library, June 1996
 A:Reference number: Z19943
 A:Accession: T24856
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-483 <WIL>
 A:Cross-references: EMBL:Z73911; PIDN:CAA98142.2; GSPDB:GN00022; CESP:T12A7.2
 A:Experimental source: clone T12A7
 C:Genetics:
 A:Gene: CESP:T12A7.2
 A:Map position: 4
 A:Introns: 36/3; 71/1; 146/1; 255/2; 287/2; 340/3; 387/1; 449/2

Query Match 21.7%; Score 61.5; DB 2; Length 483;
 Best Local Similarity 31.8%; Pred. No. 17;
 Matches 14; Conservative 5; Mismatches 20; Indels 5; Gaps 1;

QY 5 CSQNEYFDSLHACIPQLRCSNTPLTCQRYCNASVTNSVKG 48
 DB 108 CMNDGYFNHTLGRGV-----CTSNWVGEHCIFRCNSGVNKTSG 146

```
RESULT 12
G88846
Protein T12A7.2 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: G88846
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: G88846
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-520<STO>
A:Cross-references: GB:chr_IV; PIDN:CA98142.1; PID:G3879789; GSPDB:GN00022; CESP:T12A7.
A:Gene: T12A7.2
A:Map position: 4

Query Match      21.7%; Score 61.5; DB 2; Length 520;
Best Local Similarity 31.8%; Pred. No. 18;
Matches 14; Conservative 5; Mismatches 20; Indels 5; Gaps 1;

OY 5 CSQNEVFDLHACIPQQLCSNTPLTCQRCMASTNSVKG 48
DB 145 CMMDGTFNHTLGRV-----CTSMVGECIFRCNSGVNKTSG 183

RESULT 13
T13954
MEGF6 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C:Accession: T13954
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: Z14126; MUID:98360089; PMID:9693030
A:Accession: T13954
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1574 <NAK>
A:Cross-references: EMBL:AB011532; NID:G3449293; PIDN:BA032462.1; PID:G3449294
A:Experimental source: strain Sprague-Dawley; brain
C:Genetics:
A:Gene: MEGF6

Query Match      21.3%; Score 60.5; DB 2; Length 1574;
Best Local Similarity 32.2%; Pred. No. 59;
Matches 19; Conservative 8; Mismatches 19; Indels 13; Gaps 4;

OY 2 AGQCSQNEVFDLHACIPQQL-----RCSSNTPLPLT----CORVC--NASVTNSVKG 48
DB 963 ACNCSAGAPCDAYTGSCI-CPAGRWGPRCAOSCPILTFGLNCSQITCFNGASCDSVTG 1020

RESULT 14
T14119
seven-pass transmembrane receptor protein precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T14119
R:Hadjilovakakis, A.K.; Formstone, C.J.; Little, P.F.R.
submitted to the EMBL Data Library, October 1997
A:Description: The Celar family of novel evolutionarily conserved seven-pass transmembr
A:Reference number: Z17881
A:Accession: T14119
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-3034 <HAD>
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A:Cross-references: EMBL:AF031572; NID:G3800735; PID:G3800736; PIDN:AA68836.1
C:Genetics:
A:Gene: Celar1
A:Map position: 15
C:Keywords: transmembrane protein
C:Keywords: signal sequence #status predicted <SIG>
F/1-26/Domain: signal sequence #status predicted <MRT>
F/27-3034/Product: seven-pass transmembrane receptor protein #status predicted <MRT>

Query Match      21.3%; Score 60.5; DB 2; Length 3034;
Best Local Similarity 28.3%; Pred. No. 1e+02;
Matches 17; Conservative 5; Mismatches 19; Indels 19; Gaps 3;

OY 4 QCSQNEVFDLHACIPQQL-----RCSSNTPLPLTCQ-----RYCN-----ASTYN 44
DB 2001 QCKENYKPPADACLPDCFPHGSHSRACDMDTQCAKKGVLIGRCNRCNDNPFAYETS 2060

RESULT 15
T15577
hypothetical protein C23G10.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
C:Accession: T15577
R:Latreille, P.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans coemid C23G10.
A:Reference number: Z18372
A:Accession: T15577
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-758 <LAT>
A:Cross-references: EMBL:U39851; NID:G1055062; PID:G1055068; PIDN:AAA81069.1; CESP:C23G
C:Gene: CESP:C23G10.8
A:Interfam: 47/3; 237/3; 293/2; 405/3; 487/1; 577/3; 694/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C23G10.8

Query Match      20.8%; Score 59; DB 2; Length 758;
Best Local Similarity 42.9%; Pred. No. 47;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 12 DSLHACIPQQLRCSSNTPL 32
DB 260 ESVFPHLYPABIRCSADGPPL 280

Search completed: January 7, 2003, 09:41:06
Job time : 9.28572 secs
```


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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:31:39 ; Search time 12.1855 Seconds
(without alignment)
371.797 Million cell updates/sec

Title: US-09-855-158-7

Perfect score: 201

Sequence: 1 CSQNEYFDLLHACIPQLRCSSNTPLTCQRYC 34

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq 101002.*

1:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SID82/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SID82/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SID82/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SID82/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	201	100.0	34	AAE15486	Human B-cell matur
2	201	100.0	51	AAE15485	Human B-cell matur
3	201	100.0	58	AAE15501	Human B-cell matur
4	201	100.0	181	AAE15484	Human B-cell matur
5	201	100.0	184	AAE15483	Amiro acid sequenc
6	201	100.0	184	AAE15482	A human BCMA prote
7	201	100.0	184	AAE15481	Human BCMA protein
8	201	100.0	184	AAE15480	Human B-cell matur
9	201	100.0	184	AAE15479	Human B-cell matur
10	201	100.0	184	AAE15478	Human B-cell matur

11	201	100.0	184	ABB81487	Human BCMA recepto
12	201	100.0	283	AAE15488	Human BCMA-immunog
13	201	100.0	302	AAE00507	Human BCMA-immunog
14	201	100.0	302	AAE00507	Mouse IGG signal/h
15	159.5	79.4	157	AAE06099	Human BAPF recepto
16	136	67.7	185	AAE08844	Amino acid sequenc
17	136	67.7	185	AAE071980	Murine B cell matu
18	136	67.7	185	AAE15490	Mouse B cell matur
19	93.5	46.5	117	AAE15489	Mouse BCMA-human i
20	90.5	45.0	24	AAE15491	Human-murine B cel
21	71.5	35.6	249	AAE15492	A murine ztnf4, a
22	66.5	33.1	33	AAE15495	Human TACI cystein
23	66.5	33.1	37	AAE15495	Human AGP-3 recept
24	66.5	33.1	59	AAE10951	Human TACI cystein
25	66.5	33.1	59	AAE15500	Human lymphocyte s
26	66.5	33.1	166	AAE15494	Human TACI extrace
27	66.5	33.1	166	AAE15494	Human TACI splice
28	66.5	33.1	265	AAE09244	Human AGP-3 recept
29	66.5	33.1	291	AAU10949	Human lymphocyte s
30	66.5	33.1	293	AAE15493	Human neutrokin-a
31	66.5	33.1	293	AAE15493	A transmembrane ac
32	66.5	33.1	293	AAE15493	Human TACI protein
33	66.5	33.1	293	AAE15493	Human TACI-IgG Rc
34	66.5	33.1	293	AAE15493	Human tumour necro
35	66.5	33.1	293	AAE15493	Human TACI-IgG Rc
36	66.5	33.1	293	AAE15493	Human TACI-IgG Rc
37	66.5	33.1	293	AAE15493	Human TACI-IgG Rc
38	66.5	33.1	293	AAE15493	Human TACI-IgG Rc
39	66.5	33.1	293	AAE15493	Human TACI-IgG Rc
40	66.5	33.1	293	AAE15493	Human TACI-IgG Rc
41	66.5	33.1	293	AAE15493	Human TACI-IgG Rc
42	66.5	33.1	293	AAE15493	Human TACI-IgG Rc
43	66.5	33.1	293	AAE15493	Human TACI-IgG Rc
44	66.5	33.1	293	AAE15493	Human TACI-IgG Rc
45	66.5	33.1	293	AAE15493	Human TACI-IgG Rc

ALIGNMENTS

RESULT 1

AAE15486

ID AAE15486 standard; peptide; 34 AA.

AC AAE15486;

XX

XX

DT 12-MAR-2002 (first entry)

XX

XX

DE Human B-cell maturation (BCMA) protein cysteine-rich consensus region.

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PI The11 LE, Yu G;
XX
DR WPI; 2002-066686/09.
XX
PT Inhibiting activity of B cell maturation protein and/or transmembrane
XX activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor
XX family ligand
XX
PS Claim 1; Fig 10A; 94pp; English.

XX
XX The invention relates to a method for inhibiting TAC1 (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering
CC a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
CC family ligand), having the consensus region of TAC1, BCMA, or the TAC1/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
XX is human BCMA protein cysteine-rich consensus region.

SQ Sequence 34 AA;

Query Match 100.0%; Score 201; DB 23; Length 34;
Best Local Similarity 100.0%; Pred. No. 7, 4e-19;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYPDSLHACIPQLRCSSNTPTTCQRYC 34
DB 1 CSQNEYPDSLHACIPQLRCSSNTPTTCQRYC 34

RESULT 2

ID AAE15485 standard; peptide; 51 AA.

AC AAE15485;

DT 12-MAR-2002 (first entry)

DE Human B-cell maturation (BCMA) protein extracellular domain.

XX Human; transmembrane activator and intracellular CAML interactor; TAC1;
XX Cytotoxic; B cell maturation protein; BCMA; tumor necrosis factor-TNF;
XX lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
XX prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
XX drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
XX Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
XX human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
XX rheumatoid arthritis; atherosclerosis.

OS Homo sapiens.

PN WO200187979-A2.

PD 22-NOV-2001.

PF 14-MAY-2001; 2001WO-US15567.

PR 12-MAY-2000; 2000US-204039P.

PR 27-JUN-2000; 2000US-214591P.

PR 14-MAY-2001; 2001US-0214591.

PA (AMGE-) AMGEN INC.

PI The11 LE, Yu G;

DR WPI; 2002-066686/09.

XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
XX activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor
XX family ligand
XX
PS Claim 1; Fig 10A; 94pp; English.

XX
XX The invention relates to a method for inhibiting TAC1 (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering
CC a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
CC family ligand), having the consensus region of TAC1, BCMA, or the TAC1/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
XX is human BCMA protein extracellular domain.

SQ Sequence 51 AA;

Query Match 100.0%; Score 201; DB 23; Length 51;
Best Local Similarity 100.0%; Pred. No. 1, 1e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYPDSLHACIPQLRCSSNTPTTCQRYC 34
DB 5 CSQNEYPDSLHACIPQLRCSSNTPTTCQRYC 38

RESULT 3

ID AAE15501 standard; peptide; 58 AA.

AC AAE15501;

DT 12-MAR-2002 (first entry)

DE Human B cell maturation protein cysteine rich extracellular region.

XX Human; transmembrane activator and intracellular CAML interactor; TAC1;
XX Cytotoxic; B cell maturation protein; BCMA; tumor necrosis factor-TNF;
XX lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
XX prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
XX drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
XX Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
XX human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
XX rheumatoid arthritis; atherosclerosis.

OS Homo sapiens.

PN WO200187979-A2.

PD 22-NOV-2001.

PF 14-MAY-2001; 2001WO-US15567.

PR 12-MAY-2000; 2000US-204039P.

PR 27-JUN-2000; 2000US-214591P.

```

PR 14-MAY-2001; 2001US-0214591.
PA (AMGE-) AMGEN INC.
PI Theill LE, Yu G;
XX WPI; 2002-066686/09.
DR
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor
PT family ligand
XX
XX Disclosure; Fig 13; 94pp; English.
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering
CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human BCMA cysteine-rich extracellular region.
XX
XX Sequence 58 AA;
SQ
Query Match 100.0%; Score 201; DB 23; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.3e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSQNEYFDSLHACIPQLRCSNTPTPLTCQRYC 34
Db 1 CSQNEYFDSLHACIPQLRCSNTPTPLTCQRYC 34
RESULT 4
AAE15484
ID AAE15484 standard; Protein; 181 AA.
XX
XX AAE15484;
XX
XX 12-MAR-2002 (first entry)
XX
XX Human B-cell maturation (BCMA) protein.
XX
XX Human; transmembrane activator and intracellular CAML interactor; TACI;
KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.
XX
XX Homo sapiens.
XX
XX Location/Qualifiers
XX Key 5..38
XX Region /note= "Cysteine-rich consensus region; This is region
XX is specifically claimed as SEQ ID NO: 7 in claim 1 of
XX the specification"
XX 52..72
XX Domain

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FT
XX /label= Transmembrane_domain
FN WO200187979-A2.
XX
XX 22-NOV-2001.
XX
XX 14-MAY-2001; 2001WO-US15567.
XX
XX 12-MAY-2000; 2000US-204039P.
XX 27-JUN-2000; 2000US-214591P.
XX 14-MAY-2001; 2000US-0214591.
XX
XX (AMGE-) AMGEN INC.
XX
XX Theill LE, Yu G;
XX WPI; 2002-066686/09.
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor
PT family ligand
XX
XX Disclosure; Fig 10A; 94pp; English.
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering
CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human BCMA protein.
XX
XX Sequence 181 AA;
SQ
Query Match 100.0%; Score 201; DB 23; Length 181;
Best Local Similarity 100.0%; Pred. No. 4e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSQNEYFDSLHACIPQLRCSNTPTPLTCQRYC 34
Db 5 CSQNEYFDSLHACIPQLRCSNTPTPLTCQRYC 38
RESULT 5
AAB08843
ID AAB08843 standard; peptide; 184 AA.
XX
XX AAB08843;
XX
XX 02-JAN-2001 (first entry)
XX
XX Amino acid sequence of human.
XX
XX BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;
KW anti-cell death gene; apoptosis; viral infection; inflammatory response;
KW rheumatoid arthritis; inflammatory bowel disease; septic shock.
XX
XX Homo sapiens.
XX
XX Location/Qualifiers
XX Key

```

FT Domain 57..77 /note= "putative transmembrane domain"
XX
XX
XX MO200050633-A1.
XX
XX 31-AUG-2000.
XX
XX 24-FEB-2000; 2000MO-US04925.
XX
XX 24-FEB-1999; 99US-0121485.
XX
XX (GEHO) GEN HOSPITAL CORP.
XX
XX Seed B, Ting A;
XX
XX WPI; 2000-558405/51.
XX
XX
XX Identifying a modulator of gene expression for drug designing, by
XX contacting a compound library with a cell expressing an anti-cell death
XX gene and reporter gene, and determining alteration in reporter gene
XX expression -
XX
XX Claim 32; Fig 7A; 53pp; English.
XX
XX The present sequence represents a BCMA (not defined) polypeptide. BCMA
XX is a necrosis factor (NF)-KB activator. The method of the invention is
XX used to identify compounds which modulate BCMA activity (and thus NF-KB
XX activity). The specification describes a method of identifying a
XX polypeptide which increases gene expression from a promoter. The method
XX involves contacting a library of with a cell which expresses a
XX recombinant anti-cell death gene and a reporter gene operably linked to
XX the promoter, and then determining whether the expression of the
XX reporter gene is altered as a result of contact with library. The method
XX is useful for identifying polypeptides which increase or decrease gene
XX expression from a promoter. The BCMA polypeptide or nucleic acid are
XX useful for preparing a pharmaceutical composition for treating cancer,
XX aplastic, viral infections, inflammatory response, such as rheumatoid
XX arthritis, inflammatory bowel disease or septic shock. BCMA is useful for
XX identifying compounds that modulate NF-KB expression and thus for drug
XX designing.
XX
XX Sequence 184 AA;
SQ
Query Match 100.0%; Score 201; DB 21; Length 184;
Best Local Similarity 100.0%; Pred. No. 4.1e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CSQNEYPDSLHACIPQRCSSNTPTLCORYC 34
DB 8 CSQNEYPDSLHACIPQRCSSNTPTLCORYC 41
RESULT 6
AAE094001
ID AAE094001 standard; Protein; 184 AA.
XX
XX AAE094001;
XX
XX 20-OCT-2000 (first entry)
XX
XX A human BCMA protein, a B cell protein related to TACI.
XX
XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
XX transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
XX znf4 activity; antibody production; autoimmune disease; amyloidosis;
XX systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
XX rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
XX end stage renal failure; glomerulonephritis; vasculitis; neuropathy;
XX renal neoplasia; multiple myeloma; lymphoma; light chain neuropathy;
XX immune response; immunosuppression; graft rejection; joint pain;
XX graft versus host disease; inflammation; swelling; anaemia; septic shock;
XX insulin dependent diabetes mellitus; Crohn's disease; hypertension;
XX renal artery stenosis; occlusion; cholesterol; renal emboli.

XX OS Homo sapiens.
XX
XX MO200040716-A2.
XX
XX 13-JUL-2000.
XX
XX 07-JAN-2000; 2000MO-US00396.
XX
XX 07-JAN-1999; 99US-0226533.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Gross JA, Xu W, Madden K, Yee DP;
XX
XX WPI; 2000-452538/39.
XX
XX N-PSDB; AAA58559.
XX
XX Inhibiting znf4 activity in a mammal, to treat autoimmune diseases,
XX renal disease, graft versus host disease, and inflammation, comprises
XX administering a BR43x2, TACI or BCMA extracellular domain polypeptide -
XX
XX Disclosure; Page 152; 175pp; English.
XX
XX The present sequence represents a human BCMA protein, a B cell protein
XX related to transmembrane activator and CAML-interactor (TACI) receptor.
XX TACI is a tumour necrosis factor (TNF) receptor. The extracellular
XX domain of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell
XX protein) receptor contain a cysteine rich domain, and are used for
XX inhibiting znf4 activity. A znf4 is a TNF ligand, and may also be used
XX for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated
XX with activating BR43x2, TACI or BCMA receptor-ligand engagement associated
XX with activated or resting B lymphocytes, effector T-cells, or with
XX autoimmune disease selected from systemic lupus erythematosus, myasthenia
XX gravis, multiple sclerosis and rheumatoid arthritis. The znf4 activity
XX and BR43x2, TACI or BCMA receptor-ligand engagement is associated with
XX asthma, bronchitis, emphysema, end stage renal failure,
XX glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal
XX neoplasms, multiple myelomas, lymphomas, light chain neuropathy,
XX amyloidosis, moderating immune response, immunosuppression, graft
XX rejection, graft versus host disease, inflammation, insulin dependent
XX diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
XX septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,
XX agonists or antagonists can be used to treat hypertension, renal artery
XX stenosis, or occlusion, and cholesterol or renal emboli.
XX
XX Sequence 184 AA;
SQ
Query Match 100.0%; Score 201; DB 21; Length 184;
Best Local Similarity 100.0%; Pred. No. 4.1e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CSQNEYPDSLHACIPQRCSSNTPTLCORYC 34
DB 8 CSQNEYPDSLHACIPQRCSSNTPTLCORYC 41
RESULT 7
AAE09241
ID AAE09241 standard; Protein; 184 AA.
XX
XX AAE09241;
XX
XX 19-NOV-2001 (first entry)
XX
XX Human BCMA protein.
XX
XX Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
XX TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
XX autoimmune disease; rheumatoid arthritis; multiple sclerosis;
XX psoriasis.
XX
XX Homo sapiens.
OS

XX WO200160397-A1.
 XX 23-AUG-2001.
 XX 28-NOV-2000; 2000WO-US232378.
 XX 16-FEB-2000; 2000US-0182938.
 XX 22-AUG-2000; 2000US-0226986.
 XX (GETH) GENENTECH INC.
 XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
 XX Yan M;
 XX WPI; 2001-541628/60.
 XX N-PSDB; AAD15902.
 XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
 XX activity, for treating autoimmune disorders and cancer, comprises
 XX exposing the cells to TALL-1 or APRIL polypeptide agonists or
 XX antagonists -
 XX Example 2; Fig 2; 160pp; English.
 XX The invention relates to methods of using one or more agonists or
 XX antagonists to modulate the activity of the members of TNF (tumour
 XX necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
 XX e.g. TACI or BCMA. The method is useful for treating pathological
 XX conditions or diseases associated with increased TALL-1 and APRIL
 XX expression or activity. TALL-1 and APRIL antagonists are used to
 XX block the interaction between APRIL and TALL-1 with TACI or BCMA.
 XX They are useful for treating a mammal suffering from cancer such
 XX as leukaemia, lymphoma, myeloma, cancers of lung and colon and
 XX autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
 XX psoriasis and lupus erythematosus. The present sequence is human
 XX BCMA protein.
 XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 22; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4.1e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSONEYFDSLHACIPQLRCSNSTPPLTCQRYC 34
 |||||
 Db 8 CSONEYFDSLHACIPQLRCSNSTPPLTCQRYC 41

RESULT 8
 AAE00506
 ID AAE00506 standard; Protein; 184 AA.

XX AC AAE00506;
 XX 31-JUL-2001 (first entry)
 XX Human B cell maturation protein (BCMA).
 XX Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
 XX gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
 XX carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
 XX systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
 XX B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
 XX organ transplantation; HIV; human immunodeficiency virus; TNF;
 XX tumour necrosis factor; BCMA; B cell maturation protein.
 XX Homo sapiens.
 XX MO200124811-A1.
 XX 12-APR-2001.

PF 05-OCT-2000; 2000WO-US27579.
 XX 06-OCT-1999; 99US-0157933.
 PR 11-FEB-2000; 2000US-0181807.
 PR 30-JUN-2000; 2000US-0215888.
 XX (BIOJ) BIOGEN INC.
 XX (AFOT-) APOTEC R & D SA.
 XX Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
 XX WPI; 2001-266242/27.
 XX N-PSDB; AAD03844.

XX Treating a mammal for a condition associated with undesired cell
 XX proliferation such as cancer or carcinoma, comprises administering a
 XX composition comprising A Proliferation Inducing Ligand Receptor
 XX (APRIL-R) antagonist -
 XX Claim 3; Fig 3A; 85pp; English.

XX The invention relates to a method of treating a mammal for a condition
 XX associated with undesired cell proliferation such as cancer or
 XX carcinoma. The method involves administering a composition comprising
 XX A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as
 XX B cell maturation protein (BCM or BCMA) antagonist that antagonises the
 XX interaction between APRIL and its cognate receptor(s). This method is
 XX useful for treating undesired cell proliferation such as cancer or
 XX carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
 XX prostate carcinoma, and other carcinomas whose proliferation is modulated
 XX by APRIL. It is also useful for treating autoimmune diseases (Grave's
 XX disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
 XX diseases, renal disorders, B-cell lympho-proliferative disorders,
 XX immunosuppressive diseases, organ transplantation, inflammation and
 XX human immunodeficiency virus (HIV), and for treating, suppressing or
 XX altering an immune response involving a signalling pathway between
 XX APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
 XX The present sequence is human APRIL-R also referred as BCMA or
 XX BCM protein.

XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 22; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4.1e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPQLRCSNSTPPLTCQRYC 34
 |||||
 Db 8 CSONEYFDSLHACIPQLRCSNSTPPLTCQRYC 41

RESULT 9
 AAB60698
 ID AAB60698 standard; Protein; 184 AA.

XX AC AAB60698;
 XX 22-MAY-2001 (first entry)
 XX Human BAFF receptor (BAFF-R).
 XX Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
 XX immune-related disorder; B-cell growth inhibitor; BCMA; inhibitor;
 XX B-cell maturation inhibitor; immunoglobulin production disorder; hypertension;
 XX autoimmune disorder; B-cell lymphoproliferative disorder; HIV infection;
 XX renal disorder; immunosuppressive disorder; HIV infection;
 XX organ transplantation; antiinflammatory; systemic lupus erythematosus;
 XX autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
 XX B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
 XX lymphoma; gene therapy; cancer; tumour.
 XX Homo sapiens.

PN WO200112812-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 16-AUG-2000; 2000WO-US22507.
 XX
 PR 17-AUG-1999; 99US-0149378.
 PR 11-FEB-2000; 2000US-0181684.
 PR 18-FEB-2000; 2000US-0183536.
 XX
 PA (BIOI) BIOGEN INC.
 PA (APOT-) APOTEC R & D SA.
 XX
 PI Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P,
 PI Thompson J;
 XX
 DR WPI; 2001-202866/20.
 DR N-PSDB; AAF59998.
 XX
 PT Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
 PT lympho-proliferative disorder by administering BAF-R-receptor
 PT polypeptide, chimeric molecule comprising receptor or anti-BAF-R
 PT antibody homolog
 XX
 XX Claim 20; Fig 1; 59pp; English.
 XX
 CC The invention relates to the use of a BAF-R receptor (BAF-R, also known
 CC as BCMA) protein, or a BAF-R fusion protein as an agent for the
 CC treatment of a variety of immune-related disorders. BAF-R is a member of
 CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
 CC agent, and also plays a role in the development of hypertension and
 CC related disorders. BAF-R, fusion proteins containing it, and BAF-R-
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,
 CC and in the treatment of autoimmune disorders. B-cell lymphoproliferative
 CC disorders, hypertension and renal disorders. The BAF-R proteins may also
 CC be used in the treatment of immunosuppressive disorders and HIV
 CC infection, and in patients undergoing organ transplantation. The BAF-R
 CC proteins or BAF-R specific antibodies may be used for treating,
 CC suppressing or altering an immune response involving a signalling pathway
 CC between BAF-R and BAF-R, thereby inhibiting inflammation. Since BAF-R
 CC inhibits B-cell growth and maturation it is useful for treating diseases
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 CC human BAF-R may be used in gene therapy to treat tumours, lymphomas,
 CC autoimmune disorders and inherited B-cell-associated disorders. The
 CC present sequence represents human BAF-R.
 XX
 SQ Sequence 184 AA;
 Query Match 100.0%; Score 201; DB 22; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4, 1e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSQNEYFDSLHACIPQRLCSSTNPPLTCORYC 34
 DB 8 CSQNEYFDSLHACIPQRLCSSTNPPLTCORYC 41
 XX
 RESULT 10
 ID AAY71979 standard; Protein; 184 AA.
 XX
 AC AAY71979;
 XX
 DT 28-MAR-2001 (first entry)
 XX
 DE Human B cell maturation factor (BCMA) protein.
 XX
 KW Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
 KW Tumour necrosis factor and Apol-related leucocyte expressed ligand 1;
 KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;

KM systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
 KM thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
 KM haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;
 KM post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
 KM B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
 XX
 OS Homo sapiens.
 XX
 FH Key location/Qualifiers
 FT Domain 1..62 /label= Extracellular_domain
 FT
 XX WO200068378-A1.
 XX
 PD 16-NOV-2000.
 XX
 PF 05-MAY-2000; 2000WO-US12266.
 XX
 PR 06-MAY-1999; 99US-0132892.
 PR 01-MAY-2000; 2000US-0201012.
 XX
 PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.
 XX
 PI Shu HS;
 XX
 DR WPI; 2001-016094/02.
 DR N-PSDB; AAD02125.
 XX
 PT Isolated TALL-1 protein is used to identify compounds that regulate B
 PT lymphocyte proliferation, used to treat B lymphocyte associated
 PT autoimmune disorders -
 XX
 XX Claim 37; Page 104-105; 112pp; English.
 XX
 CC The present invention relates to Tumour necrosis factor (TNF) and
 CC Apol-related leucocyte expressed ligand 1 (TALL-1) nucleic acid
 CC molecules, proteins (including homologues), and their antibodies. The
 CC invention in particular relates to methods for regulating the
 CC interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell
 CC maturation factor) to regulate monocyte, macrophage and B lymphocyte
 CC mediated immune responses. TALL-1 protein is useful for identifying
 CC compounds that regulate B lymphocyte proliferation. It is also useful for
 CC treating B lymphocyte associated autoimmune disorders like rheumatoid
 CC arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes
 CC mellitus, multiple sclerosis, myasthenia gravis, Grave's disease,
 CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura,
 CC Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever,
 CC post-streptococcal glomerulonephritis, or polyarteritis nodosa.
 CC The TALL-1 protein and its corresponding nucleic acid sequence are also
 CC useful in diagnostic assays.
 CC
 CC The present sequence is a human B cell maturation factor (BCMA)
 CC protein. It is the receptor for TALL-1 protein. BCMA gene is
 CC located on chromosome 16, in human tissues. BCMA is expressed by
 CC spleen and lymph nodes but not by brain, muscle, heart, lung, kidney,
 CC pancreas, testis and placenta. BCMA mRNA is absent in the pro-B
 CC lymphocyte stage but its expression increases with B lymphocyte
 CC maturation.
 XX
 SQ Sequence 184 AA;
 Query Match 100.0%; Score 201; DB 22; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4, 1e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSQNEYFDSLHACIPQRLCSSTNPPLTCORYC 34
 DB 8 CSQNEYFDSLHACIPQRLCSSTNPPLTCORYC 41
 XX
 RESULT 11
 ID ABB81487 standard; Protein; 184 AA.
 XX

AC ABB81487;
 DT 02-SEP-2002 (first entry)
 XX Human BCMA receptor related protein SEQ ID NO:7.
 DE
 XX Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;
 KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
 KW neuroprotective; antirheumatic; antiarthritic; antiaschmatic;
 KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
 KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
 KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
 KW rheumatoid arthritis; bronchitis; emphysema; renal disease; nephritis;
 KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; amyloidosis;
 KW pyelonephritis; renal neoplasm; multiple myeloma; large vessel disease;
 KW light chain neuropathy; hypertension; large vessel disease;
 KW graft-versus host disease; graft rejection; Crohn's disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200238766-A2.
 PN
 XX
 XX 16-MAY-2002.
 PD
 XX
 XX 05-NOV-2001; 2001WO-US47018.
 PF
 XX
 XX 07-NOV-2000; 2000US-246449P.
 PR
 XX 20-DEC-2000; 2000US-257131P.
 PR
 XX 28-JUN-2001; 2001US-201715P.
 PR
 XX 29-AUG-2001; 2001US-315565P.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX
 XX Gross JA, Xu W, Henne RM, Grant FU;
 PI
 XX WPI; 2002-508212/54.
 DR
 XX
 XX Novel isolated human tumor necrosis factor receptor polypeptide, termed
 PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end
 PT stage renal failure or renal disease and lymphoma
 XX
 XX Disclosure; Page 135-136; 154pp; English.
 PS
 XX The present invention describes a human tumour necrosis factor receptor
 CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,
 CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
 CC antirheumatic, antiarthritic, antiaschmatic, nephrotropic and hypotensive
 CC activities, and can be used in gene therapy. (I) can be used for
 CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
 CC (e.g. ZTNF4), for treating disorders and diseases associated with B
 CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
 CC inhibiting the proliferation of tumour cells. (I) is useful for treating
 CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
 CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
 CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
 CC leukaemia, nephritis, and pyelonephritis, and for treating renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
 CC amyloidosis, hypertension, large vessel diseases, graft-versus host
 CC disease, graft rejection and Crohn's disease. (I) is useful for
 CC modulating the immune system, for regulating B cell responses and
 CC development, for modulating development of other cells, antibody
 CC production and cytokine production, and for modulating T and B cell
 CC communication. The present sequence represents a protein which is
 CC given in the exemplification of the present invention.
 XX
 SQ Sequence 184 AA;
 Query Match 100.0%; Score 201; DB 23; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4.1e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CSQNEYFDSLHACIPQLRCSSTNPTPLTCQRYC 34

Db 8 CSQNEYFDSLHACIPQLRCSSTNPTPLTCQRYC 41
 RESULT 12
 AAE15488
 ID AAE15488 standard; Protein; 283 AA.
 XX
 AC AAE15488;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 XX Human BCMA-immunoglobulin Fc region fusion protein.
 DE
 XX Human; transmembrane activator and intracellular CAML interactor; TAC1;
 KW cytotatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis; fusion protein.
 XX
 OS Homo sapiens.
 XX
 XX WO200187979-A2.
 PN
 XX
 PD 22-NOV-2001.
 XX
 XX 14-MAY-2001; 2001WO-US15567.
 PF
 XX
 XX 12-MAY-2000; 2000US-204039P.
 PR
 XX 27-JUN-2000; 2000US-214531P.
 PR
 XX 14-MAY-2001; 2001US-0214591.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX
 XX Theill LE, Yu G;
 PI
 XX WPI; 2002-066686/09.
 DR
 XX
 XX Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand
 XX
 XX Disclosure; Fig 10B; 94pp; English.
 PS
 XX The invention relates to a method for inhibiting TAC1 (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand) having the consensus region of TAC1, BCMA, or the TAC1/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA, and TAC1
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA protein-immunoglobulin Fc region fusion protein.
 XX
 SQ Sequence 283 AA;
 Query Match 100.0%; Score 201; DB 23; Length 283;
 Best Local Similarity 100.0%; Pred. No. 6.3e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
 DB 5 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 38

RESULT 13

AAE0507
 ID AAE0507 standard; Protein; 302 AA.

AC AAE0507;

DT 31-JUL-2001 (first entry)

XX Human BCMA-Immunoglobulin G Fc region fusion construct.

XX Human: A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
 KM gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
 KM carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
 KM systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
 KM B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
 KM organ transplantation; HIV; human immunodeficiency virus; TNF; murine;
 KM tumour necrosis factor; B cell maturation protein; BCM; fusion protein;
 KM immunoglobulin G; IgG; Fc region.

OS Chimeric - Homo sapiens.

XX Chimeric - Mus sp.

XX Key Location/Qualifiers

FT 1..22 /label= Signal peptide

FT /note= "Derived from murine Ig kappa sequence"

FT /label= Mature_human_BCMA_IgG_Fc_fusion_protein

FT /note= "Derived from human BCMA protein"

FT /note= "Derived from human IgG Fc region"

FT /label= Cysteine_rich_domain

FT /note= "Derived from human BCMA"

PN WO200124811-A1.

PD 12-APR-2001.

XX 05-OCT-2000; 2000WO-US27579.

XX 06-OCT-1999; 99US-0157933.

PR 11-FEB-2000; 2000US-0181807.

PR 30-JUN-2000; 2000US-0215688.

XX (BIOI) BIOGEN INC.

PA (APOT-) APOTEC R & D SA.

XX Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;

XX WPI, 2001-266242/27.

DR N-PSDB; AAD03847.

XX Treating a mammal for a condition associated with undesired cell

PT proliferation such as cancer or carcinoma, comprising administering a

PT composition comprising A Proliferation Inducing Ligand Receptor

PT (APRIL-R) antagonist

XX Example 1; Fig 3B; 85pp; English.

XX The invention relates to a method of treating a mammal for a condition

XX associated with undesired cell proliferation such as cancer or

XX carcinoma. The method involves administering a composition comprising

XX A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as

XX B cell maturation protein (BCM or BCMA) antagonist that antagonises the

XX interaction between APRIL and its cognate receptor(s). This method is

CC useful for treating undesired cell proliferation such as cancer or
 CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
 CC prostate carcinoma, and other carcinomas whose proliferation is modulated
 CC by APRIL. It is also useful for treating autoimmune diseases (Grave's
 CC disease, systemic lupus erythematosus-SLE), hypertension, cardiovascular
 CC diseases, renal disorders, B-cell lympho-proliferative disorders,
 CC immunosuppressive diseases, organ transplantation, inflammation and
 CC human immunodeficiency virus (HIV), and for treating, suppressing or
 CC altering an immune response involving a signalling pathway between
 CC APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
 CC The present sequence is a fusion construct containing human APRIL-R
 CC also referred as BCMA or BCM protein, Fc region of human immunoglobulin
 CC G (IgG) and a signal sequence from murine Ig kappa cDNA.

XX Sequence 302 AA;

Query Match 100.0%; Score 201; DB 22; Length 302;
 Best local similarity 100.0%; Pred. No. 6, 8e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
 DB 31 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 64

RESULT 14

AAE0699
 ID AAE0699 standard; Protein; 302 AA.

AC AAE0699;

DT 22-MAY-2001 (first entry)

XX Mouse IgG signal/human BAFF-R/human IgG Fc fusion protein, BAFF-R-Fc.

XX Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
 KM immune-related disorder; B-cell growth inhibitor;
 KM B-cell maturation inhibitor; immunoglobulin production inhibitor;
 KM autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
 KM renal disorder; immunosuppressive disorder; HIV infection;
 KM organ transplantation; antiinflammatory; systemic lupus erythematosus;
 KM autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
 KM B-cell carcinoma; leukemia; rapidly progressive glomerulonephritis;
 KM lymphoma; gene therapy; cancer; tumour; IgG Fc; fusion construct.

OS Chimeric - Homo sapiens.

XX Chimeric - Mus sp.

XX WO200112812-A2.

XX 22-FEB-2001.

XX 16-AUG-2000; 2000WO-US22507.

XX 17-AUG-1999; 99US-0149378.

PR 11-FEB-2000; 2000US-0181684.

PR 18-FEB-2000; 2000US-0183536.

XX (BIOI) BIOGEN INC.

PA (APOT-) APOTEC R & D SA.

XX Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;

XX Thompson J;

XX WPI, 2001-202866/20.

DR N-PSDB; AAF59999.

XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell

XX lympho-proliferative disorder by administering BAFF-receptor

XX polypeptide, chimeric molecule comprising receptor or anti-BAFF-R

XX antibody homolog

XX Example 4; Fig 2; 59pp; English.

XX The invention relates to the use of a BAFF receptor (BAFF-R, also known
 CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the
 CC treatment of a variety of immune-related disorders. BAFF-R is a member of
 CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
 CC agent, and also plays a role in the development of hypertension and
 CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,
 CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
 CC disorders, hypertension and renal disorders. The BAFF-R proteins may also
 CC be used in the treatment of immunosuppressive disorders and HIV
 CC infection, and in patients undergoing organ transplantation. The BAFF-R
 CC proteins or BAFF-R specific antibodies may be used for treating,
 CC suppressing or altering an immune response involving a signalling pathway
 CC between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
 CC inhibits B-cell growth and maturation it is useful for treating diseases
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
 CC autoimmune disorders and inherited B-cell-associated disorders. The
 CC present sequence represents the BAFF-R fusion protein BAFF-R-Fc,
 CC comprising a mouse IgG-kappa signal sequence, residues 1-153
 CC of human BAFF-R and a human IgG Fc sequence.

XX Sequence 302 AA;

Query Match 100.0%; Score 201; DB 22; Length 302;
 Best Local Similarity 100.0%; Pred. No. 6.8e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
 DB 31 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 64

RESULT 15

AAB60700 AAB60700 standard; Protein; 157 AA.

XX AC AAB60700;

XX DT 22-MAY-2001 (first entry)

XX DE Human BAFF receptor (BAFF-R) sequence encoded by A plasmid pJST535.

XX KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
 KW immune-related disorder; B-cell growth inhibitor; BCMA; inhibitor;
 KW B-cell maturation inhibitor; immunoglobulin production inhibitor;
 KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
 KW renal disorder; immunosuppressive disorder; HIV infection;
 KW organ transplantation; antiinflammatory; systemic lupus erythematosus;
 KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
 KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
 KW lymphoma; gene therapy; cancer; tumour; plasmid pJST535.

XX OS Homo sapiens.

XX PN WO200112812-A2.

XX PD 22-FEB-2001.

XX PF 16-AUG-2000; 2000WO-US22507.

XX PR 17-AUG-1999; 99US-0149378.

XX PR 11-FEB-2000; 2000US-0181684.

XX PR 18-FEB-2000; 2000US-0183536.

XX PA (BIOJ) BIOGEN INC.

XX PA (APOT-) APOTEC R & D SA.

XX MacKay F, Browning J, Ambrose C, Tschopp J, Schneider P;

PI Thompson J;
 XX WPI; 2001-202866/20.
 DR N-PSDB; AAF60000.

XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
 PT lympho-proliferative disorder by administering BAFF-receptor
 PT polypeptide, chimeric molecule comprising receptor or anti-BAFF-R
 PT antibody homolog -

XX Example 1; Fig 3; 59pp; English.

XX The invention relates to the use of a BAFF receptor (BAFF-R, also known
 CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the
 CC treatment of a variety of immune-related disorders. BAFF-R is a member of
 CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
 CC agent, and also plays a role in the development of hypertension and
 CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,
 CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
 CC disorders, hypertension and renal disorders. The BAFF-R proteins may also
 CC be used in the treatment of immunosuppressive disorders and HIV
 CC infection, and in patients undergoing organ transplantation. The BAFF-R
 CC proteins or BAFF-R specific antibodies may be used for treating,
 CC suppressing or altering an immune response involving a signalling pathway
 CC between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
 CC inhibits B-cell growth and maturation it is useful for treating diseases
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
 CC autoimmune disorders and inherited B-cell-associated disorders. The
 CC present sequence represents a human BAFF-R protein sequence as encoded
 CC by plasmid pJST535. However, this BAFF-R protein sequence is 27 amino
 CC acids shorter than that given in AAB60698.

XX SQ Sequence 157 AA;

Query Match 79.4%; Score 159.5; DB 22; Length 157;
 Best Local Similarity 90.6%; Pred. No. 7.4e-13;
 Matches 29; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 3 QNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34

DB 7 QNEYFDSLHACIPQCLR---NTPPLTCQRYC 35

Search completed: January 7, 2003, 09:37:26
 Job time : 13:1855 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:35:04 ; Search time 4.85714 Seconds
(without alignments)
672.941 Million cell updates/sec

Title: US-09-855-158-7

Perfect score: 201
Sequence: 1 CSQNEYPDSLHACIPQLRCSSNTPLTCQRYC 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73.*

1: Pirl.*

2: Pirl.*

3: Pirl.*

4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	201	100.0	184	2 S43486	B-cell maturation factor - human
2	67.5	33.6	1548	2 S34583	serine proteinase
3	64.5	32.1	5376	2 T42215	zonadhesin - mouse
4	61	30.3	1101	2 T16840	hypothetical prote
5	59	29.4	758	2 T15577	hypothetical prote
6	58	28.9	1299	2 T43251	furin (EC 3.4.21.7
7	57.5	28.6	63	2 S07127	chymotrypsin/elast
8	57.5	28.6	1680	2 A43434	furin (EC 3.4.21.7
9	57	28.4	1717	1 A45558	epidermal growth f
10	56	27.9	2476	2 T34022	zonadhesin - pig
11	55.5	27.6	989	2 T01519	hypothetical prote
12	55	27.4	330	2 T25169	hypothetical prote
13	55	27.4	1513	2 T23681	hypothetical prote
14	54.5	27.1	2155	2 T30197	alpha tectorin - m
15	54	26.9	1980	2 S4307	myosin heavy chain
16	54	26.9	2022	2 A32256	myosin-Ikb (slimila
17	53.5	26.6	758	2 S46625	finger protein YJL
18	53	26.4	1574	2 T13954	MSGF6 protein - ra
19	53	26.4	2824	2 T22759	hypothetical prote
20	52.5	26.1	118	2 S61051	hypothetical prote
21	52	25.9	255	2 A84544	hypothetical prote
22	52	25.9	294	2 T23682	hypothetical prote
23	52	25.9	547	2 T34318	hypothetical prote
24	52	25.9	1474	2 D88550	protein ZC84.6 lim
25	52	25.9	2844	2 S28291	hypothetical prote
26	51.5	25.6	63	2 S57816	antimicrobial pept
27	51.5	25.6	282	2 S35754	siab-1B protein -
28	51.5	25.6	282	2 I48763	siab-1A protein -
29	51.5	25.6	497	2 T27827	hypothetical prote

30	51.5	25.6	915	2 T21773	hypothetical prote
31	51.5	25.6	927	2 T21772	hypothetical prote
32	51.5	25.6	999	2 T19275	hypothetical prote
33	51.5	25.6	2120	2 T30243	alpha tectorin - c
34	51	25.4	641	2 E96612	probable transcrip
35	51	25.4	653	2 G96675	hypothetical prote
36	51	25.4	746	2 G84605	hypothetical prote
37	50.5	25.1	610	1 I46001	C4b-binding protei
38	50	24.9	63	2 S08572	chymotrypsin/elast
39	50	24.9	74	2 S10332	ubiquitin / riboso
40	50	24.9	342	2 T30370	hypothetical prote
41	50	24.9	376	2 C81272	probable aminotran
42	50	24.9	455	1 G8HUT1	tumor necrosis fac
43	50	24.9	561	2 T27318	hypothetical prote
44	50	24.9	626	2 T27319	hypothetical prote
45	50	24.9	922	2 T23573	hypothetical prote

ALIGNMENTS

RESULT 1

S43486
B-cell maturation factor - human
N;Alternate names: BCM protein; BCMA protein; BEL protein
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence revision 27-Jan-1995 #text_change 21-Jul-2000
C;Accession: S43486; S31208; S36661
R;Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
Nucleic Acids Res. 22, 1147-1154, 1994
A;Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bidire
A;Reference number: S43486; MUID:94218235; PMID:1365126
A;Accession: S43486
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-184 <LA2>
A;Cross-references: EMBL:Z29574; NID:G471244; PIDN:CAA82690.1; PID:G471245
R;Laabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis,
EMBO J. 11, 3897-3904, 1992
A;Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;1
A;Reference number: S31208; MUID:93010984; PMID:1396583
A;Accession: S31208
A;Molecule type: mRNA
A;Residues: 1-184 <LA2>
A;Cross-references: EMBL:Z14954; NID:G29407; PIDN:CAA78679.1; PID:G29408
A;Accession: S36661
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 4-184 <LA3>
A;Cross-references: EMBL:Z14955
C;Genetics:
A;Gene: GDB:BCMA
A;Cross-references: GDB:135977; OMIM:109545
A;Map position: 16p13.1-16p13.1
A;Introns: 44/1; 93/1
C;Superfamily: human B-cell maturation factor

Query Match 100.0%; Score 201; DB 2; Length 184;

Best Local Similarity 100.0%; Pred No. 2.7e-17; Mismatches 0; Indels 0; Gaps 0;

Matches 34; Conservative 0;

QY 1 CSQNEYPDSLHACIPQLRCSSNTPLTCQRYC 34

Db 8 CSQNEYPDSLHACIPQLRCSSNTPLTCQRYC 41

RESULT 2

S34583

serine proteinase (EC 3.4.21.-) PC6B - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999

C;Accession: S34583

R;Nakagawa, T.; Murakami, K.; Nakayama, K.

FEBS Lett. 327, 165-171, 1993
A:Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a
A:Reference number: S34583; MUID:93327934; PMID:8355106
A:Accession: S34583
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1548 <NAK>
A:Cross-references: GB:D17583; NID:9407344; PIDN:BAA04507.1; PID:01005033; PID:9440374
C:Keywords: hydrolase; serine proteinase

Query Match 33.6%; Score 67.5; DB 2; Length 1548;
Best Local Similarity 37.8%; Pred. No. 2.3;
Matches 14; Conservative 4; Mismatches 14; Indels 5; Gaps 1;

Qy 1 CSONEYFDSLHACIPCOLRCSNTPP-----LTCOR 32
Db 1152 CAVEYWDGSHRCQPCCHKKSCSGSPSEDQCTCPR 1188

RESULT 3
T42215
zonadhesin - mouse
N:Alternate names: sperm-specific membrane protein
C:Species: Mus musculus (house mouse)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T42215
R:Qao, Z.; Garbers, D.L. 1998
J. Biol. Chem. 273, 3415-3421, 1998
A:Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane pro
A:Reference number: 222080; MUID:98123114; PMID:9452463
A:Accession: T42215
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-5376 <GAO>
A:Cross-references: EMBL:U97068; NID:93327420; PID:93327421; PIDN:AAC26680.1
C:Genetics:
A:Gene: Zan
A:Map position: 5
A:Function:
A:Description: functions in multiple cell adhesion processes
A:Note: found exclusively on the apical region of the sperm head
C:Keywords: cell adhesion

Query Match 32.1%; Score 64.5; DB 2; Length 5376;
Best Local Similarity 35.1%; Pred. No. 16;
Matches 13; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

Qy 1 CSONEYFDSLHACIPCOLRCSNTPP---PLTCOR 34
Db 3300 CPTNSQFTDCLPSCVPSCSNRCVTSVPSSCREGC 3336

RESULT 4
T16840
hypothetical protein T10E10.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16840
R:Geisel, C.
submitted to the EMBL Data Library, October 1995
A:Description: The sequence of C. elegans cosmid T10E10.
A:Reference number: Z18588
A:Accession: T16840
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1101 <GEI>
A:Cross-references: EMBL:U39644; NID:91049339; PID:91049343; PIDN:AAA80360.1; CESP:T10E1
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:T10E10.4
A:Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7
Query Match 30.3%; Score 61; DB 2; Length 1101;

Best Local Similarity 37.5%; Pred. No. 11;
Matches 12; Conservative 7; Mismatches 11; Indels 2; Gaps 1;

Qy 1 CSONEYFDSLHACIPCOLR--CSNTPPLTC 30
Db 351 CSQSTVFNSDLVNVCVPLAIONSCDSSTOQPCV 382

RESULT 5
T15577
hypothetical protein C23G10.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
C:Accession: T15577
R:Latreille, P.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid C23G10.
A:Reference number: Z18372
A:Accession: T15577
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-758 <LAT>
A:Cross-references: EMBL:U39851; NID:91055062; PID:91055068; PIDN:AAA81069.1; CESP:C23G
A:Gene: CESP:C23G10.8
A:Introns: 47/3; 237/3; 293/2; 405/3; 487/1; 577/3; 694/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C23G10.8

Query Match 29.4%; Score 59; DB 2; Length 758;
Best Local Similarity 42.9%; Pred. No. 14;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 8 DSLHACIPCOLRCSNTPPL 28
Db 260 BSVFHLVPAERICSGADGPPL 280

RESULT 6
T43251
furin (RC 3.4.21.75) - fall armyworm
N:Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; seri
C:Species: Spodoptera frugiperda (fall armyworm)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C:Accession: T43251
R:Cieplik, M.; Klenk, H.
submitted to the EMBL Data Library, January 1996
A:Description: Cloning and functional characterization of FURIN from Spodoptera frugipe
A:Reference number: Z22368
A:Accession: T43251
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1299 <CIE>
A:Cross-references: EMBL:Z6888; NID:9167859; PID:9219690; PIDN:CAA93116.1
A:Experimental source: clone Sfurin 6; ovary
A:Function:
A:Description: responsible for the endoproteolytic processing of proproteins with speci
C:Keywords: hydrolase; serine proteinase

Query Match 28.9%; Score 58; DB 2; Length 1299;
Best Local Similarity 37.1%; Pred. No. 28;
Matches 13; Conservative 5; Mismatches 9; Indels 8; Gaps 2;

Qy 1 CSONEYFDSLHACIPCOLRCS-----SNTPPLTC 30
Db 1150 CSRPLRIDRLNQCVCPC---CSRGVNSTPTPTC 1181

RESULT 7
S07127
chymotrypsin/elastase inhibitor - common roundworm
C:Species: Ascaris lumbricoides (common roundworm)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S07127

Rabin, D.R.; Peanasky, R.J.; Goos, S.M.
Arch. Biochem. Biophys. 232, 143-161, 1984
A:Title: The inhibitors of chymotrypsin/elastase from Ascaris lumbricoides: the prima
A:Reference number: S07127; PMID:84255715; PMID:6564898
A:Accession: S07127
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-63 <BAB>
C:Superfamily: roundworm trypsin inhibitor

Query Match 28.6%; Score 57.5; DB 2; Length 63;
Best Local Similarity 37.1%; Pred. No. 2.5;
Matches 13; Conservative 5; Mismatches 10; Indels 7; Gaps 3;

QY 1 CSQNEFYDLSLLHACIPQLRCS--SSNTP-PLTQCR 32
DB 5 CGPNEVWTE---CTGCEMKGPDENTPCPLMCRR 35

RESULT 8
A43434
furin (EC 3.4.21.75) 2 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Mar-2000
C:Accession: A43434
R:Roederoek, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, E.
J. Biol. Chem. 267, 17208-17215, 1992
A:Title: Cloning and functional expression of Dfurin2, a subtilisin-like proprotein proc
A:Reference number: A43434; PMID:92381036; PMID:1512259
A:Accession: A43434
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1680 <ROB>
A:Cross-references: GB:M94375; NID:G157461; PID:G157462
A:Note: sequence extracted from NCBI backbone (NCBIN:111933, NCBI:P:111934)
C:Genetics:
A:Gene: FlyBase:Fur2
A:Cross-references: FlyBase:FBGN0004598
C:Superfamily: subtilisin homology
C:Keywords: hydrolase; serine proteinase; transmembrane protein
F:409-652/Domain: subtilisin homology <SBT>
F:418,457,638/Active site: Asp, His, Ser #status predicted

Query Match 28.6%; Score 57.5; DB 2; Length 1680;
Best Local Similarity 34.3%; Pred. No. 41;
Matches 12; Conservative 5; Mismatches 17; Indels 1; Gaps 1;

QY 1 CSQNEFYDLSLLHACIPQLRCS--NTPPTTCQRYC 34
DB 1199 CSESEFYQVQGRPCFCHASCGSGFADTCTSC 1233

RESULT 9
A45558
epidermal growth factor receptor homolog precursor - fluke (Schistosoma mansoni)
N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
C:Species: Schistosoma mansoni
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A45558; S27836
R:Shoemaker, C.B.; Ramachandran, H.; Landa, A.; dos Reis, M.G.; Stein, L.D.
Mol. Biochem. Parasitol. 53, 17-32, 1992
A:Title: Alternative splicing of the Schistosoma mansoni gene encoding a homologue of ep
A:Reference number: A45558; PMID:92365727; PMID:1501637
A:Accession: A45558
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1717 <SHO>
A:Cross-references: EMBL:M86396; NID:G160957; PIDN:AAA29866.1; PID:G160958
A:Note: sequence extracted from NCBI backbone (NCBI:P:111129)
C:Genetics:
A:Gene: SER

C:Superfamily: fluke epidermal growth factor receptor homolog 1; protein kinase homology
C:Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; phosphoprotein

F:1-19/Domain: signal sequence #status predicted <SIG>
F:2-117/Product: epidermal growth factor receptor homolog 1 #status predicted <MAT>
F:1018-1323/Domain: protein kinase homology <KIN>
F:1026-1034/Region: protein kinase ATP-binding motif

Query Match 28.4%; Score 57; DB 1; Length 1717;
Best Local Similarity 40.9%; Pred. No. 48;
Matches 9; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSQNEFYDLSLLHACIPQLRCS 22
DB 646 CPRNTYIDPQTRHCLPCNCS 667

RESULT 10
T34022
zonadhesin - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C:Accession: T34022
R:Hardy, D.M.; Garbers, D.L.
J. Biol. Chem. 270, 26025-26028, 1995
A:Title: A sperm membrane protein that binds in a species-specific manner to the egg ext
A:Reference number: Z21464; PMID:96064658; PMID:7592795
A:Accession: T34022
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2476 <HAR>
A:Cross-references: EMBL:U40024; NID:G1066465; PID:G1066466; PIDN:AAC48486.1
A:Experimental source: strain Meishan; testis
C:Genetics:
A:Gene: Zan
C:Function:
A:Description: may be involved in sperm adhesion to the zona pellucida

Query Match 27.9%; Score 56; DB 2; Length 2476;
Best Local Similarity 31.6%; Pred. No. 86;
Matches 12; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

QY 1 CSQNEFYDLSLLHACIP--CQ--LRCSNTPPLTTCQRYC 34
DB 1851 CSAHSVTVTSCLPSCQDPQEGCTGAGAPSTCEGC 1888

RESULT 11
T01519
hypothetical protein T10M13.17.1 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 24-Mar-1999
C:Accession: T01519
R:Johnson, A.F.; de la Bastide, M.; Lodhi, M.; Hoffman, J.; Hasegawa, A.; Gnoj, L.; Gott
Martienssen, R.; McCombie, W.
submitted to the EMBL Data Library, May 1997 .
A:Description: The sequence of the Arabidopsis thaliana T10M13 BAC.

A:Reference number: Z14346
A:Accession: T01519
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-989 <JOH>
A:Cross-references: EMBL:AF001308; NID:G2104523; PID:G3912931
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4S
A:Introns: 31/3
A:Note: T10M13.17.1

Query Match 27.6%; Score 55.5; DB 2; Length 989;
Best Local Similarity 41.9%; Pred. No. 45;
Matches 13; Conservative 3; Mismatches 10; Indels 5; Gaps 2;

QY 1 CSQNEFYDLSLLHACIP--LRCSNTPPP 27
DB 540 CARN-IDRLFLYHCSPCNFTLDRCLVNLPPP 569

```
RESULT 12
T25169
hypothetical protein T23F1.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T25169
R:Wilkinson, J.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19990
A:Accession: T25169
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-330 <MIL>
A:Cross-references: EMBL:Z81129; PIDN:CA803405.1; GSPDB:GN00023; CESP:T23F1.6
A:Experimental source: clone T23F1
C:Genetics:
A:Gene: CESP:T23F1.6
A:Map position: 5
A:Introns: 16/3
C:Superfamily: gliadin

Query Match          27.4%; Score 55; DB 2; Length 330;
Best Local Similarity 28.6%; Pred. No. 20;
Matches 12; Conservative 7; Mismatches 15; Indels 8; Gaps 2;

QY 1 CSQNEYPFDSLHACIP-----COLRCSNTPLTCORYC 34
DB 59 CASSQYQYLOTSCMCAACQSCSCQCCSNTNTCCPTCCQSC 100

RESULT 13
T23681
hypothetical protein M02G9.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T23681
R:Matthews, L.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19781
A:Accession: T23681
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1513 <MIL>
A:Cross-references: EMBL:Z81573; PIDN:CA804625.1; GSPDB:GN00020; CESP:M02G9.1
A:Experimental source: clone M02G9
C:Genetics:
A:Gene: CESP:M02G9.1
A:Map position: 2
A:Introns: 23/3; 71/3; 121/3; 183/1; 1083/3; 1141/3; 1408/1; 1449/1

Query Match          27.4%; Score 55; DB 2; Length 1513;
Best Local Similarity 44.8%; Pred. No. 74;
Matches 13; Conservative 3; Mismatches 11; Indels 2; Gaps 2;

QY 8 DSLHAC-IPQQLRC-SSNTPLTCORYC 34
DB 141 DSCQNVQNVCGACVSONSPAVCOOTC 169

RESULT 14
T30197
alpha tectorin - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C:Accession: T30197
R:legan, P.K.; Rau, A.; Keene, J.N.; Richardson, G.P.
J. Biol. Chem. 272, 8791-8801, 1997
A:Title: The mouse tectorins. Modular matrix proteins of the inner ear homologous to com
A:Reference number: Z20771; MUID:97236843; PMID:9079715
A:Accession: T30197
A:Status: preliminary; translated from GB/EMBL/DBJ
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A:Molecule type: mRNA
A:Residues: 1-2155 <LEBG>
A:Cross-references: EMBL:X99805; MUID:G1915908; PIDN:CAA68138.1; PID:G1915909
A:Experimental source: strain CD1; whole cochlea
A>Note: non-collagenous protein only expressed in the inner ear, by cells both in and s

Query Match          27.1%; Score 54.5; DB 2; Length 2155;
Best Local Similarity 29.4%; Pred. No. 1.2e+02;
Matches 10; Conservative 6; Mismatches 15; Indels 3; Gaps 1;

QY 1 CSQNEYPFDSLHACIPQQLRCSNTPLTCORYC 34
DB 1372 CPPNSHYSCVSCVCP--RCALRLKSDCNHYC 1402

RESULT 15
S54307
myosin heavy chain - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 02-Mar-2001
C:Accession: S54307
R:Reinhard, J.; Scheel, A.A.; Diekmann, D.; Hall, A.; Ruppert, C.; Baehler, M.
EMBO J. 14, 697-704, 1995
A:Title: A novel type of myosin implicated in signalling by rho family GTPases.
A:Reference number: S54307; MUID:95188874; PMID:7882973
A:Accession: S54307
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1980 <RI>
A:Cross-references: EMBL:X72609; MUID:9639998; PIDN:CAA54700.1; PID:9639999
C:Superfamily: rat myosin heavy chain; myosin motor domain homology; protein kinase C
C:Keywords: nucleotide binding; P-loop
F:143-942/Domain: myosin motor domain homology <NMOT>
F:139-246/Region: nucleotide-binding motif A (P-loop)
F:11593-1641/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match          26.9%; Score 54; DB 2; Length 1980;
Best Local Similarity 52.9%; Pred. No. 1.2e+02;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 16 PCQLRCSNTPLTCOR 32
DB 1812 PCLRLCPDPSDPLTSMK 1828
```

Search completed: January 7, 2003, 09:41:08
Job time : 6.85714 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:31:59 ; Search time 2.55639 Seconds
(without alignments)
551.635 Million cell updates/sec

Title: US-09-855-158-7
Perfect score: 201
Sequence: 1 CSQNEYFDSLHACIPQLRCSNTPPLTCQRYC 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	201	100.0	184	1	TR17_HUMAN
2	136	67.7	185	1	Q02223
3	71.5	35.6	249	1	T13X_MOUSE
4	67.5	33.6	1877	1	PCX3_MOUSE
5	66.5	33.1	293	1	T13X_HUMAN
6	64.5	32.1	5376	1	ZAN_MOUSE
7	60	29.9	867	1	SSPO_BOVIN
8	58	28.9	175	1	T13C_MOUSE
9	57.5	28.6	63	1	ICB1_ASCSU
10	57.5	28.6	1680	1	FUR2_DROME
11	56	27.9	2476	1	YAN_FIG
12	55	27.4	708	1	YB40_HUMAN
13	54	26.9	1980	1	MY9B_RAT
14	54	26.9	2114	1	MY9B_MOUSE
15	54	26.9	2158	1	MY3B_HUMAN
16	53.5	26.6	381	1	P33 CANFA
17	53.5	26.6	758	1	YU06_YEAST
18	53	26.4	131	1	ALK1_MOUSE
19	52.5	26.1	1592	1	SORL1_CHICK
20	51.5	25.6	63	1	AME2_WIRJA
21	50.5	25.1	610	1	CABP_BOVIN
22	50.5	25.1	1013	1	PRML_DROME
23	50	24.9	72	1	RL40_TOBAC
24	50	24.9	455	1	TRIA_HUMAN
25	50	24.9	1696	1	PCK5_BRACL
26	49	24.4	297	1	MED3_HUMAN
27	49	24.4	321	1	MED3_CAEEL
28	49	24.4	350	1	PAX4_HUMAN
29	49	24.4	461	1	TRIA_FIG
30	49	24.4	1483	1	UFPA_YEAST
31	49	24.4	1984	1	YL_DROME
32	49	24.4	2531	1	NTC1_MOUSE
33	49	24.4	3718	1	LMA5_MOUSE

34	48.5	24.1	323	1	TNR6_BOVIN
35	48.5	24.1	608	1	ALB1_SALSA
36	48.5	24.1	608	1	ALB2_SALSA
37	48.5	24.1	3034	1	CLRI_MOUSE
38	48	23.9	56	1	ITR4_RADMA
39	48	23.9	304	1	TFPI_MACMU
40	48	23.9	448	1	EDAF_HUMAN
41	48	23.9	450	1	RMIL_AVEVR
42	48	23.9	500	1	SAH2_HUMAN
43	48	23.9	515	1	APX1_CAEEL
44	48	23.9	611	1	SAH3_HUMAN
45	48	23.9	681	1	COG2_CAEEL

PS1867 bos taurus
P21848 salmo salar
O03156 salmo salar
O35161 mus musculus
P16344 radianchus
Q28864 macaca mula
Q99802 homo sapien
P27966 avian tois-
O43855 homo sapien
P41990 caenorhabdi
Q96nm2 homo sapien
Q21444 caenorhabdi

ALIGNMENTS

RESULT 1

TR17_HUMAN

ID TR17_HUMAN STANDARD; PRT; 184 AA.

AC Q02223;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 17 (B-cell maturation protein).

DE TNFRSF17 OR BCMA OR BCM.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. AND CHROMOSOMAL TRANSLOCATION.

RC ISSUES=Peripheral blood leukocytes, and lymph node;

RX MEDLINE=93010984; PubMed=1396583;

RA Laabi Y., Gras M.P., Carbonnel F., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;

RT "A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma.";

RL EMBO J. 11:3897-3904(1992).

[2]

RP SEQUENCE FROM N.A.

RX MEDLINE=94218235; PubMed=8165126;

RA Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;

RT "The BCMA gene, preferentially expressed during B lymphoid maturation, is bidirectionally transcribed.";

RL Nucleic Acids Res. 22:1147-1154(1994).

[3]

RP SEQUENCE FROM N.A.

RX MEDLINE=99425270; PubMed=10493829;

RA Loftus B.J., Kim U.-J., Sneddon V.P., Kalush P., Brandon R., Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L., Deallates Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S., Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;

RT "Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";

RL Genomics 60:295-308(1999).

[4]

RP SEQUENCE FROM N.A. AND VARIANT THR-153.

RX MEDLINE=21419161; PubMed=11528522;

RA Kawasaki A., Teuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;

RT "Presence of four major haplotypes in human BCMA gene: lack of association with systemic lupus erythematosus and rheumatoid arthritis.";

RL Genes Immun. 2:276-279(2001).

[5]

RP FUNCTION.

RX MEDLINE=20363816; PubMed=10903733;

RA Hatzoglou A., Rousset J., Bourgeade M.-F., Rogier E., Madry C., Inoue J., Devergne O., Tsapis A.;

RT "TNF receptor family member BCMA (B cell maturation) associates with TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38

RT J. Immunol. 165:1322-1330(2000).
 [6]
 RP FUNCTION.
 RA MEDLINE=20259066; PubMed=10801128; Enselman R., Dillon S.R.,
 RA Gross J.A., Johnston J., Murti S., Foster D., Lofton-Day C.,
 RA Madden K., Xu W., Parrish-Novak K., Foster D., Lofton-Day C.,
 RA Moore M., Litzau A., Grossman A., Haugen H., Foley K., Blumberg H.,
 RA Harrison K., Kindsvogel W., Clegg C.H.,
 RT TAC1 and B2M are receptors for a TNF homologue implicated in B-cell
 RT autoimmune disease.
 RT Nature 404:995-999(2000).
 RN (7)
 RP FUNCTION, AND INTERACTION WITH APRIL AND BAFF.
 RA MEDLINE=21170294; PubMed=10973284;
 RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
 RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
 RA Boyle W.J., Sarsol I., Hsu H., Senaldi G., Theil L.E.,
 RT "APRIL and TALL-1 and receptors BCMA and TAC1: system for regulating
 RT humoral immunity."
 RT Nat. Immunol. 1:252-256(2000).
 RN [8]
 RP INTERACTION WITH TRAF5 AND TRAF6.
 RA MEDLINE=20381353; PubMed=10908663;
 RA Shu H.-B., Johnson H.,
 RT "B cell maturation protein is a receptor for the tumor necrosis factor
 RT family member TALL-1."
 RT Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
 CC -1- FUNCTION: Receptor for TNFSF13B/BLYS/BAFF and TNFSF13/APRIL.
 CC promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK.
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
 CC and perinuclear Golgi-like structures.
 CC -1- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
 CC cells or monocytes.
 CC -1- DISSEMINATION: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS
 CC CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16) (Q26;P13)
 CC WHICH INVOLVES BCMA AND IL2.
 CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
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 CC -----
 DR EMBL: Z14954; CAAT78679.1; -
 DR EMBL: Z29575; CAAB2691.1; -
 DR EMBL: Z29574; CAAB2690.1; -
 DR EMBL: U95743; AAB67251.1; -
 DR EMBL: AB052772; BAB60895.1; -
 DR PIR: S31208; S31208.
 DR PIR: S31209; S31209.
 DR Gene; HGNC:11913; TNFRSF17.
 DR MIM: 109545; -
 KW Receptor; Immune response; Proto-oncogene; Signal-anchor;
 KW Transmembrane; Chromosomal translocation; Polymorphism.
 KW DOMAIN 1 54 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 55 77 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 78 184 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 7 4 TNFR-CYS.
 FT SITE 3 4 BREAKPOINT FOR TRANSLOCATION TO FORM
 FT DISULFID 8 21 INTERLEUKIN 2/BCM ONCOGENE.
 FT DISULFID 24 37 BY SIMILARITY.
 FT DISULFID 28 41 BY SIMILARITY.
 FT VARIANT 153 153 A -> T.
 FT /FTID=VAR_012234.
 FT SEQUENCE 184 AA; 20138 MW; 277AF11E2767D32 CRC64;

Query Match 100.0%; Score 201; DB 1; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4.8e-19;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CSONEYPDSILHACIPCOLRCSNTPPLTCORYC 34
 8 CSONEYPDSILHACIPCOLRCSNTPPLTCORYC 41
 Db
 RESULT 2
 TR17_MOUSE
 ID TR17_MOUSE STANDARD, PRT; 185 AA.
 AC 088472;
 DT 15-UN-2002 (Rel. 41, Created)
 DT 15-UN-2002 (Rel. 41, Last sequence update)
 DT 15-UN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 17 (B-cell
 DE maturation protein).
 GN TNFSF17 OR BCMA OR BCM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=BALEB; TISSUE=Spleen;
 RX MEDLINE=99061155; PubMed=9846698;
 RA Madry C., Laabi Y., Callebaut I., Roussel J., Hatzoglou A.,
 RA Le Coniat M., Morion J.P., Berger R., Traais A.,
 RT "The characterization of murine BCMA gene defines it as a new member
 RT of the tumor necrosis factor receptor superfamily."
 RT Int. Immunol. 10:1693-1702(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=21083660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batelov S., Casavant T.,
 RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peeole G., Quackenbush J.,
 RA Schmitt L.M., Steubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weir C., Whitaker C., Wilming L.,
 RA Wyanhaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Konteski S.,
 RA Hayashizaki Y.,
 RT Functional annotation of a full-length mouse cDNA collection."
 RT Nature 409:685-690(2001).
 RL -1- FUNCTION: Receptor for TNFSF13B/BLYS/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK (by similarity).
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6
 CC (similarity).
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Detected in spleen, thymus, bone marrow and
 CC heart, and at lower levels in kidney and lung.
 CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
 CC -----
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DR EMBL; AF061505; AAC23799.1; -;
 DR EMBL; AK020247; BAB32038.1; -;
 DR MGD; MGI:1343050; Tnftrsf17.
 KW Receptor; Immune response; Signal-anchor; Transmembrane;
 KW Alternative splicing.
 FT DOMAIN 1 49
 FT TRANSMEM 50 70
 FT SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT CYTOPLASMIC (POTENTIAL).
 FT TNR-CYS.
 FT REPEAT 4 36
 FT BY SIMILARITY.
 FT DISULFID 5 18
 FT BY SIMILARITY.
 FT DISULFID 21 32
 FT BY SIMILARITY.
 FT DISULFID 25 36
 FT BY SIMILARITY.
 FT VARSPLIC 87 91
 FT MISSING (IN ISOFORM 2).
 SQ SEQUENCE 185 AA; 20442 MW; 890635284FD26A8E CRC64;

Query Match 67.7%; Score 136; DB 1; Length 185;
 Best Local Similarity 70.6%; Pred. No. 1e-10; Gaps 1;
 Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 CSQNEYFDSLLHACIPQLRCSSNTPPLTCQRYC 34
 DB 5 CPHSBYFDSLLHACKPCHLRCSN--PPATCQPYC 36

RESULT 3

ID T13X MOUSE STANDARD; PRT; 249 AA.
 AC Q9ET35; Q9DBZ3;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE tumor necrosis factor receptor superfamily member 13B (Transmembrane
 DE activator and CAML interactor).
 OS TNFBSF13B OR TACI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=21177254; PubMed=1081172;
 RA Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A.,
 RA Dixit V.M.;
 RA "Identification of a receptor for BlyS demonstrates a crucial role in
 RA humoral immunity.";
 RL Nat. Immunol. 1:37-41 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saio T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA Fletschmann W., Gaasterland T., Glasi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo T., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 RN [3]
 RP FUNCTION.
 RX MEDLINE=20341628; PubMed=10880535;
 RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
 RA Theill L.E., Colombero A., Solovyev I., Lee P., McCabe S., Elliott R.,
 RA Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,
 RA Meng S.-Y., Boyle W.J., Hsu H.;
 RA "TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis
 RT factor family member involved in B cell regulation.";
 RL J. Exp. Med. 192:137-143 (2000).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=21322748; PubMed=11429548;
 RA Wang H., Marsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,
 RA Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.;
 RA "TACI-ligand interactions are required for T cell activation and
 RT collagen-induced arthritis in mice.";
 RL Nat. Immunol. 2:632-637 (2001).
 CC -1- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS
 CC that binds both ligands with similar high affinity. Mediates
 CC calcineurin-dependent activation of NF-AT, as well as activation
 CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
 CC cell function and the regulation of humoral immunity (by
 CC similarity).
 CC -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
 CC domain of CAMLG with its C-terminus (by similarity).
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
 CC -----
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EMBL; AF257673; BAB00081.1; -;
 EMBL; AK004668; BAB23457.1; -;
 MGD; MGI:1889411; Tnftrsf13b.
 PROSITE; PS00652; TNFR_NGFR_1; 1.
 PROSITE; PS00550; TNFR_NGFR_2; 2.
 DR Receptor; Immune response; Signal-anchor; Transmembrane; Repeat.
 FT DOMAIN 1 128
 FT EXTRACELLULAR (POTENTIAL).
 FT SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT TRANSMEM 129 149
 FT (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT REPEAT 5 38
 FT TNFR-CYS 1.
 FT TNFR-CYS 2.
 FT BY SIMILARITY.
 FT DISULFID 6 19
 FT BY SIMILARITY.
 FT DISULFID 22 34
 FT BY SIMILARITY.
 FT DISULFID 26 38
 FT BY SIMILARITY.
 FT DISULFID 43 58
 FT BY SIMILARITY.
 FT DISULFID 61 72
 FT BY SIMILARITY.
 FT DISULFID 65 76
 FT BY SIMILARITY.
 FT CONFLICT 137 137
 FT I -> F (IN REF. 2).
 SQ SEQUENCE 249 AA; 26947 MW; CB2F2D61C2931D81 CRC64;

Query Match 35.6%; Score 71.5; DB 1; Length 249;
 Best Local Similarity 35.3%; Pred. No. 0.025; 13; Indels 1; Gaps 1;
 Matches 12; Conservative 8; Mismatches 13;
 QY 1 CSQNEYFDSLLHACIPQLRCSSNTPPLTCQRYC 34
 DB 6 CPKQYWDSSRKSCVSCALTCQSRS-ORTCTDFC 39
 RESULT 4
 PKCS MOUSE
 ID _PCK5_MOUSE STANDARD; PRT; 1877 AA.

AC Q04592; Q62040; (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 41, Last annotation update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
DE (Proprotein convertase PCS5) (Subtilisin/kexin-like protease PCS4)
DE (Convertase PCS5) (PC6) (Subtilisin-like proprotein convertase 6)
DE (SPC6).
GN PCSK5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE OF 330-1877 FROM N.A. (ISOFORM PCS5B).
RC STRAIN=ICR; TISSUE=Intestine;
RX MEDLINE=93327934; PubMed=8335106;
RA Nakagawa T., Murakami K., Nakayama K.;
RT "Identification of an isoform with an extremely large Cys-rich region
of PC6, a Kex2-like processing endoprotease.";
RL FEBS Lett. 327:165-171(1993).
[2]
RN SEQUENCE FROM N.A. (ISOFORM PCS5A).
RP TISSUE=Brain, and Intestine;
RX MEDLINE=933224489; PubMed=8466318;
RA Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,
RA Nakayama K.;
RT "Identification and functional expression of a new member of the
mammalian Kex2-like processing endoprotease family: its striking
structural similarity to PAC64.";
RL J. Biochem. 113:132-135(1993).
[3]
RN SEQUENCE FROM N.A. (ISOFORM PCS5A).
RP TISSUE=Adrenal cortex;
RX MEDLINE=93342056; PubMed=8341687;
RA Lussan J., Vreau D., Hamelin J., Day R., Christian M., Seidah N.G.;
RT "cDNA structure of the mouse and rat subtilisin/kexin-like PCS5: a
candidate proprotein convertase expressed in endocrine and
nonendocrine cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
[4]
RN PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.
RP MEDLINE=97105178; PubMed=8947550;
RX De Bie I., Marcinkiewicz M., Walide D., Lazure C., Nakayama K.,
RA Berdyaev N., Seidah N.G.;
RT "The isoforms of proprotein convertase PCS are sorted to different
subcellular compartments.";
RL J. Cell Biol. 135:1261-1275(1996).
[5]
RN DEVELOPMENTAL EXPRESSION.
RP MEDLINE=96293359; PubMed=6696813;
RX Constam D.B., Calton M., Robertson E.J.;
RT "SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone
morphogenetic proteins at distinct sites during embryogenesis.";
RL J. Cell Biol. 134:181-191(1996).
[6]
RN DEVELOPMENTAL EXPRESSION.
RP MEDLINE=97436919; PubMed=9291583;
RX Rancourt S.L., Rancourt D.E.;
RT "Murine subtilisin-like proteinase SPC6 is expressed during embryonic
implantation, somitogenesis, and skeletal formation.";
RL Dev. Genet. 21:75-81(1997).
[7]
RN FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPEPTASE ACTIVITY
WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE
OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF. MAY BE RESPONSIBLE
FOR THE MATURATION OF GASTROINTESTINAL PEPTIDES. MAY BE INVOLVED
IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA THE ACTIVATION
OF GROWTH FACTORS.
[8]
RN CATALYTIC ACTIVITY. RELEASE OF MATURE PROTEINS FROM THEIR
PROPEPTIDES BY CLEAVAGE OF ARG-XAA-YAA-ARG-1-ZAA BONDS, WHERE XAA
CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
[9]
RN SUBCELLULAR LOCATION: PCSA IS SECRETED THROUGH THE REGULATED
SECRETORY PATHWAY. PCSB IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO

CC A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH
CC EARLY ENDOCYTES.
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS, PCSB/LONG (SHOWN HERE)
CC AND PCSA/SHORT; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: PCSA IS EXPRESSED IN MOST TISSUES BUT IS MOST
CC ABUNDANT IN THE INTESTINE AND ADRENALS. PCSB IS EXPRESSED IN THE
CC INTESTINE, ADRENALS AND LUNG BUT NOT IN THE BRAIN.
CC -1- DEVELOPMENTAL STAGE: WEAKLY EXPRESSED THROUGHOUT THE EMBRYO,
CC EXCEPT IN THE DEVELOPING NERVOUS SYSTEM, THE RIBS AND THE LIVER,
CC BUT MARKEDLY UPREGULATED AT DISCRETE SITES DURING DEVELOPMENT. AT
CC E6.5, PROMINENT EXPRESSION OBSERVED IN DIFFERENTIATED DECIDUA. AT
CC E7.5, INTENSE EXPRESSION IN EXTRAEMBRYONIC ENDODERM, ANIONIC AND YOLK
CC NASCENT MESODERM. AT 8.5, ABUNDANT EXPRESSION IN SOMITES AND YOLK
CC SAC FOLLOWED BY A COMBINATION TO DERMATOME COMPARTMENT. BETWEEN
CC E9.5 AND E11.5, ABUNDANT EXPRESSION IN AER (THICKENED ECTODERMAL
CC CELLS OF LIMB BUDS). AT E12.5, EXPRESSION IN THE LIMBS IS CONFINED
CC TO THE CONDENSING MESENCHYM SURROUNDING THE CARPITALS. AT THIS
CC STAGE, STRONG EXPRESSION ALSO DETECTED IN VESTIBULAR AND FACIAL
CC CARTILAGE PRIMORDIA AND IN THE MUSCLE OF THE TONGUE. AT E15.5, 1.
CC ABUNDANT EXPRESSION IN EPITHELIAL CELLS OF THE INTESTINAL VILUS.
CC ISOFORM A IS MOST ABUNDANT AT ALL STAGES BUT SIGNIFICANT LEVELS OF
CC ISOFORM B OCCUR AT E12.5.
CC -1- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
CC ASSISTING THE FOLDING OF THE ZMOGEN WITHIN THE ENDOPLASMIC
CC RETICULUM.
CC -1- DOMAIN: AC 1 AND AC 2 (CLUSTERS OF ACIDIC AMINO ACIDS) CONTAIN
CC SORTING INFORMATION. AC 1 DIRECTS TGN LOCALIZATION AND INTERACTS
CC WITH THE TGN SORTING PROTEIN PACS-1.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
CC -1- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
CC -----
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CC -----
DR EMBL: D17583; BAA04507.1; -
DR EMBL: D12619; BAA02143.1; -
DR EMBL: I14932; AAA74636.1; -
DR PIR: JX0248; JX0248
DR PIR: A48235; A48235.
DR HSPB: O96403; AIMP1.
DR MEROSES: S08.076; -
DR WGD; MGI:97315; PCSKS.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR002174; Furin-like.
DR InterPro: IPR002884; P_domain.
DR InterPro: IPR000209; Peptidase_S8.
DR Pfam: PF00082; Peptidase_S8; 1.
DR Pfam: PF01483; P_PARTIAL.
DR PRINTS: PR00723; SUBTILISIN.
DR PRODOM: PD000717; P_domain; 1.
DR SMART: SM00181; EGF; 3.
DR SMART: SM00001; EGF_like; 2.
DR SMART: SM00261; FU; 22.
DR PROSITE: PS00136; SUBTILASE ASP; 1.
DR PROSITE: PS00137; SUBTILASE HIS; 1.
DR PROSITE: PS00138; SUBTILASE_SRR; 1.
KW Hydroxylase, Serine protease; Glycoprotein; Zymogen; Signal;
KW Cleavage on pair of basic residues; Repeat; Alternative splicing;
KW Transmembrane.
FT SIGNAL 1 34
FT PROPEP 35 116
FT CHAIN 117 1677
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FT DOMAIN 117 1768
FT TRANSMEM 1769 1877
FT DOMAIN 117 452
FT DOMAIN 464 602
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FT HOMO B.
FT-----
FT PROTEIN CONVERTASE SUBTILISIN/KEXIN
FT TYPE 5
FT-----
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL. (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT CATALYTIC.
FT HOMO B.

GN ZAN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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RP SEQUENCE FROM N.A.
RC TISSUE-Testis;
RX MEDLINE=9812314; PubMed=9452463;
RA Gao Z., Garbers D.L.;
RT "Species diversity in the structure of zonadhesin, a sperm-specific
RT membrane protein containing multiple cell adhesion molecule-like
RT domains.";
RL J. Biol. Chem. 273:3415-3421(1998).
RN [2]
RP SEQUENCE OF 4864-5376 FROM N.A.
RC TISSUE-Testis;
RX MEDLINE=97271566; PubMed=9126492;
RA Gao Z., Hartumi T., Garbers D.L.;
RT "Chromosome localization of the mouse zonadhesin gene and the human
RT zonadhesin gene (ZAN).";
RL Genomics 41:119-122(1997).
CC -1- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA
CC OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR
CC SIGNALING.
CC -1- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE
CC APICAL REGION OF THE SPERM HEAD.
CC -1- TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPLOID SPERMATIDS.
CC -1- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATES SPERM ADHESION TO THE
CC ZONA PELLUCIDA.
CC -1- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS,
CC THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF
CC SPERMATOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMS.
CC -1- DOMAIN: THE VWFD DOMAIN 2 MAY MEDATE COVALENT
CC OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MU22).
CC -1- SIMILARITY: CONTAINS 3 MAM DOMAINS.
CC -1- SIMILARITY: CONTAINS 25 VWFD DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -----
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CC -----
DR EMBL; U97068; AAC26680.1; -;
DR EMBL; U83190; AAC53125.1; -;
DR MGD; MGI:106656; Zan.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR003645; FOLN.
DR InterPro; IPR000998; MAM domain.
DR InterPro; IPR002919; TIL_Cysrich.
DR InterPro; IPR003328; TIL_Cysrich.
DR InterPro; IPR001007; VWF_C.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF00094; vwd; 4.
DR Pfam; PF00629; MAM; 3.
DR Pfam; PF01826; TIL; 25.
DR Pfam; PF02345; Tila; 25.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00274; FOLN; 11.
DR SMART; SM00137; MAM; 2.
DR SMART; SM00214; VWC; 17.
DR SMART; SM00216; VWD; 4.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 18.
DR PROSITE; PS00740; MAM_1; FALSE_NEG.
DR PROSITE; PS00600; MAM_2; 3.
DR Signal; Glycoprotein; Transmembrane; EGF-like domain; Cell adhesion;
KW Repeat.
FT SIGNAL 1 17
FT CHAIN 18 5376
FT DOMAIN 18 5310
FT TRANSMEM 5311 5337
FT TRANSMEM 5338 5376
FT DOMAIN 45 210
FT DOMAIN 215 374
FT DOMAIN 377 542
FT DOMAIN 547 1170
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 Best Local Similarity 35.1%; Pred. No. 3.3; Mismatches 3; Gaps 2;
 Matches 13; Conservative 5;
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RESULT 7
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 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE SCO-spondin (Fragment)
 OS Bos taurus (Bovine)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Eutheria; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=ependymocyte;
 RX MEDLINE=96338614; PubMed=8743952;
 RA Gabor S., Monnerie H., Meinert R., Creveaux I., Lehmann W.,
 RA Lamalle D., Dastugue B., Meinert A.;
 RA "SCO-spondin: a new member of the thrombospondin family secreted by
 RT the subcommissural organ is a candidate in the modulation of neuronal
 RT aggregation.";
 RL J. Cell Sci. 109:1053-1061(1996).
 CC -!- FUNCTION: INVOLVED IN THE MODULATION OF NEURONAL AGGREGATION.
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- TISSUE SPECIFICITY: SUBCOMMISSURAL ORGAN.
 CC -!- DEVELOPMENTAL STAGE: EMBRYO.
 CC -!- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
 CC -!- SIMILARITY: CONTAINS AT LEAST 4 TSP TYPE-1 DOMAINS.
 CC -!- SIMILARITY: CONTAINS AT LEAST 2 EGF-LIKE DOMAINS.
 CC -!- SIMILARITY: CONTAINS AT LEAST 1 F5/8 TYPE C DOMAIN.
 CC -!- SIMILARITY: CONTAINS AT LEAST 3 LDL-RECEPTOR CLASS A DOMAINS.
 CC
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 CC
 CC EMBL; X93922; CAA63815.1; -.
 CC HSP; P01130; IAUJ.
 CC InterPro; IPR000421; FAS8 C.
 CC InterPro; IPR002172; LDL_recept_A.
 CC InterPro; IPR002919; TIL_Cysrich.
 CC InterPro; IPR000884; TSF1.
 CC InterPro; IPR001007; VWF C.
 CC Pfam; PF00057; ldl_recept_a; 3.
 CC Pfam; PF00090; tsp_1; 4.
 CC Pfam; PF00754; F5_F8_type_C; 1.
 CC Pfam; PF01826; TIL; 1.
 CC SMART; SM00231; FAS8C; 1.
 CC SMART; SM00192; LDLA; 3.
 CC SMART; SM00209; TSF1; 4.
 CC SMART; SM00214; VWC; 1.
 CC PROSITE; PS01285; FAS8C_1; 1.
 CC PROSITE; PS01286; FAS8C_2; 1.
 CC PROSITE; PS01209; LDLA_1; 3.
 CC PROSITE; PS01268; LDLA_2; 3.
 CC PROSITE; PS00692; TSF1; 4.
 CC PROSITE; PS00692; Cell adhesion; Calcium-binding; Repeat; EGF-like domain.
 KW Glycoprotein; Cell adhesion; Calcium-binding; Repeat; EGF-like domain.
 FT NON_TER 1

FT DOMAIN 26 81 TSP TYPE-1 1.
 FT DOMAIN 103 142 EGF-LIKE 1.
 FT DOMAIN 143 180 EGF-LIKE 2.
 FT DOMAIN 185 243 TSP TYPE-1 2.
 FT DOMAIN 344 502 F5/8 TYPE C.
 FT DOMAIN 506 544 LDL-RECEPTOR CLASS A 1.
 FT DOMAIN 663 701 LDL-RECEPTOR CLASS A 2.
 FT DOMAIN 723 761 LDL-RECEPTOR CLASS A 3.
 FT DOMAIN 762 813 TSP TYPE-1 3.
 FT DOMAIN 814 867 TSP TYPE-1 4.
 FT DISULFID 107 122 BY SIMILARITY.
 FT DISULFID 116 127 BY SIMILARITY.
 FT DISULFID 129 141 BY SIMILARITY.
 FT DISULFID 147 166 BY SIMILARITY.
 FT DISULFID 149 169 BY SIMILARITY.
 FT DISULFID 171 179 BY SIMILARITY.
 FT DISULFID 344 502 BY SIMILARITY.
 FT DISULFID 508 520 BY SIMILARITY.
 FT DISULFID 515 533 BY SIMILARITY.
 FT DISULFID 527 542 BY SIMILARITY.
 FT DISULFID 665 677 BY SIMILARITY.
 FT DISULFID 672 690 BY SIMILARITY.
 FT DISULFID 684 699 BY SIMILARITY.
 FT DISULFID 725 737 BY SIMILARITY.
 FT DISULFID 732 750 BY SIMILARITY.
 FT DISULFID 744 759 BY SIMILARITY.
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 309 309 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 409 409 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT NON_TER 867 867
 SQ SEQUENCE 867 AA; 91817 MM; 9538F2108E787B49 CRC64;
 Query Match 29.9%; Score 60; DB 1; Length 867;
 Best Local Similarity 42.9%; Pred. No. 2.3;
 Matches 9; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
 QY 10 LLHACIPCOLRCSNTPPLTC 30
 DB 96 VFHACVCPPLTCDDISQATC 116

RESULT 8
 T13C_MOUSE
 ID T13C_MOUSE STANDARD; PRT; 175 AA.
 AC Q9D8D0;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE tumor necrosis factor receptor superfamily member 13C (B cell-
 DE activating factor receptor) (BAFF receptor) (BAFF-R) (Blys receptor
 DE 3) (B-cell maturation defect).
 GN TNFRSF13C OR BAFFR OR BCMO OR BR3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=BALB/c; TISSUE=B-cell lymphoma;
 RX MEDLINE=21442025; PubMed=11509692;
 RA Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
 RA Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C.,
 RA Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L.,
 RA Ambrose C.;
 RT "BAFF-R, a newly identified TNF receptor that specifically interacts
 RT with BAFF.";
 RL Science 293:2108-2111(2001).
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND DISEASE.
 RC STRAIN=A/J;
 RX MEDLINE=21475520; PubMed=11591325;
 RA Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M.,
 RA Cancro M.P., Grewal I.S., Dixit V.M.;

RT "Identification of a novel receptor for B lymphocyte stimulator that is mutated in a mouse strain with severe B cell deficiency.";
 RT Curr. Biol. 11:1547-1552(2001).
 RN [3]

RP SOURCE FROM N.A. (ISOPFORM 1).
 RC STRAIN-C57BL/6J; TISSUE-Small intestine;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawal J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Atakawa I., Hara A., Fukunishi Y., Komio H., Adachi J., Fukuda S.,
 RA Atzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamahata I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [4]

RP FUNCTION
 RX MEDLINE=21614654; PubMed=11747827;
 RA Harless S.M., Hentz V.M., San A.P., Hsu B.L., Clise-Dwyer K.,
 RA Hilbert D.M., Hayes C.E., Cancro M.P.;
 RT Competition for Blyc-mediated signaling through Bcnd/BR3 regulates peripheral B lymphocyte numbers.";
 RL Curr. Biol. 11:1986-1989(2001).
 CC - FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/BLYS.
 CC Promotes the survival of mature B-cells and the B-cell response.
 CC - SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC - ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.
 CC - TISSUE SPECIFICITY: Highly expressed in spleen and testis;
 CC detected at lower levels in lung and thymus.
 CC - DISEASE: Defects in TNFSF13C are a cause of severe B-cell deficiency. B-cell deficient strain A/WySnJ has a 4.7 kb insertion in the BAFF gene leading to an altered C-terminus. The mutant RNA is not detectable. B-cell lymphoproliferation is normal, but the life span of peripheral B-cells is much reduced.
 CC - SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.

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CC EMBL: AF373847; AAK91827.1; -;
 DR EMBL: AK008142; BAB25490.1; -;
 DR MGD: MGI:1919299; Tnfrsf13c.
 KM Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;
 KM alternative splicing.
 FT DOMAIN 1 71 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 72 92 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT DOMAIN 93 175 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 22 38 TNFR-CYS (PARTIAL).
 FT DISULFID 27 35 BY SIMILARITY.
 FT CARBOHYD 23 38 N-LINKED (GLCNAC.) (POTENTIAL).
 FT VARSPLIT 133 143 MISSING (IN ISOPFORM 2).
 SQ SEQUENCE 173 AA; 18798 MW; 28BC7C1A02FB87EF CRC64;

Query Match 28.9%; Score 58; DB 1; Length 175;
 Best Local Similarity 47.4%; Pred. No. 0.95;
 Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GSONEYFDSLHACIPCOL 19
 Db 22 CQTECFDPLVANCYCEL 40

RESULT 9

ICEL_ASCSU STANDARD; PRT; 63 AA.

AC P07851;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 15-JUL-1999 (Rel. 36, Last annotation update)
 DE Chymotrypsin/elastase isoform 1 (C/E-1 inhibitor).
 OS Ascaris suum (pig roundworm) (Ascaris lumbricoides).
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;
 CC NCB1_TaxID=6253;
 RN [1]
 RP MEDLINE=84255715; PubMed=6564898;
 RA Babin D.R., Peanasky R.J., Goos S.M.;
 RT "The inhibitors of chymotrypsin/elastase from Ascaris lumbricoides: the primary structure.";
 RL Arch. Biochem. Biophys. 232:143-161(1984).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH ELASTASE.
 RX MEDLINE=95006335; PubMed=792044;
 RA Huang K., Strynacka N.C., Bernard V.D., Peanasky R.J., James M.N.;
 RT "The molecular structure of the complex of Ascaris chymotrypsin/elastase inhibitor with porcine elastase.";
 RL Structure 2:679-689(1994).
 CC - FUNCTION: DEFEND THE ORGANISM AGAINST THE HOST'S PROTEINASES.
 CC - SIMILARITY: BELONGS TO THE ASCARIS TRYPSIN INHIBITOR FAMILY.

DR PIR: S07127; S07127.
 DR PDB: 1EAI; 05-APR-99.
 DR InterPro: IPR002919; TIL_Cysrich.
 KW Serine protease inhibitor; 3D-structure.
 FT DISULFID 5 38
 FT DISULFID 14 33
 FT DISULFID 17 29
 FT DISULFID 21 60
 FT DISULFID 40 54
 FT ACT SITE 31 32
 SQ SEQUENCE 63 AA; 6862 MW; 5DC10DE75B375F16 CRC64;

Query Match 28.6%; Score 57.5; DB 1; Length 63;
 Best Local Similarity 37.1%; Pred. No. 0.43;
 Matches 13; Conservative 5; Mismatches 10; Indels 7; Gaps 3;

Qy 1 GSONEYFDSLHACIPCOLRC--SSNP-PLTCOR 32
 Db 5 CGPNEVWTE---CTGCEMKCGPDENTPCPLMCCR 35

RESULT 10

FT22_DROME STANDARD; PRT; 1680 AA.

AC P30432;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Furin-like protease 2 precursor (EC 3.4.21.75) (Furin 2).
 GN Fur2.
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7277;

RN SEQUENCE FROM N.A. PubMed=1512259;
 RP MEDLINE=92381036; Pauli I.G.L., Kurzik-Dumke U.,
 RX Roebrock A.J.M., Cremers J.W.M.,
 RA Roebrock A.J.M., Gelfand E.A.F., Leunissen J.A.M., van de Ven W.J.;
 "Cloning and functional expression of Dfurnin2, a subtilisin-like
 RI protease and functional enzyme of Drosophila melanogaster with multiple
 RT repeats of a cysteine motif.";
 RL J. Biol. Chem. 267:17208-17215 (1992).
 CC -!- FUNCTION: FURIN IS LIKELY TO REPRESENT THE UBIQUITOUS ENDOPEPTASE
 CC ACTIVITY WITHIN CONSTITUTIVE SECRETORY PATHWAYS AND CAPABLE OF
 CC CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: Release of mature proteins from their
 CC propeptides by cleavage of Arg-Xaa-Yaa-Arg-|-Zaa bonds, where Xaa
 CC can be any amino acid and Yaa is Arg or Lys. Releases albumin,
 CC complement component C3 and von Willebrand factor from their
 CC respective precursors.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8. FURIN SUBFAMILY.
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 CC EMBL; W94375; AA28551.1; -.
 DR PIR; A43434; A43434.
 DR HSP; Q99405; IMPT.
 DR MEROPS; S08.049; -.
 DR FLYBASE; Fgn0004598; Fur2.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR002174; Furin-like.
 DR InterPro; IPR002884; P domain.
 DR InterPro; IPR00209; Peptidase S8.
 DR Pfam; PF00082; Peptidase S8; 1.
 DR Pfam; PF01483; P; PARTIAL.
 DR PRINTS; PR00723; SUBTILISIN.
 DR ProDom; PD000717; P domain; 1.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00261; FU; 10.
 DR PROSITE; PS00136; SUBTILASE ASP; 1.
 DR PROSITE; PS00137; SUBTILASE HIS; 1.
 DR PROSITE; PS00138; SUBTILASE SER; 1.
 DR Hydrolase; Serine protease; Glycoprotein; Signal; Transmembrane;
 KW Multigene family; Zymogen; Repeat.
 FT SIGNAL; 1; 2; POTENTIAL.
 FT PROPEP; 319; POTENTIAL.
 FT CHAIN; 320; 1690; FURIN-LIKE PEPTASE 2.
 FT ACT_SITE; 418; 418; CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE; 457; 457; CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE; 638; 638; CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DOMAIN; 962; 1444; 10 X TANDEN REPEATS, CYS-RICH.
 FT REPEAT; 962; 1007; 1.
 FT REPEAT; 1008; 1057; 2.
 FT REPEAT; 1058; 1104; 3.
 FT REPEAT; 1105; 1153; 4.
 FT REPEAT; 1154; 1205; 5.
 FT REPEAT; 1206; 1254; 6.
 FT REPEAT; 1255; 1299; 7.
 FT REPEAT; 1300; 1346; 8.
 FT REPEAT; 1347; 1393; 9.
 FT REPEAT; 1394; 1444; 10.
 FT TRANSMEM; 1508; 1532; POTENTIAL.
 FT DOMAIN; 1533; 1690; CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD; 3; 3; N-LINKED (GLCNAC...); (POTENTIAL).
 FT CARBOHYD; 109; 109; N-LINKED (GLCNAC...); (POTENTIAL).
 FT CARBOHYD; 130; 130; N-LINKED (GLCNAC...); (POTENTIAL).
 FT CARBOHYD; 203; 203; N-LINKED (GLCNAC...); (POTENTIAL).
 FT CARBOHYD; 443; 443; N-LINKED (GLCNAC...); (POTENTIAL).
 FT CARBOHYD; 481; 481; N-LINKED (GLCNAC...); (POTENTIAL).
 FT CARBOHYD; 928; 928; N-LINKED (GLCNAC...); (POTENTIAL).

FT CARBOHYD; 1061; 1061; N-LINKED (GLCNAC...); (POTENTIAL).
 FT CARBOHYD; 1182; 1182; N-LINKED (GLCNAC...); (POTENTIAL).
 FT CARBOHYD; 1275; 1275; N-LINKED (GLCNAC...); (POTENTIAL).
 FT CARBOHYD; 1276; 1276; N-LINKED (GLCNAC...); (POTENTIAL).
 FT CARBOHYD; 1440; 1440; N-LINKED (GLCNAC...); (POTENTIAL).
 SQ SEQUENCE 1680 AA; 183599 MW; 0A99CE8770A8E293 CRC64;
 Query Match 28.8%; Score 57.5; DB 1; Length 1680;
 Best Local Similarity 34.3%; Pred. No. 8.9; Mismatches 17; Indels 1; Gaps 1;
 Matches 12; Conservative 5;
 QY 1 CSQNEYFDSLHACIPQLRCSS-NTPPLTCQRYC 34
 Db 1199 CSESEFYQVEGQCRCHASCSCGSPADTCTSC 1233
 RESULT 11
 ZAN_PIG
 ID_ZAN_PIG STANDARD; PRT; 2476 AA.
 AC Q28983;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Zonadhesin precursor.
 GN ZAN.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN
 RP SEQUENCE FROM N.A.; AND SEQUENCE OF 823-830; 859-872; 883-890;
 RP 920-925; 960-967; 1235-1244; 1349-1354; 1518-1532; 1624-1656;
 RP 1658-1667; 1777-1795 AND 1914-1921.
 RC STRAIN=Meishan; TISSUE=Testis;
 RX MEDLINE=96064658; PubMed=7592795;
 RA Hardy D.M., Garbers D.L.;
 RT "A sperm membrane protein that binds in a species-specific manner to
 RT the egg extracellular matrix is homologous to von Willebrand
 RT factor.";
 RL J. Biol. Chem. 270:26025-26028 (1995).
 CC -!- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA
 CC OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR
 CC SIGNALING.
 CC -!- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE
 CC APICAL REGION OF THE SPERM HEAD (BY SIMILARITY).
 CC -!- TISSUE SPECIFICITY: IN TESTIS, PRIMARILY IN HAPLOID SPERMATIDS.
 CC NOT IN LUNG, LIVER, HEART, SPLEEN, BRAIN, KIDNEY, EPIDIDYMIS.
 CC -!- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE
 CC ZONA PELLUCIDA.
 CC -!- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS,
 CC THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF
 CC SPERMATOZOEA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS.
 CC -!- DOMAIN: THE WFED DOMAINS 2 AND 3 MAY MEDIATE COVALENT
 CC OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).
 CC -!- PTM: THE MAM DOMAINS AND THE MUCIN-LIKE DOMAINS ARE MISSING
 CC FROM THE ZONADHESIN THAT BINDS TO THE EGG EXTRACELLULAR MATRIX.
 CC PROCESSING MIGHT OCCUR DURING SPERM MATURATION AND/OR
 CC CAPACITATION.
 CC -!- SIMILARITY: CONTAINS 2 MAM DOMAINS.
 CC -!- SIMILARITY: CONTAINS 4.5 WFED DOMAINS.
 CC -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
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 CC EMBL; U40024; AAC48486.1; -.
 DR HSP; P56682; 1CCV.

[illegible]

Query Match	27.9%	Score 56	DB 1	Length 2476
Best Local Similarity	31.6%	Pred. No. 20		
Matches 12	Conservative 8	Mismatches 14	Indels 4	Gaps 2

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QY      1 CSQNEYFDSLHACIP-CQ--LRCSNTPELTQRYC 34
      ||:::|::|::|::|::|::|
Db    1851 CSAHSVYTSVCVPSCLPSCQDPEGGCTGAGAPSTCEEGC 1888

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RESULT 12
YB40 HUMAN

ID	YB40	HUMAN	STANDARD;	PRT;	708	AA.
AC	QUILTO					
DT	16-OCT-2001	(Rel. 40, Created)				
DT	16-OCT-2001	(Rel. 40, Last sequence update)				
DT	15-JUN-2002	(Rel. 41, Last annotation update)				
DE	Hypothetical protein KIAA1140 (Fragment).					
GN	KIAA1140.					
OS	Homo sapiens (Human).					
OC	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;					
OC	Mammalia, Eubacteria, Primates, Catarrhini, Hominiidae, Homo.					
OX	NCBI_TaxID=9606;					
RA	(1)					
RA	SEQUENCE FROM N.A.					
RP	TISSUE=Brain.					
RC	MEBLINB=2003618; PubMed=10574461;					
RX	Hiroswa M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,					
RA	Ohara O.;					
RT	"Characterization of cDNA clones selected by the Genemark analysis					
RT	from size-fractionated cDNA libraries from human brain".					
RL	DNA Res. 6:329-336(1999).					
CC	-1 SIMILARITY: CONTAINS 8 TPR REPEATS.					
CC	-----					
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CC	-----					
DR	EMBL; AB032966; BAA86454.1; -					
DR	InterPro; IPR001440; TPR.					
DR	Pfam; PF00515; TPR; 7.					
DR	SMART; SM00028; TPR; 3.					
KW	Hypothetical protein; Repeat; TPR repeat.					
FT	NON TER	1				
FT	REPEAT	27	60	TPR 1.		
FT	REPEAT	264	297	TPR 2.		
FT	REPEAT	347	381	TPR 3.		
FT	REPEAT	383	415	TPR 4.		
FT	REPEAT	416	449	TPR 5.		
FT	REPEAT	595	628	TPR 6.		
FT	REPEAT	630	662	TPR 7.		
FT	REPEAT	663	696	TPR 8.		
SEQUENCE	708 AA;	79140 MW;	8593440B522CFIC	CRG64;		

Query Match	27.4%	Score 55	DB 1	Length 708
Best Local Similarity	38.2%	Pred. NO	8.4	
Matches 13	Conservative	5	Mismatches	14
			Indels	2
			Gaps	1

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QY      1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCGRYC 34
      | : | | | : | | | | : |
Db      277 CGKSAAYAVSLIRECV--KLRPSPDPYPLMAAKVC 308

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RESULT 13
MY9B RAT

DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)

DE MYOSIN IAD (UNCONVENTIONAL MYOSIN-5b) :
GN MYO9B OR MYR5.
OS Rattus norvegicus (Rat) :

OC Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

RC STRAIN=Sprague-Dawley; TISSUE=Brain stem, and Spinal cord;
RX MEDLINE=9518874; PubMed=7882973;
RA Reinhard J., Scheel A.A., Diekmann D., Hall A., Ruppert C.,

BAehler M.;
 RA "A novel type of myosin implicated in signalling by rho family
 RT GFases";
 RL EMBL J. 14:697-704 (1995).
 CC -!- FUNCTION: MYOSINS ARE ACTIN-BASED MOTOR MOLECULES WITH ATPASE
 CC ACTIVITY. UNCONVENTIONAL MYOSINS SERVE IN INTRACELLULAR MOVEMENTS.
 CC MAY BE INVOLVED IN THE REMODELING OF THE ACTIN CYTOSKELETON. BINDS
 CC ACTIN WITH HIGH AFFINITY BOTH IN THE ABSENCE AND PRESENCE OF ATP
 CC AND ITS MECHANOCHEMICAL ACTIVITY IS INHIBITED BY CALCIUM IONS.
 CC ALSO ACTS AS A GTPASE ACTIVATING PROTEIN ON RHO.
 CC -!- SUBCELLULAR LOCATION: IN UNDIFFERENTIATED CELLS COLOCALIZES WITH
 CC F-ACTIN IN THE CELL PERIPHERY WHILE IN DIFFERENTIATED CELLS ITS
 CC LOCALIZATION IS CYTOPLASMIC WITH THE HIGHEST LEVELS IN THE
 CC PERINUCLEAR REGION (BY SIMILARITY).
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN TESTIS, LUNG, THYMUS, BRAIN,
 CC LIVER, AND SPLEEN.
 CC -!- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
 CC BINDING DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
 CC -!- SIMILARITY: CONTAINS 4 IQ DOMAINS.
 CC -----
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 CC -----
 CC EMBL; X77609; CRA54700.1; -.
 CC HSSP; P08799; LMND.
 CC InterPro; IPR002219; DAG_PE-BIND.
 CC InterPro; IPR000048; IQ region.
 CC InterPro; IPR000159; RA domain.
 CC InterPro; IPR000198; RUGAP.
 CC InterPro; IPR001609; myosin_head.
 CC Pfam; PF00063; myosin_head; 2.
 CC Pfam; PF00130; DAG_PE-BIND; 1.
 CC Pfam; PF00612; IQ_4.
 CC Pfam; PF00620; RhoGAP; 1.
 CC Pfam; PF00788; RA; 1.
 CC PRINTS; PR00193; MYOSINHEAVY.
 CC PRODOM; PR000355; myosin_head; 2.
 CC SMART; SM00109; C1; 1.
 CC SMART; SM00242; MYSC; 1.
 CC SMART; SM00314; RA; 1.
 CC SMART; SM00324; RhoGAP; 1.
 CC PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
 CC PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
 CC PROSITE; PS50096; IQ; 3.
 CC Myosin; Repeat; ATP-binding; Calmodulin-binding; Actin-binding;
 KW Cytoskeleton; Coiled coil; GTPase activation; Phorbol-ester binding;
 KW Zinc.
 FT DOMAIN 1 940 HEAD OR MOTOR DOMAIN.
 FT DOMAIN 941 1045 NECK OR REGULATORY DOMAIN.
 FT DOMAIN 1046 1980 TAIL.
 FT DOMAIN 1841 1861 COILED COIL (POTENTIAL).
 FT DOMAIN 1918 1948 COILED COIL (POTENTIAL).
 FT DOMAIN 845 856 ACTIN-BINDING.
 FT DOMAIN 958 978 IQ 1.
 FT DOMAIN 981 1001 IQ 2.
 FT DOMAIN 1002 1024 IQ 3.
 FT DOMAIN 1025 1054 IQ 4.
 FT DOMAIN 1593 1641 PHORBOL-ESTER AND DAG BINDING.
 FT DOMAIN 1673 1822 RHO-GAP.
 FT NP_BIND 239 246 ATP (POTENTIAL).
 FT SEQUENCE 1980 AA; 225035 MW; D79FECDADF0AE0C05 CRC64;
 Query Match 26.9%; Score 54; DB 1; Length 1980;
 Best Local Similarity 52.9%; Pred. NO. 29;
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 16 PCOLRCSSNTPPLTQCR 32
 DB 1812 PCLLRCPDSDPLTSMK 1828
 RESULT 14
 MY9B MOUSE
 ID MY9B MOUSE STANDARD; PRT; 2114 AA.
 AC Q9QY06; Q9QY07; Q9QY08; Q9QY09;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myosin Ixb (Unconventional myosin-9b).
 GN MYO9B OR MYR5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10030;
 RN [1]
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND VARIANTS.
 RC STRAIN=C57BL/6;
 RX MEDLINE=20047919; PubMed=10580159;
 RA Grewal P.K., Jones A.-M., Macnouchie M., Lemmers R.J.F., Frants R.R.,
 RA Hewitt J.E.;
 RT Cloning of the murine unconventional myosin gene Myo9b and
 RT identification of alternative splicing.;
 RL Gene 240:389-398(1999).
 CC -!- FUNCTION: MYOSINS ARE ACTIN-BASED MOTOR MOLECULES WITH ATPASE
 CC MAY BE INVOLVED IN THE REMODELING OF THE ACTIN CYTOSKELETON. BINDS
 CC ACTIN WITH HIGH AFFINITY BOTH IN THE ABSENCE AND PRESENCE OF ATP
 CC AND ITS MECHANOCHEMICAL ACTIVITY IS INHIBITED BY CALCIUM IONS.
 CC ALSO ACTS AS A GTPASE ACTIVATING PROTEIN ON RHO.
 CC -!- SUBCELLULAR LOCATION: IN UNDIFFERENTIATED CELLS COLOCALIZES WITH
 CC F-ACTIN IN THE CELL PERIPHERY WHILE IN DIFFERENTIATED CELLS ITS
 CC LOCALIZATION IS CYTOPLASMIC WITH THE HIGHEST LEVELS IN THE
 CC PERINUCLEAR REGION (BY SIMILARITY).
 CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2/Q AND 3/C ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE BRAIN, HEART, MUSCLE AND
 CC INNER EAR.
 CC -!- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
 CC BINDING DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
 CC -!- SIMILARITY: CONTAINS 4 IQ DOMAINS.
 CC -----
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 CC -----
 CC EMBL; AF143687; AAF00122.1; -.
 CC EMBL; AF143685; AAF00120.1; -.
 CC EMBL; AF143686; AAF00121.1; ALT_FRAME.
 CC EMBL; AF143683; AAF00118.1; -.
 CC HSSP; P08799; LMND.
 CC MGD; MGI:106624; Myo9b.
 CC InterPro; IPR002219; DAG_PE-BIND.
 CC InterPro; IPR000048; IQ region.
 CC InterPro; IPR000159; RA domain.
 CC InterPro; IPR000198; RhoGAP.
 CC InterPro; IPR001609; myosin_head.
 CC Pfam; PF00063; myosin_head; 2.
 CC Pfam; PF00130; DAG_PE-BIND; 1.
 CC Pfam; PF00612; IQ; 4.
 CC Pfam; PF00620; RhoGAP; 1.
 CC Pfam; PF00788; RA; 1.
 CC PRINTS; PR00193; MYOSINHEAVY.

DR SMART; SM00242; MYSC; 1.
 DR SMART; SM00314; RA; 1.
 DR SMART; SM00324; RHOGAP; 1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
 DR PROSITE; PSS0081; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE; PSS0096; IQ; 3.
 KW Myosin; Repeat; ATP-binding; Calmodulin-binding; Actin-binding;
 KW Cytoskeleton; Coiled coil; GTPase activation; Phorbol-ester binding;
 KW Zinc; Alternative splicing.
 FT DOMAIN 1 939
 FT DOMAIN 940 1044
 FT DOMAIN 1045 2158
 FT DOMAIN 1046 1071
 FT DOMAIN 1880 1901
 FT DOMAIN 1959 1989
 FT DOMAIN 844 855
 FT DOMAIN 957 977
 FT DOMAIN 979 1000
 FT DOMAIN 1001 1023
 FT DOMAIN 1024 1053
 FT DOMAIN 1633 1681
 FT DOMAIN 1713 1862
 FT NP BIND 239 246
 FT VARSPPLIC 2022 2023
 FT VARSPPLIC 2024 2158
 FT CONFLICT 1917 1939
 FT CONFLICT 1947 1947
 FT CONFLICT 2040 2045
 FT CONFLICT 2049 2049
 FT CONFLICT 2067 2067
 FT CONFLICT 2157 2158
 SQ SEQUENCE 2158 AA; 243556 MW; 4978f1d70f56d28 CRC64;

Query Match 26.9%; Score 54; DB 1; Length 2158;
 Best Local Similarity 52.9%; Pred. No. 32;
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 16 PCQLRCSSNTPELTQOR 32
 |||||:||||:
 Db 1852 PCLLRCPDNDSELTSMK 1868

Search completed: January 7, 2003, 09:38:05
 Job time : 4.55639 secs

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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:34:29 ; Search time 9.62907 Seconds
(without alignments)
727.547 Million cell updates/sec

Title: US-09-855-158-7

Perfect score: 201
Sequence: 1 CSQNEYFDSLHACIPQLRCSSNTPLTCORYC 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriaph.*
17: sp_archaeap.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72.5	36.1	499	11	O88714 mus musculus
2	64.5	32.1	5374	11	Q99ND0 mus musculus
3	61	30.3	966	5	Q22378 caenorhabdi
4	60	29.9	5146	6	Q8SPM4 bos taurus
5	59.5	29.6	353	5	Q9VW81 drosophila
6	59.5	29.6	353	5	Q8SZ58 drosophila
7	59	29.4	937	5	Q9GYR5 caenorhabdi
8	58	28.9	175	11	Q8R4W8 mus musculus
9	58	28.9	1299	5	Q26489 spodoptera
10	57.5	28.6	62	5	O77419 ascaris suu
11	57.5	28.6	1376	5	Q8SZS2 drosophila
12	57.5	28.6	1679	5	Q24301 drosophila
13	57	28.4	321	10	Q9MAM0 arabidopsis
14	57	28.4	1717	5	Q26566 schistosoma
15	56	27.9	341	11	Q9D351 mus musculus
16	56	27.9	387	13	Q9PVD4 xenopus lae

17	55.5	27.6	146	12	Q9EP28
18	55.5	27.6	225	5	Q9VE40
19	55.5	27.6	955	4	Q96DN2
20	55.5	27.6	989	10	Q9ZU00
21	55.5	27.6	2820	5	Q9VLT6
22	58	27.4	330	5	O18118
23	58	27.4	344	11	Q924K7
24	58	27.4	450	4	Q8EUS3
25	58	27.4	1074	5	Q964D1
26	55	27.4	1101	5	Q964D2
27	55	27.4	1127	12	Q993K9
28	55	27.1	1513	5	O19770
29	54.5	27.1	146	12	Q9EP23
30	54.5	27.1	1752	4	Q9C091
31	54.5	27.1	1792	13	O57484
32	54.5	27.1	2155	4	O75443
33	54.5	27.1	2155	11	O08523
34	54	26.9	375	4	Q8WVD2
35	54	26.9	718	5	Q9B107
36	54	26.9	2447	5	Q9NEF9
37	54	26.9	4072	5	Q9W4Y4
38	53.5	26.6	146	12	Q9EP09
39	53.5	26.6	246	6	Q9TUX4
40	53.5	26.6	281	6	Q29475
41	53.5	26.6	285	6	Q95326
42	53.5	26.6	414	12	Q68813
43	53.5	26.6	1069	5	Q9BPS2
44	53.5	26.6	2843	4	Q9Y6R7
45	53	26.4	305	2	Q9F917

ALIGNMENTS

RESULT 1

O88714 PRELIMINARY; PRT; 499 AA.
ID AC O88714
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Gastric mucin-like protein (fragment)
GN GASTRIC MUCIN-LIKE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=STOMACH;
RA Tomasetto C., Masson R., Wendling C., Lefebvre O., Chenard M.P.,
RA Rio M.C.
RT "Identification of interactions between trefoil peptides and members
of the mucin protein family using the Yeast two-hybrid system.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ010752; CAA09343.1; -
DR HSSP; P56682; CCV
DR InterPro; IPR002919; TIL_Cysrich.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF01826; TIL; 1.
DR Pfam; PF00094; vwd; 1.
DR SMART; SM00216; vwd; 1.
FT NON_TER 1
FT NON_TER 499
SQ SEQUENCE 499 AA; 54190 MW; 04F89EF4F23EE61E CRC64;

Query Match 36.1%; Score 72.5; DB 11; Length 499;

Best Local Similarity 48.3%; Pred. NO. 0.0053;

Matches 14; Conservative

Mismatches 7; Indels 7; Gaps 1;

Oy 1 CSQNEYFDSLHACIPQLRCSSNTPLT 29

|||||

Db 430 CSQNEYFDHSEGTCTVPC-----APPTT 451

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RESULT 2
ID 099ND0 PRELIMINARY; PRT; 5374 AA.
AC 099ND0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE ZAN (Zonadhesin).
GN ZAN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=21138439; PubMed=11239002;
RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
RA Miller W., Koop B.F.;
RT "Comparative analysis of the gene-dense ACHE/TPR2 region on human
RT chromosome 7q22 with the orthologous region on mouse chromosome 5."
RT Nucleic Acids Res. 29:11352-11355(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RA Cheung T.L., Wilson M.D., Koop B.F., Hardy D.M.;
RT "Genomic Basis of Inter- and Intra-species Variation in Zonadhesin
RT Domain Structure."
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC - - STIMILARITY: CONTAINS 3 MAM DOMAINS.
DR EMBL; AF312033; AAK28824.1; -
DR MGD; MG1:106656; AAL04416.1; -
DR DR MGD; MG1:106656; ZAN.
DR InterPro; IPR0010561; EGF-like.
DR InterPro; IPR003645; FOLN.
DR InterPro; IPR000998; MAM domain.
DR InterPro; IPR003328; TILA_Cysrich.
DR InterPro; IPR002919; TILA_Cysrich.
DR InterPro; IPR001007; VWF_C.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF00629; MAM; 3.
DR Pfam; PF01826; TIL; 25.
DR Pfam; PF02345; TIL; 25.
DR Pfam; PF00094; vwd; 4.
DR SMART; SM00001; EGF-like; 1.
DR SMART; SM00274; FOLN; 21.
DR SMART; SM00137; MAM; 3.
DR SMART; SM00214; VMC; 25.
DR SMART; SM00216; VMD; 4.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 18.
DR PROSITE; PS50060; MAM_2; 3.
DR PROSITE; PS50060; MAM_2; 3.
DR BEE-like domain; Glycoprotein.
SQ SEQUENCE 5374 AA; 579536 MW; 90D2D8CFE5DE24EB CRC64;

Query Match 32.1%; Score 64.5; DB 11; Length 5374;
Best Local Similarity 35.1%; Pred. No. 0.93;
Matches 13; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

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RESULT 3
ID 022378 PRELIMINARY; PRT; 966 AA.
AC 022378;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)

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DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 102.5 kDa protein.
GN T10B10.4
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Telodermidae; Caenorhabditis.
OC NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium."
RT Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Geisel C.;
RT "The sequence of C. elegans cosmid T10B10."
RT Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission."
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U39644; AAB80360.2; -
DR HSRP; P10962; IMGT.
DR InterPro; IPR002557; Chitin_bind_Petr.
DR InterPro; IPR00794; ketoacyl-synt.
DR InterPro; IPR003571; Snake_toxin.
DR InterPro; IPR002899; WRI/EB.
DR Pfam; PF01607; GEM_14; 2.
DR SMART; SM00289; WRI; 12.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
DR PROSITE; PS00272; SNAKE_TOXIN; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 966 AA; 102460 MW; B565A3CDD25216D9 CRC64;

Query Match 30.3%; Score 61; DB 5; Length 966;
Best Local Similarity 37.5%; Pred. No. 0.63;
Matches 12; Conservative 7; Mismatches 11; Indels 2; Gaps 1;

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RESULT 4
ID 08SPM4 PRELIMINARY; PRT; 5146 AA.
AC 08SPM4;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE SCO-spndin.
GN SCO-SPONDIN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SUBCOMMISSURAL ORGAN;
RA Meinel A.;
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=SUBCOMMISSURAL ORGAN;
RX MEDLINE=20465125; PubMed=11008217;
RA Goltson S.;

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RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Latreille P., Woldmann P., Zidanic M.;
RT "the sequence of C. elegans cosmid C23G10."
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RC SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U99851; AAF99879.1; -.
KW Hypothetical protein.
SQ SEQUENCE 937 AA; 106668 MW; 1C140595DFD3ACE4 CRC64;

Query Match
Best Local Similarity 29.4%; Score 59; DB 5; Length 937;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 8 DSLHACIPCOLRCSNTPL 28
DB 439 ESVEFHPYPAERCSADGPL 459

RESULT 8
ID O8R4W8 PRELIMINARY; PRT; 175 AA.
AC O8R4W8;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE TRAF3 binding protein.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno K., Irie S., Sato T.-A.;
RT "Identification of novel TRAF3 binding protein, T3BP, which increases
RT cellular F-actin content."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF350257; AAL83914.1; -.
SQ SEQUENCE 175 AA; 18846 MW; B64EFP4B52EB93B1 CRC64;

Query Match
Best Local Similarity 28.9%; Score 58; DB 11; Length 175;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 CSQNEVFDLHACIPCOL 19
DB 22 CNOTCEPFLVRCVSCCL 40

RESULT 9
ID Q26489 PRELIMINARY; PRT; 1299 AA.
AC Q26489;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Endoprotease furin.
GN FURIN.
OS Spodoptera frugiperda (Fall armyworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Noctuidae; Noctuidae; Amphipyrinae; Spodoptera.
NCBI_TaxID=7108;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SF9;
RA Cieplik M., Klenk H.;
RT "Cloning and functional characterization of FURIN from Spodoptera

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RT frugiperda (SF9) cells."
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z68888; CAA93116.1; -.
DR HSSP; Q99405; IMPT.
DR InterPro; IPR002174; Furin-like.
DR InterPro; IPR000209; Peptidase_S8.
DR InterPro; IPR002884; P_domain.
DR Pfam; PF01483; P_1.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISTIN.
DR ProDom; PD000717; P_domain; 1.
DR SMART; SM00261; FU; 10.
DR PROSITE; PS00136; SUBTILASE_ASP; 1.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Protease.
SQ SEQUENCE 1299 AA; 142020 MW; 4C3799C7BEC572AB CRC64;

Query Match
Best Local Similarity 28.9%; Score 58; DB 5; Length 1299;
Matches 13; Conservative 5; Mismatches 9; Indels 8; Gaps 2;

OY 1 CSQNEVFDLHACIPCOLRCS-----SNTPPLTC 30
DB 1150 CSRPLRIDRLNNQCVC---CSRGVNTSTPTPTDC 1181

RESULT 10
ID O77419 PRELIMINARY; PRT; 62 AA.
AC O77419;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Chymotrypsin/elastase inhibitor-1 (Fragment).
GN ChC/E-1.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
NCBI_TaxID=6253;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98297373; PubMed=9635450;
RA Lu C.C., Nguyen T., Morris S., Hill D., Sakanari J.A.;
RT "Antisense simple: mutational bursts in the reactive site centers of
RT serine protease inhibitors from an ascarid nematode."
RL Exp. Parasitol. 89:257-261 (1998).
DR EMBL; U94499; AAC61300.1; -.
DR HSSP; P07851; IEAI.
DR InterPro; IPR002919; TIL_Cystrich.
DR Pfam; PF01826; TIL; 1.
DR NON_TER 1.
FT NON_TER 62.
SQ SEQUENCE 62 AA; 6794 MW; 154CE25A375E0B2C CRC64;

Query Match
Best Local Similarity 28.6%; Score 57.5; DB 5; Length 62;
Matches 13; Conservative 5; Mismatches 10; Indels 7; Gaps 3;

OY 1 CSQNEVFDLHACIPCOLRCS--SNTP-PLTCR 32
DB 5 CGPNEVWTE---CTGCEMKCGDPENTPCPLMKRR 35

RESULT 11
ID O85ZS2 PRELIMINARY; PRT; 1376 AA.
AC O85ZS2;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE ID3018zp.
GN FUR2.

```


OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RN [1]_TaxID=7227;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA Straub-Con M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY070553; AAL48024.1; -;
 SQ SEQUENCE 1376 AA; 149716 MW; B6704BA89A3A88FB CRC64;
 Query Match 28.6%; Score 57.5; DB 5; Length 1376;
 Best Local Similarity 34.3%; Pred. No. 3.1;
 Matches 12; Conservative 5; Mismatches 17; Indels 1; Gaps 1;
 Db 895 CSSEFYQVGEQCRPCHASCSCGNGPADTCTCTSC 929
 QY 1 CSQNEFYDLSLHACIPCOLRCSS-NTPPLTCQRYC 34
 |||:::|
 DB 895 CSSEFYQVGEQCRPCHASCSCGNGPADTCTCTSC 929
 |||:::|
 RESULT 12
 ID Q24301 PRELIMINARY; PRT; 1679 AA.
 AC Q24301;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE FUR2 protein.
 GN FUR2 OR DFUR2 OR CG4235 OR CG18734.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RN [1]_TaxID=7227;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Wan K.H., Doyle C., Rogers Y.-H.C., Blazer V.G., Champe M., Pfeiffer B.D.,
 RA Abul J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Chalkley E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lin X.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lai X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.M.G.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupeki M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirkka R., Tector C., Turner R., Ventres E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh K.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RL "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ISO-1;
 RX MEDLINE=92381036; PubMed=1512259;
 RA Roebroek A.J., Creemers J.W., Pauli I.G., Kurzik-Dumke U., Rentrop M.,
 RA Gateff E.A., Leunissen J.A., de Ven W.J.;
 RT "Cloning and functional expression of Dfurin2, a subtilisin-like
 RT proprotein processing enzyme of Drosophila melanogaster with multiple
 RT repeats of a cysteine motif.";
 RL J. Biol. Chem. 267:17208-17215 (1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ISO-1;
 RX MEDLINE=95186060; PubMed=7880443;
 RA Roebroek A.J., Ayoubi T.A., Creemers J.W., Pauli I.G., Ven W.J.;
 RT "The Dfur2 gene of Drosophila melanogaster: Genetic organization,
 RT expression during embryogenesis, and pro-protein processing activity
 RT of its translational product Dfurin2.";
 RL DNA Cell Biol. 14:223-234 (1995).
 DR EMBL; AB003502; AAF48596.1; -;
 DR EMBL; L33831; AAA69860.1; -;
 DR HSP; Q99405; IMPT.
 DR MEROPS; S08.049; -;
 DR FlyBase; FBgn004598; Fur2.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR002174; Furin-like.
 DR InterPro; IPR000209; Peptidase_S8.
 DR InterPro; IPR002884; P_domain.
 DR Pfam; PF01483; P; 1.
 DR Pfam; PF00082; Peptidase_S8; 1.
 DR PRINTS; PR00723; SUBTILISIN.
 DR ProDom; PD000717; P_domain; 1.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00261; PU; 10.
 DR PROSITE; PS00136; SUBTILASE ASP; 1.
 DR PROSITE; PS00137; SUBTILASE_HIS; 1.
 DR PROSITE; PS00138; SUBTILASE_SER; 1.
 SQ SEQUENCE 1679 AA; 183368 MW; 3F9E749F0B021CF6 CRC64;
 Query Match 28.6%; Score 57.5; DB 5; Length 1679;
 Best Local Similarity 34.3%; Pred. No. 3.8;
 Matches 12; Conservative 5; Mismatches 17; Indels 1; Gaps 1;
 QY 1 CSQNEFYDLSLHACIPCOLRCSS-NTPPLTCQRYC 34
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 DB 1198 CSSEFYQVGEQCRPCHASCSCGNGPADTCTCTSC 1232
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 RESULT 13
 ID Q9MAM0 PRELIMINARY; PRT; 321 AA.
 AC Q9MAM0;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE T25K16.14.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Dunn P., Shim P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 RA Khan S., Kim C., Altfelt H., Bel O., Chin C., Chou J., Choi E.,
 RA Com L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharbeky N.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 RA Thavert A., Toriumi M., Vayberg M., Yu G., Federspiel N.A.,
 RA Theologis A., Becker J.R.;
 RT "Genomic sequence for Archidopsis thaliana BAC T25K16 from chromosome
 RT 1";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 CC - - - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC - - - SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.
 DR EMBL: AC007123; AAF6467.1; -.
 DR HSSP: P54274; 1BA5.
 DR InterPro: IPR001005; Myb_DNA_binding.
 DR Pfam: PF00249; myb_DNA-binding; 1.
 DR SMART: SM00395; SANT; 1.
 DR PROSITE: PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE: PS00090; MYB_3; 1.
 DR DNA-binding; Nuclear protein.
 KW SEQUENCE 321 AA; 36643 MW; F3411A75DBC0B406 CRC64;
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 Query Match 28.4%; Score 57; DB 10; Length 321;
 Best Local Similarity 41.4%; Pred. No. 0.92; Mismatches 6; Gaps 1;
 Matches 12; Conservative 1; Indels 10; Gaps 1;
 QY 12 HACPQCLR-----GSSNPPLTCORYC 34
 DB 63 HACTVCDIADGVPCGSGNCPPLAVHRKC 91
 RESULT 14
 ID Q26566 PRELIMINARY; PRT; 1717 AA.
 AC Q26566;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Epidermal growth factor receptor precursor.
 GN SER.
 OS Schistosoma mansoni (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
 OC Schistosomatoidea; Schistosomatidae; Schistosoma.
 NCBI_TaxId=6183;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=PUERTO RICAN;
 RX MEDLINE=92365727; PubMed=1501637;
 RA Shoemaker C.B., Ramachandran H., Landa A., dos Reis M.G., Stein L.;
 RT "Alternative splicing of the Schistosoma mansoni gene encoding a
 RT homologue of epidermal growth factor receptor.";
 RL Mol. Biochem. Parasitol. 53:117-32(1992).
 DR EMBL: M86395; A329866.1; -.
 DR HSSP: P11382; 1FGK.
 DR InterPro: IPR000494; EGFR_L_domain.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002174; Furin-like.
 DR InterPro: IPR001245; Tyr_Pkinase.
 DR InterPro: IPR000822; ZnF_C2H2.
 DR Pfam: PF00757; Furin-like; 2.
 DR Pfam: PF00069; Pkinase; 1.
 DR Pfam: PF01030; Recep_L_domain; 2.
 DR ProDom: PD000001; Euk_Pkinase; 1.
 DR SMART: SM00261; FU; 6.
 DR SMART: SM00219; TYKC; 1.
 DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE: PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE: PS00028; ZINC FINGER C2H2_1; UNKNOWN_1.
 KW ATP-binding; Receptor_Signal; Transferase; Tyrosine-protein kinase.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 1717 EPIDERMAL GROWTH FACTOR RECEPTOR.
 SQ SEQUENCE 1717 AA; 192304 MW; 1101A338C1653D8C CRC64;

Query Match 28.4%; Score 57; DB 5; Length 1717;
 Best Local Similarity 40.9%; Pred. No. 4.6;
 Matches 9; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
 QY 1 CSONEYFDSLHACPQCLRCSSNTPPLTCORYC 22
 DB 646 CERNRYIDPQRHGLCPNCSGS 667
 RESULT 15
 ID Q9D351 PRELIMINARY; PRT; 341 AA.
 AC Q9D351;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE 7420700M05RIK protein.
 GN 7420700M05RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=IN VITRO FERTILIZED EGGS;
 RX MEDLINE=C57BL/6J; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Katsukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischiemann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Marcano Y., Mikado I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Blake J., Botfield D., Bruno M., Carninci F., de Bonaldo M.F.,
 RA Brownstein M.J., But C., Fletcher C., Fujita W., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Momtaz S.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyokawa K., Wang K.H., Welter C., Whitaker C., Wilming L.,
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK018361; BAB31177.1; -.
 DR HSSP: P08047; 1SP1.
 DR MGD: MGI:1923003; 7420700M05RIK.
 DR InterPro: IPR000822; ZnF_C2H2.
 DR Pfam: PF00096; ZF_C2H2_3.
 DR ProDom: PD000003; ZnF_C2H2_1.
 DR SMART: SM00355; ZnF_C2H2; 3.
 DR PROSITE: PS00028; ZINC FINGER C2H2_1; 2.
 DR PROSITE: PS0157; ZINC FINGER C2H2_2; 3.
 KW DNA-binding; Metal-binding; Zinc-finger.
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 Job time : 11.6291 secs

us-09-855-158-7.rai

Tue Jan 7 10:36:58 2003

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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:35:14 ; Search time 4.17544 Seconds
(without alignments)
239.587 Million cell updates/sec

Title: US-09-855-158-7
Perfect score: 201
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues 262574
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*
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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66.5	33.1	166	2	US-08-810-572A-6
2	66.5	33.1	166	4	US-09-290-333-6
3	66.5	33.1	293	2	US-08-810-572A-2
4	66.5	33.1	293	4	US-09-290-333-2
5	56	27.9	2476	2	US-08-276-967-2
6	53.5	26.6	381	4	US-09-257-580-2
7	53.5	26.6	5405	4	US-08-718-388-9
8	52	25.9	547	4	US-09-877-730-26
9	52	25.9	624	4	US-09-877-730-24
10	52	25.9	712	4	US-09-877-730-16
11	52	25.9	826	4	US-09-877-730-12
12	52	25.9	904	4	US-09-877-730-6
13	52	25.9	991	4	US-09-877-730-12
14	52	25.9	1069	4	US-09-877-730-2
15	51.5	25.6	63	1	US-08-117-080-12
16	51.5	25.6	63	1	US-08-471-329-12
17	51.5	25.6	63	2	US-08-915-142-12
18	51.5	25.6	77	2	US-08-465-380-40
19	51.5	25.6	77	2	US-08-465-380-40
20	51.5	25.6	77	2	US-08-480-478-33
21	51.5	25.6	77	2	US-08-486-397-4
22	51.5	25.6	77	2	US-08-486-397-40
23	51.5	25.6	77	2	US-08-486-399-4
24	51.5	25.6	77	2	US-08-486-399-40
25	51.5	25.6	77	2	US-08-461-965-4
26	51.5	25.6	77	2	US-08-461-965-40
27	51.5	25.6	77	2	US-08-326-110A-33

28	51.5	25.6	77	2	US-08-634-641-4	Sequence 4, Appli
29	51.5	25.6	77	2	US-08-634-641-40	Sequence 40, Appli
30	51.5	25.6	77	3	US-09-249-471-4	Sequence 4, Appli
31	51.5	25.6	77	3	US-09-249-471-40	Sequence 40, Appli
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35	51.5	25.6	77	3	US-09-249-451-40	Sequence 40, Appli
36	51.5	25.6	77	3	US-08-809-455-4	Sequence 4, Appli
37	51.5	25.6	77	3	US-08-809-455-40	Sequence 40, Appli
38	51.5	25.6	77	3	US-09-249-461-4	Sequence 4, Appli
39	51.5	25.6	77	3	US-09-249-461-40	Sequence 40, Appli
40	51.5	25.6	77	3	US-09-249-448-4	Sequence 4, Appli
41	51.5	25.6	77	3	US-09-249-448-40	Sequence 40, Appli
42	51.5	25.6	81	2	US-08-465-380-7	Sequence 7, Appli
43	51.5	25.6	81	2	US-08-480-478-36	Sequence 36, Appli
44	51.5	25.6	81	2	US-08-486-397-7	Sequence 7, Appli
45	51.5	25.6	81	2	US-08-486-399-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-810-572A-6
Sequence 6, Application US/08810572A
Patent No. 5969102
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
APPLICANT: von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,572A
FILING DATE: 28-FEB-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-810-572A-6

Query Match 33.1%; Score 66.5; DB 2; Length 166;
Best Local Similarity 32.4%; Pred. No. 0.48;

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Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;
QY 1 CSONEYFDSLHACIPQCLRGSSNTPPLTCQRYC 34
DB 34 CPEQYWDPLGTGCMSCKTCINHQ5-QRTCAFC 66

RESULT 2
US-09-290-333-6
; Sequence 6, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/290.333
; FILING DATE: 12-Apr-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq, David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-290-333-6

Query Match 33.1%; Score 66.5; DB 4; Length 166;
Best Local Similarity 32.4%; Pred. No. 0.48; 14; Indels 1; Gaps 1;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;
QY 1 CSONEYFDSLHACIPQCLRGSSNTPPLTCQRYC 34
DB 34 CPEQYWDPLGTGCMSCKTCINHQ5-QRTCAFC 66

RESULT 3
US-08-810-572A-2
; Sequence 2, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810.572A
; FILING DATE: 28-Feb-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-810-572A-2

Query Match 33.1%; Score 66.5; DB 2; Length 293;
Best Local Similarity 32.4%; Pred. No. 0.84; 14; Indels 1; Gaps 1;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;
QY 1 CSONEYFDSLHACIPQCLRGSSNTPPLTCQRYC 34
DB 34 CPEQYWDPLGTGCMSCKTCINHQ5-QRTCAFC 66

RESULT 4
US-09-290-333-2
; Sequence 2, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/290.333
; FILING DATE: 12-Apr-1999
; CLASSIFICATION: unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq. David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2
Query Match 33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 0.84;
Matches 11; Conservative 14; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEFYDLSLHACIPQLRCSNTPTLTQRYC 34
Db 34 CPSEQYDPLIGTCMSCKTICNQS-QRTCAAPC 66

RESULT 5
US-08-276-967-2
; Sequence 2, Application US/08276967
; Patent No. 5851817
; GENERAL INFORMATION:
; APPLICANT: Hardy, Daniel M.
; APPLICANT: Gathers, David L.
; TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of
; TITLE OF INVENTION: Sperm
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: Submitted Herewith
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UTSD.418/KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-276-967-2
Query Match 27.9%; Score 56; DB 2; Length 2476;
Best Local Similarity 31.6%; Pred. No. 1.2e+02;
Matches 12; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

QY 1 CSQNEFYDLSLHACIP-CQ---LRCSSNTPTLTQRYC 34
Db 1851 CSAHSVYTSCVPLSCPQDPGQCTGAGAPSTCEGC 1888

RESULT 6
US-09-257-580-2
; Sequence 2, Application US/09257580
; Patent No. 6307036
; GENERAL INFORMATION:
; APPLICANT: Yorkshire Cancer Research
; TITLE OF INVENTION: Tumour Suppressor Gene
; FILE REFERENCE: Canine p53
; CURRENT APPLICATION NUMBER: US/09/257,580
; CURRENT FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: 9804178.3
; PRIOR FILING DATE: 1998-02-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Canis
; US-09-257-580-2
Query Match 26.6%; Score 53.5; DB 4; Length 381;
Best Local Similarity 48.3%; Pred. No. 38;
Matches 14; Conservative 1; Mismatches 13; Indels 1; Gaps 1;

QY 4 NEYFDSLHACIPQLRCSNTPTLTQRCR 32
Db 118 NKLFCQLAKTC-EVQLWVSSPPPTCVR 145

RESULT 7
US-08-718-388-9
; Sequence 9, Application US/08718388
; Patent No. 6271362
; GENERAL INFORMATION:
; APPLICANT: MORIKAWA, MINORU
; APPLICANT: HARADA, NAOKI
; TITLE OF INVENTION: GENE ENCODING IGF FC REGION-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,388
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 0230-111
; TELECOMMUNICATION INFORMATION:

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Tue Jan 7 10:36:58 2003

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Page 4

TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 5405 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-718-388-9

Query Match 26.6%; Score 53.5; DB 4; Length 5405;
Best Local Similarity 34.3%; Pred. No. 4.9e+02;
Matches 12; Conservative 5; Mismatches 13; Indels 5; Gaps 2;

QY 1 CSQNEYFDSLHACI-PCQLRGSSNTPPLTCQRYC 34
DB 3934 CPQNSHYE---LCADTCSLGSALSAFLQCPDGC 3964

RESULT 8
US-09-877-730-26
Sequence 26, Application US/09877730
Patent No. 6465632
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Abuin, Alejandro
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
FILE REFERENCE: LEX-0189-USA
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,607
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 547
TYPE: PRT
ORGANISM: homo sapiens
US-09-877-730-26

Query Match 25.9%; Score 52; DB 4; Length 547;
Best Local Similarity 33.3%; Pred. No. 80;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 4 NEYFDSLHACI-PCQLRGSSNTPPLTCQRYC 33
DB 503 NSFIDAKVLSGICISRSISIPPCVCKMY 532

RESULT 9
US-09-877-730-24
Sequence 24, Application US/09877730
Patent No. 6465632
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Abuin, Alejandro
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
FILE REFERENCE: LEX-0189-USA
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US/09/877,730
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 31

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 624
TYPE: PRT
ORGANISM: homo sapiens
US-09-877-730-24

Query Match 25.9%; Score 52; DB 4; Length 624;
Best Local Similarity 33.3%; Pred. No. 91;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 4 NEYFDSLHACI-PCQLRGSSNTPPLTCQRYC 33
DB 580 NSFIDAKVLSGICISRSISIPPCVCKMY 609

RESULT 10
US-09-877-730-22
Sequence 22, Application US/09877730
Patent No. 6465632
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Abuin, Alejandro
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
FILE REFERENCE: LEX-0189-USA
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,607
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 712
TYPE: PRT
ORGANISM: homo sapiens
US-09-877-730-22

Query Match 25.9%; Score 52; DB 4; Length 712;
Best Local Similarity 33.3%; Pred. No. 1e+02;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 4 NEYFDSLHACI-PCQLRGSSNTPPLTCQRYC 33
DB 668 NSFIDAKVLSGICISRSISIPPCVCKMY 697

RESULT 11
US-09-877-730-16
Sequence 16, Application US/09877730
Patent No. 6465632
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Abuin, Alejandro
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
FILE REFERENCE: LEX-0189-USA
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,607
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 826

; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-16

Query Match 25.9%; Score 52; DB 4; Length 826;
Best Local Similarity 33.3%; Pred. No. 1.2e+02;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

OY 4 NEYFDSLHACIPQCLRCSSNTPTPLTCQRY 33
DB 782 NSFIDAKVLSCGICISRSSIPPPCVCKMY 811

RESULT 12
US-09-877-730-6
; Sequence 6, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0189-USA
; CURRENT APPLICATION NUMBER: US/09/877,730
; PRIOR FILING DATE: 2001-06-08
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 904
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-6

Query Match 25.9%; Score 52; DB 4; Length 904;
Best Local Similarity 33.3%; Pred. No. 1.3e+02;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

OY 4 NEYFDSLHACIPQCLRCSSNTPTPLTCQRY 33
DB 860 NSFIDAKVLSCGICISRSSIPPPCVCKMY 889

RESULT 13
US-09-877-730-12
; Sequence 12, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0189-USA
; CURRENT APPLICATION NUMBER: US/09/877,730
; PRIOR FILING DATE: 2001-06-08
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 991
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-12

Query Match 25.9%; Score 52; DB 4; Length 991;
Best Local Similarity 33.3%; Pred. No. 1.4e+02;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

OY 4 NEYFDSLHACIPQCLRCSSNTPTPLTCQRY 33
DB 947 NSFIDAKVLSCGICISRSSIPPPCVCKMY 976

RESULT 14
US-09-877-730-2
; Sequence 2, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0189-USA
; CURRENT APPLICATION NUMBER: US/09/877,730
; PRIOR FILING DATE: 2001-06-08
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1069
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-2

Query Match 25.9%; Score 52; DB 4; Length 1069;
Best Local Similarity 33.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

OY 4 NEYFDSLHACIPQCLRCSSNTPTPLTCQRY 33
DB 1025 NSFIDAKVLSCGICISRSSIPPPCVCKMY 1054

RESULT 15
US-08-117-080-12
; Sequence 12, Application US/08117080
; Patent No. 5482928
; GENERAL INFORMATION:
; APPLICANT: DE BOLLE, MIGUEL
; APPLICANT: BROEKAERT, WILLEM F
; APPLICANT: CAMMUE, BRUNO PA
; APPLICANT: VANDERLEIDEN, JOZEF
; APPLICANT: REES, SARAH B
; TITLE OF INVENTION: BIOTIDAL PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, NW; NINTH FLOOR, EAST
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,080
; FILING DATE:

Tue Jan 7 10:36:58 2003

us-09-855-158-7.rat

Page 6

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00423
FILING DATE: 10-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9105052.6
FILING DATE: 11-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9105684.6
FILING DATE: 19-MAR-1991
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861 3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: FIGURE 7 AMINO ACID SEQUENCE MJ-AMP2
US-08-117-080-12

Query March 25.64; Score 51.5; DB 1; Length 63;
Best Local Similarity 38.54; Pred. No. 11;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;
OY 10 LHAACIFQALGSSNT-PRLTCORYC 34
DB 24 MIRAIGNGRCNENVGPPYCCSGPC 49

Search completed: January 7, 2003, 09:42:03
Job time: 5.17544 secs

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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:40:20 ; Search time 2.55639 Seconds
(without alignments)
252.055 Million cell updates/sec

Title: US-09-855-158-7
Perfect score: 201
Sequence: 1 CSONEYFDSLHACIPQLRCSSNTPPLTCQRYC 34

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Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	201	100.0	34	10	US-09-854-864-7
2	201	100.0	51	10	US-09-854-864-6
3	201	100.0	58	10	US-09-854-864-21
4	201	100.0	81	10	US-09-854-864-13
5	201	100.0	181	10	US-09-854-864-5
6	201	100.0	184	9	US-10-077-438-1
7	201	100.0	184	9	US-10-077-438-7
8	201	100.0	184	9	US-10-077-137-1
9	201	100.0	184	9	US-10-077-137-7
10	201	100.0	283	10	US-09-854-864-9
11	181	90.0	207	9	US-10-077-438-3
12	181	90.0	207	9	US-10-077-137-3
13	136	67.7	185	10	US-09-854-864-11
14	136	67.7	281	10	US-09-854-864-1
15	93.5	46.5	117	10	US-09-854-864-12
16	66.5	33.1	37	9	US-09-779-050A-45
17	66.5	33.1	59	10	US-09-854-864-20
18	66.5	33.1	67	10	US-09-854-864-16
19	66.5	33.1	166	10	US-09-854-864-15

20	66.5	33.1	231	9	US-09-779-050A-43	Sequence 43, Appl
21	66.5	33.1	233	9	US-09-779-050A-42	Sequence 42, Appl
22	66.5	33.1	233	9	US-10-084-971-2	Sequence 2, Appl
23	66.5	33.1	233	10	US-09-879-919-22	Sequence 22, Appl
24	66.5	33.1	233	10	US-09-854-864-14	Sequence 14, Appl
25	66.5	33.1	233	10	US-09-961-376-2	Sequence 2, Appl
26	66.5	33.1	337	10	US-09-854-864-18	Sequence 18, Appl
27	59.5	29.6	418	9	US-09-886-429-2	Sequence 2, Appl
28	59.5	29.6	735	10	US-09-898-570-10	Sequence 10, Appl
29	59.5	29.6	845	10	US-09-898-570-12	Sequence 12, Appl
30	59.5	29.6	974	10	US-09-898-570-14	Sequence 14, Appl
31	59.5	29.6	1009	10	US-09-898-570-16	Sequence 16, Appl
32	59	29.4	38	9	US-09-779-050A-46	Sequence 46, Appl
33	55	27.4	162	10	US-09-798-789-10	Sequence 10, Appl
34	53.5	26.6	5405	9	US-10-025-380-1116	Sequence 1116, Ap
35	53.5	26.6	5405	10	US-09-922-217-1116	Sequence 1116, Ap
36	53	26.4	108	9	US-09-950-933A-61	Sequence 61, Appl
37	53	26.4	131	10	US-09-790-264-61	Sequence 61, Appl
38	52	25.9	115	9	US-09-950-933A-65	Sequence 65, Appl
39	51.5	25.6	136	10	US-09-893-737-302	Sequence 302, App
40	51	25.4	78	9	US-09-749-637A-324	Sequence 324, App
41	51	25.4	117	9	US-09-950-933A-62	Sequence 62, Appl
42	51	25.4	119	9	US-09-950-933A-63	Sequence 63, Appl
43	50.5	25.1	131	9	US-09-950-933A-66	Sequence 66, Appl
44	50	24.9	153	10	US-09-800-909-3	Sequence 3, Appl
45	50	24.9	153	10	US-09-884-987-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-854-864-7
; Sequence 7, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-7

Query Match 100.0%; Score 201; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CSONEYFDSLHACIPQLRCSSNTPPLTCQRYC 34
Db 1 CSONEYFDSLHACIPQLRCSSNTPPLTCQRYC 34

RESULT 2
US-09-854-864-6
; Sequence 6, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI

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Page 2

FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 6
LENGTH: 51
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-6

Query Match 100.0%; Score 201; DB 10; Length 51;
Best Local Similarity 100.0%; Pred. No. 1,6e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSONEYFDSLHACIPQOLRCSSNTPPLTCQRYC 34
DB 5 CSONEYFDSLHACIPQOLRCSSNTPPLTCQRYC 38

RESULT 3
US-09-854-864-21
Sequence 21, Application US/09854864
Patent No. US20020081296A1
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
FILE REFERENCE: BLYS/AGP-3, AND TACI
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 21
LENGTH: 58
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-21

Query Match 100.0%; Score 201; DB 10; Length 58;
Best Local Similarity 100.0%; Pred. No. 1,8e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSONEYFDSLHACIPQOLRCSSNTPPLTCQRYC 34
DB 1 CSONEYFDSLHACIPQOLRCSSNTPPLTCQRYC 34

RESULT 4
US-09-854-864-13
Sequence 13, Application US/09854864
Patent No. US20020081296A1
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
FILE REFERENCE: BLYS/AGP-3, AND TACI
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 13
LENGTH: 81
TYPE: PRT
ORGANISM: Consensus
US-09-854-864-13

Query Match 100.0%; Score 201; DB 10; Length 81;
Best Local Similarity 100.0%; Pred. No. 2,5e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSONEYFDSLHACIPQOLRCSSNTPPLTCQRYC 34
DB 1 CSONEYFDSLHACIPQOLRCSSNTPPLTCQRYC 34

RESULT 5
US-09-854-864-5
Sequence 5, Application US/09854864
Patent No. US20020081296A1
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
FILE REFERENCE: BLYS/AGP-3, AND TACI
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 5
LENGTH: 181
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-5

Query Match 100.0%; Score 201; DB 10; Length 181;
Best Local Similarity 100.0%; Pred. No. 5,1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSONEYFDSLHACIPQOLRCSSNTPPLTCQRYC 34
DB 5 CSONEYFDSLHACIPQOLRCSSNTPPLTCQRYC 38

RESULT 6
US-10-077-438-1
Sequence 1, Application US/10077438
Patent No. US20020165156A1
GENERAL INFORMATION:
APPLICANT: Mackay, Fabienne
APPLICANT: Browning, Jeffrey
APPLICANT: Ambrose, Christine
APPLICANT: Teschopp, Jurg
APPLICANT: Schneider, Pascal
APPLICANT: Thompson, Jeffrey
APPLICANT: Biogen, Inc.
APPLICANT: Apotech R&D S.A.
TITLE OF INVENTION: Baff Receptor (BCMA), An
TITLE OF INVENTION: Immunosuppressive Agent
FILE REFERENCE: A080PCT
CURRENT APPLICATION NUMBER: US/10/077,438
CURRENT FILING DATE: 2002-02-18
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/181,684
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/183,536

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; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-1

Query Match
Best Local Similarity 100.0%; Score 201; DB 9; Length 184;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPQCLRCSSNTPTLTCQRYC 34
Db 8 CSONEYFDSLHACIPQCLRCSSNTPTLTCQRYC 41

RESULT 7
US-10-077-438-7
; Sequence 7, Application US/10077438
; Patent No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; PRIOR FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-7

Query Match
Best Local Similarity 100.0%; Score 201; DB 9; Length 184;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPQCLRCSSNTPTLTCQRYC 34
Db 8 CSONEYFDSLHACIPQCLRCSSNTPTLTCQRYC 41

RESULT 8
US-10-077-137-1
; Sequence 1, Application US/10077137
; Patent No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; PRIOR FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-7

Query Match
Best Local Similarity 100.0%; Score 201; DB 9; Length 184;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 8 CSONEYFDSLHACIPQCLRCSSNTPTLTCQRYC 41

RESULT 9
US-10-077-137-7
; Sequence 7, Application US/10077137
; Patent No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; PRIOR FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-7

Query Match
Best Local Similarity 100.0%; Score 201; DB 9; Length 184;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPQCLRCSSNTPTLTCQRYC 34
Db 8 CSONEYFDSLHACIPQCLRCSSNTPTLTCQRYC 41

RESULT 10
US-09-854-864-9
; Sequence 9, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
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us-09-855-158-7.rapb

Page 4

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; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-05-12
; PRIOR FILING DATE: 2000-06-27
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-9
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Best Local Similarity 100.0%; Pred. No. 7,6e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
Db 5 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 38
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RESULT 11
US-10-077-438-3
; Sequence 3, Application US/10077438
; Patent No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoep, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; PRIOR FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-3
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Best Local Similarity 63.0%; Pred. No. 1e-13;
Matches 34; Conservative 0; Mismatches 20; Indels 20; Gaps 1;
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Oy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
Db 46 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 99
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RESULT 12
US-10-077-137-3
; Sequence 3, Application US/10077137
; Patent No. US20020172674A1
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; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoep, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; PRIOR FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-3
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Query Match 90.0%; Score 181; DB 9; Length 207;
Best Local Similarity 63.0%; Pred. No. 1e-13;
Matches 34; Conservative 0; Mismatches 20; Indels 20; Gaps 1;
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Oy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
Db 46 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 99
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RESULT 13
US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11
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Db 5 CFHSEYFDSLHACKCHLRCN--PPATCOPYC 36
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RESULT 14
US-09-854-864-10
; Sequence 10, Application US/09854864
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; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10

Query Match 67.7%; Score 136; DB 10; Length 281;
Best Local Similarity 70.6%; Pred. No. 1.4e-08;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

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DB 5 CFHSEYFDSLLHACKPCHLRCSN--PPATCQPYC 36

RESULT 15
US-09-854-864-12
; Sequence 12, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-854-864-12

Query Match 46.5%; Score 93.5; DB 10; Length 117;
Best Local Similarity 69.7%; Pred. No. 0.00037;
Matches 23; Conservative 1; Mismatches 2; Indels 7; Gaps 4;

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Title: US-09-855-158-7

Perfect score: 201
Sequence: 1 CSQNEYFDSLHACIPQLRCSSNTPLTCORVC 34

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Post-processing: Minimum Match 0%
Maximum Match 100%
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SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	201	100.0	34	1	PCT-US02-34376-11
2	201	100.0	34	1	Sequence 11, Appl
3	201	100.0	184	1	Sequence 6, Appl
4	201	100.0	184	1	Sequence 39, Appl
5	201	100.0	184	5	Sequence 2, Appl
6	201	100.0	184	6	Sequence 6, Appl
7	201	100.0	184	6	Sequence 39, Appl
8	67.5	33.6	1548	6	Sequence 2, Appl
9	66.5	33.1	33	1	Sequence 13, Appl
10	66.5	33.1	33	6	Sequence 13, Appl
11	66.5	33.1	166	6	Sequence 6, Appl
12	66.5	33.1	293	6	Sequence 22, Appl
13	66.5	33.1	293	6	Sequence 1, Appl
14	66.5	33.1	293	6	Sequence 2, Appl
15	66.5	33.1	301	6	Sequence 12, Appl
16	66.5	33.1	334	6	Sequence 8, Appl
17	66.5	33.1	366	6	Sequence 6, Appl
18	66.5	33.1	404	6	Sequence 15, Appl
19	59	25.4	34	1	Sequence 14, Appl
20	59	25.4	34	6	Sequence 14, Appl
21	55	27.4	162	6	Sequence 420, App
22	53.5	26.6	4360	5	Sequence 66993, A
23	53.5	26.6	4360	5	Sequence 66993, A
24	53	26.4	131	6	Sequence 61, Appl
25	52.5	26.1	976	6	Sequence 1565, Ap
26	51	25.4	87	1	Sequence 2251, Ap

27 51 25.4 87 6 PCT-US02-34376-11
28 51 25.4 334 1 PCT-US02-32727-21573
29 51 25.4 334 6 US-10-057-498-21573
30 50.5 25.1 133 6 US-10-057-498-21573
31 50.5 25.1 710 1 PCT-US02-29560-308
32 50 24.9 161 5 US-09-898-234B-4
33 50 24.9 161 5 US-09-899-422A-6
34 50 24.9 161 5 US-09-899-422A-6
35 50 24.9 162 5 US-09-898-234B-73
36 50 24.9 162 5 US-09-899-422A-6
37 50 24.9 162 5 US-09-899-422A-6
38 50 24.9 162 6 US-10-218-102-419
39 50 24.9 162 6 US-10-218-102-424
40 50 24.9 162 6 US-10-218-102-425
41 50 24.9 162 6 US-10-218-102-427
42 50 24.9 162 6 US-10-218-102-431
43 50 24.9 172 5 US-09-898-234B-20
44 50 24.9 172 5 US-09-899-422A-20
45 50 24.9 173 5 US-09-898-234B-16

ALIGNMENTS

RESULT 1
PCT-US02-34376-11
Sequence 11, Application PC/TUS0234376
GENERAL INFORMATION:
APPLICANT: Zhang, Gongyi
APPLICANT: Shu, Hong-Bing
APPLICANT: Liu, Yingfang
APPLICANT: Xu, Liangguo
TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
TITLE OF INVENTION: Modified Proteins and Methods Related Thereo
FILE REFERENCE: 2879-86-PCT PCT/US02/34376
CURRENT APPLICATION NUMBER: 2002-10-24
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 60/345,106
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 60/348,962
PRIOR FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: 60/354,966
PRIOR FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: 60/403,364
PRIOR FILING DATE: 2002-08-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 34
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-34376-11

Query Match 100.0%; Score 201; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQLRCSSNTPLTCORVC 34
DB 1 CSQNEYFDSLHACIPQLRCSSNTPLTCORVC 34

RESULT 2
US-10-281-053-11
Sequence 11, Application US/10281053
GENERAL INFORMATION:
APPLICANT: Zhang, Gongyi
APPLICANT: Shu, Hong-Bing
APPLICANT: Liu, Yingfang
APPLICANT: Xu, Liangguo
TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
TITLE OF INVENTION: Modified Proteins and Methods Related Thereo
FILE REFERENCE: 2879-86

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us-09-855-158-7.rapn

Page 2

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; CURRENT APPLICATION NUMBER: US/10/281,053
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,106
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/348,962
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/354,966
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/403,364
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 11
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-281-053-11
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Query Match          100.0%; Score 201; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 4,9e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CSONEYFDSLHACIPCOLRCSSTPPLTCORYC 34
Db 1 CSONEYFDSLHACIPCOLRCSSTPPLTCORYC 34
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RESULT 3
PCT-US02-34376-6
; Sequence 6, Application PC/TUS0234376
; GENERAL INFORMATION:
; APPLICANT: Zhang, Gongyi
; APPLICANT: Shu, Hong-Bing
; APPLICANT: Liu, Yingfang
; APPLICANT: Xu, Lianguo
; TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
; FILE REFERENCE: 2879-86-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/34376
; PRIOR FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,106
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/348,962
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/354,966
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/403,364
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 6
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-34376-6
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Query Match          100.0%; Score 201; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 1,5e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CSONEYFDSLHACIPCOLRCSSTPPLTCORYC 34
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RESULT 4
PCT-US02-06001-39
; Sequence 39, Application PC/TUS0206001
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Markowitz, Sanford David
; APPLICANT: Eos Biotechnology, Inc.
; APPLICANT: Case Western Reserve University
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; TITLE OF INVENTION: Novel Methods of Diagnosis of Metastatic Colorectal
; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
; FILE REFERENCE: 018501-000840PC
; CURRENT APPLICATION NUMBER: PCT/US02/06001
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/272,206
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/281,149
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/284,555
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 39
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: tumor necrosis factor receptor superfamily, member
PCT-US02-06001-39
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Query Match          100.0%; Score 201; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 1,5e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CSONEYFDSLHACIPCOLRCSSTPPLTCORYC 34
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RESULT 5
US-09-848-271-2
; Sequence 2, Application US/09848271
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven
; APPLICANT: Baker, Kevin
; TITLE OF INVENTION: Human Tumor Necrosis Factor TR18 and Methods Based Thereon
; FILE REFERENCE: PF526
; CURRENT APPLICATION NUMBER: US/09/848,271
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/254,931
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/236,038
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/201,852
; PRIOR FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 2
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-848-271-2
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Query Match          100.0%; Score 201; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 1,5e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CSONEYFDSLHACIPCOLRCSSTPPLTCORYC 34
Db 8 CSONEYFDSLHACIPCOLRCSSTPPLTCORYC 41
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RESULT 6
US-10-281-053-6
; Sequence 6, Application US/10281053
; GENERAL INFORMATION:
; APPLICANT: Zhang, Gongyi
; APPLICANT: Shu, Hong-Bing
; APPLICANT: Liu, Yingfang
; APPLICANT: Xu, Lianguo
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Tue Jan 7 10:36:59 2003

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; TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
; TITLE OF INVENTION: Modified Proteins and Methods Related Thereto
; FILE REFERENCE: 2879-86
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US/10/281,053
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,106
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/348,962
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/354,966
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/403,364
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-281-053-6

Query Match      100.0%; Score 201; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 7
US-10-087-080-39
; Sequence 39, Application US/10087080
; GENERAL INFORMATION:
; APPLICANT: Mack, David H
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Cancer Methods of Diagnosis of Metastatic Colorectal
; TITLE OF INVENTION: Cancer Compositions and Methods of Screening for
; TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
; FILE REFERENCE: 018501-080840US
; CURRENT APPLICATION NUMBER: US/10/087,080
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/272,206
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/281,149
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/284,555
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: tumor necrosis factor receptor superfamily, member
; OTHER INFORMATION: 17 (TNFRSF17)
US-10-087-080-39

Query Match      100.0%; Score 201; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 8
US-10-180-903-2
; Sequence 2, Application US/10180903

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; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: SPC6 SERINE PROTEASE GENE DISRUPTIONS,
; TITLE OF INVENTION: AND COMPOSITIONS AND METHODS RELATED THERETO
; FILE REFERENCE: R-720
; CURRENT APPLICATION NUMBER: US/10/180,903
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/300,978
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/324,820
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1548
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-180-903-2

Query Match      33.6%; Score 67.5; DB 6; Length 1548;
Best Local Similarity 37.8%; Pred. No. 2.3;
Matches 14; Conservative 4; Mismatches 14; Indels 5; Gaps 1;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 32
Db 1152 CAAVEYWDGSHRCPCPKKCRSGSPEDQCYTCPR 1188

RESULT 9
PCT-US02-34376-13
; Sequence 13, Application PC/TUS0234376
; GENERAL INFORMATION:
; APPLICANT: Zhang, Gongyi
; APPLICANT: Shu, Hong-Bing
; APPLICANT: Liu, Yingfang
; APPLICANT: Xu, Lianguo
; TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
; FILE REFERENCE: 2879-86-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/34376
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,106
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/348,962
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/354,966
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/403,364
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-34376-13

Query Match      33.1%; Score 66.5; DB 1; Length 33;
Best Local Similarity 32.4%; Pred. No. 0.26;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

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Db 1 CPBEQYWDPLLGTCMSCKTICNHQS-QRTCAAF 33

RESULT 10
US-10-281-053-13
; Sequence 13, Application US/10281053
; GENERAL INFORMATION:
; APPLICANT: Zhang, Gongyi
; APPLICANT: Shu, Hong-Bing
; APPLICANT: Liu, Yingfang

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/ APPLICANT: Xu, Liangguo
/ TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
/ FILE REFERENCE: 2879-86
/ CURRENT FILING DATE: 2002-10-24
/ PRIOR APPLICATION NUMBER: US/10/281,053
/ PRIOR FILING DATE: 2002-10-24
/ PRIOR APPLICATION NUMBER: 60/345,106
/ PRIOR FILING DATE: 2001-10-24
/ PRIOR APPLICATION NUMBER: 60/348,962
/ PRIOR FILING DATE: 2002-01-14
/ PRIOR APPLICATION NUMBER: 60/354,966
/ PRIOR FILING DATE: 2002-02-07
/ PRIOR APPLICATION NUMBER: 60/403,364
/ PRIOR FILING DATE: 2002-08-13
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn Version 3.1
/ SEQ ID NO 13
/ LENGTH: 33
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-281-053-13

Query Match      33.1%; Score 66.5; DB 6; Length 33;
Best Local Similarity 32.4%; Pred. No. 0.26;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY      1 CSQNEYPDSLHACIPQCLRCSSNTPLTCORYC 34
Db      1 CPEQYWDPLGTGCMCKTICNHQS-ORTCAAF 33

RESULT 11
US-10-293-816-6
/ Sequence 6 Application US/10293816
/ GENERAL INFORMATION:
/ APPLICANT: Bram, Richard J.
/ APPLICANT: Von, Bulow, Goltz
/ TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
/ FILE REFERENCE: 44158/254623
/ CURRENT FILING DATE: 2002-11-12
/ CURRENT APPLICATION NUMBER: US/10/293,816
/ PRIOR FILING DATE: 2001-02-14
/ PRIOR APPLICATION NUMBER: US 09/782,857
/ PRIOR FILING DATE: 1999-04-12
/ PRIOR APPLICATION NUMBER: US 08/810,572
/ PRIOR FILING DATE: 1997-03-03
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6
/ LENGTH: 166
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-293-816-6

Query Match      33.1%; Score 66.5; DB 6; Length 166;
Best Local Similarity 32.4%; Pred. No. 0.73;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY      1 CSQNEYPDSLHACIPQCLRCSSNTPLTCORYC 34
Db      34 CPEQYWDPLGTGCMCKTICNHQS-ORTCAAF 66

RESULT 12
US-10-268-951-22
/ Sequence 22 Application US/10268951
/ GENERAL INFORMATION:
/ APPLICANT: Yu, Guo-Liang, et al.
/ TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
/ FILE REFERENCE: PP253P2
/ CURRENT APPLICATION NUMBER: US/10/268,951
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/ CURRENT FILING DATE: 2002-10-11
/ PRIOR APPLICATION NUMBER: 10/082,260
/ PRIOR FILING DATE: 2002-02-26
/ PRIOR APPLICATION NUMBER: 09/879,919
/ PRIOR FILING DATE: 2001-06-14
/ PRIOR APPLICATION NUMBER: 08/815,783
/ PRIOR FILING DATE: 1997-03-12
/ PRIOR APPLICATION NUMBER: 60/328,401
/ PRIOR FILING DATE: 2001-10-12
/ PRIOR APPLICATION NUMBER: 60/293,812
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,978
/ PRIOR FILING DATE: 2001-03-23
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/254,875
/ PRIOR FILING DATE: 2000-12-13
/ PRIOR APPLICATION NUMBER: 60/241,952
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/211,537
/ PRIOR FILING DATE: 2000-06-15
/ Remaining prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 22
/ LENGTH: 293
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-268-951-22

Query Match      33.1%; Score 66.5; DB 6; Length 293;
Best Local Similarity 32.4%; Pred. No. 1.1;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY      1 CSQNEYPDSLHACIPQCLRCSSNTPLTCORYC 34
Db      34 CPEQYWDPLGTGCMCKTICNHQS-ORTCAAF 66

RESULT 13
US-10-258-368-1
/ Sequence 1 Application US/10258368
/ GENERAL INFORMATION:
/ APPLICANT: Ambrose, Christine
/ APPLICANT: Thompson, Jeffrey
/ APPLICANT: Schneider, Pascal
/ APPLICANT: Renner, Paul
/ TITLE OF INVENTION: TacI As Anti-Tumor Agent
/ FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
/ CURRENT FILING DATE: 2002-10-21
/ CURRENT APPLICATION NUMBER: US/10/258,368
/ PRIOR FILING DATE: 2000-04-27
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: PatentIn Version 3.1
/ SEQ ID NO 1
/ LENGTH: 293
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-258-368-1

Query Match      33.1%; Score 66.5; DB 6; Length 293;
Best Local Similarity 32.4%; Pred. No. 1.1;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

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Db      34 CPEQYWDPLGTGCMCKTICNHQS-ORTCAAF 66

RESULT 14
US-10-293-816-2
/ Sequence 2 Application US/10293816
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; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; FILE REFERENCE: 44158/254623
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US/10/293,816
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-293-816-2

Query Match 33.1%; Score 66.5; DB 6; Length 293;
Best Local Similarity 32.4%; Pred. No. 1.1;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 34 CPBEQYWDPLLGTCMSCKTICNHQS-QRTCAAPC 66

RESULT 15
US-10-258-368-12
; Sequence 12 Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; APPLICANT: Rennert, Paul
; TITLE OF INVENTION: Tac1 As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCI/US01/40626
; CURRENT APPLICATION NUMBER: US/10/258,368
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: USSN 60/199,946
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-258-368-12

Query Match 33.1%; Score 66.5; DB 6; Length 301;
Best Local Similarity 32.4%; Pred. No. 1.1;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 42 CPBEQYWDPLLGTCMSCKTICNHQS-QRTCAAPC 74

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Job time : 4.43108 secs

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OM protein - protein search, using sw model
Run on: January 7, 2003, 09:31:39 ; Search time 29.0301 Seconds
(without alignments)
371.797 Million cell updates/sec

Title: US-09-855-158-13
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Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*

7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*

8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*

9: /SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*

10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*

11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*

12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*

13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*

14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*

15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*

16: /SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*

17: /SID22/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*

18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*

19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*

20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*

21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*

22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	205	41.2	302	AAE00507	Human BCMA-Immunoglobulin G
2	205	41.2	302	AAE00507	Mouse IgG signal/h
3	201.5	40.5	283	AAE15488	Human BCMA-Immunoglobulin G
4	201	40.4	34	AAE15485	Human B-cell matur
5	201	40.4	51	AAE15485	Human B-cell matur
6	201	40.4	58	AAE15485	Human B-cell matur
7	201	40.4	181	AAE15484	Amino acid sequenc
8	201	40.4	184	AAE08843	A human BCMA prote
9	201	40.4	184	AAE08843	Human BCMA protein
10	201	40.4	184	AAE09241	Human BCMA protein

11	201	40.4	184	AAE00506	Human B cell matur
12	201	40.4	184	AAE00506	Human B cell matur
13	201	40.4	184	AAE00506	Human B cell matur
14	201	40.4	184	AAE00506	Human B cell matur
15	159.5	32.0	157	AAE0700	Human B cell matur
16	153	30.7	124	AAE15492	Human-murine BCMA
17	153	30.7	117	AAE15491	Human-murine B cell
18	139.5	28.0	281	AAE15489	Mouse BCMA-human i
19	136	27.3	185	AAE08844	Amino acid sequenc
20	136	27.3	185	AAE08844	Murine B cell matur
21	136	27.3	185	AAE15490	Protein of hTACI (
22	100.5	20.2	334	AAE15490	Protein of hTACI (
23	100.5	20.2	366	AAE15490	Protein of hTACI (
24	98	19.7	249	AAE15490	A murine ztnf4, a
25	96.5	19.4	301	AAE15490	Human protein SEO
26	95	19.1	256	AAE15490	Novel human diagno
27	95	19.1	351	AAE15490	Novel human diagno
28	93	18.7	166	AAE15490	Human lymphocyte s
29	93	18.7	166	AAE15490	Human TACI extrace
30	93	18.7	265	AAE15490	Human TACI splice
31	93	18.7	291	AAE15490	Human AGP-3 recept
32	93	18.7	293	AAE15490	Human lymphocyte s
33	93	18.7	293	AAE15490	Human neutrokin-a
34	93	18.7	293	AAE15490	A transmembrane ac
35	93	18.7	293	AAE15490	Human TACI protein
36	93	18.7	293	AAE15490	Human tumour necro
37	93	18.7	293	AAE15490	Human TACI-IgG Fc
38	93	18.7	293	AAE15490	Human TACI recepto
39	93	18.7	293	AAE15490	Human transmembran
40	93	18.7	293	AAE15490	Tumour necrosis fa
41	93	18.7	293	AAE15490	Human transmembran
42	93	18.7	293	AAE15490	Human AGP-3 relate
43	93	18.7	312	AAE15490	Protein of N-termi
44	93	18.7	397	AAE15498	Human TACI-immunog
45	93	18.7	404	AAE15498	Protein of a compl

ALIGNMENTS

RESULT 1
AAE00507
ID AAE00507 standard; Protein; 302 AA.
XX AAE00507;
AC AAE00507;
XX 31-JUL-2001 (first entry)
DT Human BCMA-Immunoglobulin G Fc region fusion construct.
XX Human; A proliferation inducing Ligand Receptor; APRIL-R; cytostatic;
XX gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
XX carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
XX systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
XX B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
XX organ transplantation; HIV; human immunodeficiency virus; TNF; murine;
XX tumour necrosis factor; B cell maturation protein; BCMA; fusion protein;
XX immunoglobulin G; IgG; Fc region.
XX Chimeric - Homo sapiens.
OS Chimeric - Mus sp.
FH Key Location/Qualifiers
FT 1..22 /label= Signal peptide
FT 23..302 /note= "Derived from murine Ig kappa sequence"
FT 23..302 /label= Mature_human_BCMA_IgG_Fc_fusion_protein
FT 23..75 /note= "Derived from human BCMA protein"
FT 76..302 /note= "Derived from human IgG Fc region"
FT 24..302 /note= "Derived from human IgG Fc region"

FT /label= Cysteine-rich domain
FT /note= "Derived from human BCMA"
XX
XX MO200124811-A1.
XX
XX 12-APR-2001.
XX
XX 05-OCT-2000; 2000MO-US27579.
XX
XX 06-OCT-1999; 99US-0157933.
XX 11-FEB-2000; 2000US-0181807.
XX 30-JUN-2000; 2000US-0215688.
XX
XX (BIOJ) BIOGEN INC.
XX (APOT-) APOTEC R & D SA.
XX
XX Schneider P, Thompson J, Cachero T, Ambrose C, Rennett P,
XX WPI, 2001-266242/27.
XX N-PSDB; AAD03847.
XX
XX Treating a mammal for a condition associated with undesired cell
XX proliferation such as cancer or carcinoma, comprises administering a
XX composition comprising A proliferation inducing ligand Receptor
XX (APRIL-R) antagonist -
XX
XX Example 1; Fig 3B; 85pp; English.
XX
XX The invention relates to a method of treating a mammal for a condition
XX associated with undesired cell proliferation such as cancer or
XX carcinoma. The method involves administering a composition comprising
XX A proliferation inducing ligand Receptor (APRIL-R) also referred as
XX B cell maturation protein (BCM or BCMA) antagonist that antagonises the
XX interaction between APRIL and its cognate receptor(s). This method is
XX useful for treating undesired cell proliferation such as cancer or
XX carcinoma, e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
XX prostate carcinoma, and other carcinomas whose proliferation is modulated
XX by APRIL. It is also useful for treating autoimmune diseases (Grave's
XX disease, systemic lupus erythematosus-SLE), hypertension, cardiovascular
XX diseases, renal disorders, B-cell lympho-proliferative disorders,
XX immunosuppressive diseases, organ transplantation, inflammation and
XX human immunodeficiency virus (HIV), and for treating, suppressing or
XX altering an immune response involving a signalling pathway between
XX APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
XX The present sequence is a fusion construct containing human APRIL-R
XX also referred as BCMA or BCM protein, Fc region of human immunoglobulin
XX G (IgG) and a signal sequence from murine Ig kappa cDNA.
XX
XX Sequence 302 AA;
XX
XX Query Match 41.2%; Score 205; DB 22; Length 302;
XX Best Local Similarity 67.8%; Pred. No. 2.3e-10;
XX Matches 40; Conservative 2; Mismatches 9; Indels 8; Gaps 3;
XX
XX 1 CSQNEVPSDLHACIPQCLRCSSNTPPLTCORYC-CYFDSL-----LHACPCLRCSP 53
XX Db 31 CSQNEVPSDLHACIPQCLRCSSNTPPLTCORICNASVTVNSVGVKHTCP--PCPAP 87
XX
XX RESULT 2
XX AAB60699 standard; Protein; 302 AA.
XX ID AAB60699;
XX AC AAB60699;
XX XX
XX DT 22-MAY-2001 (first entry)
XX XX
XX DE Mouse IgG signal/human BAF-R/human IgG Fc fusion protein, BAF-R-Fc.
XX KM Human BAF-R; BAF-R receptor; TNF family; immunoregulatory agent;
XX KM immune-related disorder; B-cell growth inhibitor;
XX KM B-cell maturation inhibitor; immunoglobulin production inhibitor;
XX KM autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;

KM renal disorder; immunosuppressive disorder; HIV infection;
KM organ transplantation; antiinflammatory; systemic lupus erythematosus;
KM autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
KM B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
KM lymphoma; gene therapy; cancer; tumour; IgG Fc; fusion construct.
XX
XX Chimeric - Homo sapiens.
XX OS Chimeric - Mus sp.
XX
XX MO200112812-A2.
XX
XX 22-FEB-2001.
XX
XX 16-AUG-2000; 2000MO-US22507.
XX
XX 17-AUG-1999; 99US-0149378.
XX 11-FEB-2000; 2000US-0181684.
XX 18-FEB-2000; 2000US-0183536.
XX
XX (BIOJ) BIOGEN INC.
XX (APOT-) APOTEC R & D SA.
XX
XX McKay F, Browning J, Ambrose C, Tschopp J, Schneider P,
XX Thompson J;
XX WPI, 2001-202866/20.
XX N-PSDB; AAF59999.
XX
XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
XX lympho-proliferative disorder by administering BAF-R-receptor
XX polypeptide, chimeric molecule comprising receptor or anti-BAF-R
XX antibody homolog -
XX
XX Example 4; Fig 2; 59pp; English.
XX
XX The invention relates to the use of a BAF-R receptor (BAF-R, also known
XX as BCMA) protein, or a BAF-R fusion protein as an agent for the
XX treatment of a variety of immune-related disorders. BAF-R is a member of
XX the TNF (tumour necrosis factor) family, acting as an immunoregulatory
XX agent, and also plays a role in the development of hypertension and
XX related disorders. BAF-R, fusion proteins containing it, and BAF-R-
XX specific antibodies can be used for inhibiting B-cell growth, dendritic
XX cell-induced B-cell growth and maturation, and immunoglobulin production,
XX and in the treatment of autoimmune disorders, B-cell lymphoproliferative
XX disorders, hypertension and renal disorders. The BAF-R proteins may also
XX be used in the treatment of immunosuppressive disorders and HIV
XX infection, and in patients undergoing organ transplantation. The BAF-R
XX proteins or BAF-R specific antibodies may be used for treating,
XX suppressing or altering an immune response involving a signalling pathway
XX between BAF-R and BAF-R, thereby inhibiting inflammation. Since BAF-R
XX inhibits B-cell growth and maturation it is useful for treating diseases
XX such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
XX Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
XX progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
XX human BAF-R may be used in gene therapy to treat tumours, lymphomas,
XX autoimmune disorders and inherited B-cell-associated disorders. The
XX present sequence represents the BAF-R fusion protein BAF-R-Fc,
XX comprising a mouse IgG-kappa signal sequence, residues 1-153
XX of human BAF-R and a human IgG Fc sequence.
XX
XX Sequence 302 AA;
XX
XX Query Match 41.2%; Score 205; DB 22; Length 302;
XX Best Local Similarity 67.8%; Pred. No. 2.3e-10;
XX Matches 40; Conservative 2; Mismatches 9; Indels 8; Gaps 3;
XX
XX 1 CSQNEVPSDLHACIPQCLRCSSNTPPLTCORYC-CYFDSL-----LHACPCLRCSP 53
XX Db 31 CSQNEVPSDLHACIPQCLRCSSNTPPLTCORICNASVTVNSVGVKHTCP--PCPAP 87
XX
XX RESULT 3
XX AAB15488

us-09-855-158-13.rag

Tue Jan 7 10:36:45 2003

AAE15488 standard; Protein; 283 AA.
AAE15486
12-MAR-2002 (first entry)
Human BCMA-immunoglobulin Fc region fusion protein.
Human; transmembrane activator and intracellular CAML interactor; TAC1; cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatitis; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis; fusion protein.
Homo sapiens.
WO200187979-A2.
22-NOV-2001.
14-MAY-2001; 2001WO-US15567.
12-MAY-2000; 2000US-204039P.
27-JUN-2000; 2000US-214591P.
14-MAY-2001; 2001US-0214591.
(AMGE-) AMGEN INC.
Theill LE, Yu G;
WPI; 2002-066686/09.
Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family ligand -
Disclosure; Fig 10B; 94pp; English.
The invention relates to a method for inhibiting TAC1 (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TAC1, BCMA, or the TAC1/BCMA extracellular consensus sequence, but not the extracellular region of TAC1 or BCMA. The method is useful for inhibiting B-cell or T-cell and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour, APRIL, BCMA and TAC1 antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCMA protein-immunoglobulin Fc region fusion protein.
Sequence 283 AA;
Query Match 40.5%; Score 201.5; DB 23; Length 283;
Best Local Similarity 60.6%; Pred. No. 4; 4e-10;
Matches 40; Conservative 2; Mismatches 9; Indels 15; Gaps 3;
1 CSQNEVFDLLHACIPCLRCSSNTPPLTCQYVC-CEYFDSL-
5 CSQNEVFDLLHACIPCLRCSSNTPPLTCQYCNASVNSVKGNTAGGGGDKTKTCP- 63
48 LRCSP 53

Db 64 -PCPAP 68
RESULT 4
AAE15486
ID AAE15486 standard; peptide; 34 AA.
XX AAE15486;
XX 12-MAR-2002 (first entry)
XX Human B-cell maturation (BCMA) protein cysteine-rich consensus region.
XX Human; transmembrane activator and intracellular CAML interactor; TAC1; cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatitis; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.
XX Homo sapiens.
XX WO200187979-A2.
XX 22-NOV-2001.
XX 14-MAY-2001; 2001WO-US15567.
XX 12-MAY-2000; 2000US-204039P.
XX 27-JUN-2000; 2000US-214591P.
XX 14-MAY-2001; 2001US-0214591.
XX (AMGE-) AMGEN INC.
XX Theill LE, Yu G;
XX WPI; 2002-066686/09.
XX Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family ligand -
XX Claim 1; Fig 10A; 94pp; English.
XX The invention relates to a method for inhibiting TAC1 (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TAC1, BCMA, or the TAC1/BCMA extracellular consensus sequence, but not the extracellular region of TAC1 or BCMA. The method is useful for inhibiting B-cell or T-cell and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour, APRIL, BCMA and TAC1 antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCMA protein-immunoglobulin Fc region fusion protein.
XX Sequence 34 AA;
XX Query Match 40.4%; Score 201; DB 23; Length 34;
XX Best Local Similarity 100.0%; Pred. No. 7; 8e-11;
XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQOLRCSSNTPPLTCQRYC 34
DB 1 CSQNEYFDSLHACIPQOLRCSSNTPPLTCQRYC 34

RESULT 5
AAE15485
ID AAE15485 standard; peptide; 51 AA.
XX
AC AAE15485;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human B-cell maturation (BCMA) protein extracellular domain.
XX
KW Human: transmembrane activator and intracellular CAML interactor; TACI;
KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.
XX
OS Homo sapiens.
XX
PN WO200187979-A2.
XX
PD 22-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-US15567.
XX
PR 12-MAY-2000; 2000US-204039P.
XX
PR 27-JUN-2000; 2000US-214591P.
XX
PR 14-MAY-2001; 2001US-0214591.
XX
PA (AMGE-) AMGEN INC.
XX
PI The11 LE, Yu G;
XX
PI WPI; 2002-066686/09.
XX
DR Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor
PT family ligand -
XX
PS Claim 1; Fig 10A; 94pp; English.
XX
PS The invention relates to a method for inhibiting TACI (transmembrane
XX activator and intracellular CAML interactor) and/or B cell maturation
XX protein (BCMA) activity in a mammal. The method comprises administering
XX a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
XX family ligand), having the consensus region of TACI, BCMA, or the TACI/
XX BCMA extracellular consensus sequence, but not the extracellular region
XX of TACI or BCMA. The method is useful for inhibiting activity of TACI
XX and/or BCMA in a mammal which is useful for treating B-cell or T-cell
XX lymphoproliferative disorders, one or more solid tumours such as lung,
XX gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
XX antagonists are useful for treating inflammation and immune function
XX diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
XX dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
XX disease), drug and insect sting allergy, inflammatory bowel disease
XX (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
XX sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
XX bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
XX with leucocyte infiltration of the skin or organs. The present sequence
XX is human BCMA protein extracellular domain.
XX
SQ Sequence 51 AA;

Query Match 40.4%; Score 201; DB 23; Length 51;

Best Local Similarity 100.0%; Pred. No. 1,1e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQOLRCSSNTPPLTCQRYC 34
DB 5 CSQNEYFDSLHACIPQOLRCSSNTPPLTCQRYC 38

RESULT 6
AAE15501
ID AAE15501 standard; peptide; 58 AA.
XX
AC AAE15501;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human B cell maturation protein cysteine rich extracellular region.
XX
KW Human: transmembrane activator and intracellular CAML interactor; TACI;
KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.
XX
OS Homo sapiens.
XX
PN WO200187979-A2.
XX
PD 22-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-US15567.
XX
PR 12-MAY-2000; 2000US-204039P.
XX
PR 27-JUN-2000; 2000US-214591P.
XX
PR 14-MAY-2001; 2001US-0214591.
XX
PA (AMGE-) AMGEN INC.
XX
PI The11 LE, Yu G;
XX
PI WPI; 2002-066686/09.
XX
DR Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor
PT family ligand -
XX
PS Disclosure; Fig 13; 94pp; English.
XX
PS The invention relates to a method for inhibiting TACI (transmembrane
XX activator and intracellular CAML interactor) and/or B cell maturation
XX protein (BCMA) activity in a mammal. The method comprises administering
XX a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
XX family ligand), having the consensus region of TACI, BCMA, or the TACI/
XX BCMA extracellular consensus sequence, but not the extracellular region
XX of TACI or BCMA. The method is useful for inhibiting activity of TACI
XX and/or BCMA in a mammal which is useful for treating B-cell or T-cell
XX lymphoproliferative disorders, one or more solid tumors such as lung,
XX gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
XX antagonists are useful for treating inflammation and immune function
XX diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
XX dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
XX disease), drug and insect sting allergy, inflammatory bowel disease
XX (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
XX sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
XX bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
XX with leucocyte infiltration of the skin or organs. The present sequence
XX is human BCMA cysteine-rich extracellular region.
XX
SQ Sequence 58 AA;

Query Match	40.4%;	Score 201;	DB 23;	Length 58;
Best Local Similarity	100.0%;	Pred. No. 1.2e-10;	Indels	0; Gaps
Matches	34;	Conservative	0; Mismatches	0;
1 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34				
1 CSONEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34				
DB				
RESULT 7				
ID	AAE15484			
XX	AAE15484 standard; Protein; 181 AA.			
AC	AAE15484;			
CC				
DT	12-MAR-2002 (first entry)			
DE	Human B-cell maturation (BCMA) protein.			
XX				
XX	Human; transmembrane activator and intracellular CAML interactor; TACI;			
KW	cytotoxic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;			
KW	lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;			
KW	prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;			
KW	drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;			
KW	Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;			
KW	human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;			
KW	rheumatoid arthritis; atherosclerosis.			
XX				
XX	Homo sapiens.			
XX				
Key	Location/Qualifiers			
FT	5..38			
FT	Note= "Cysteine-rich consensus region; This is region			
FT	specifically claimed as SEQ ID NO: 7 in claim 1 of			
FT	the specification"			
FT	52..72			
FT	/label= Transmembrane_domain			
XX				
XX	WO200187979-A2.			
XX				
PD	22-NOV-2001.			
XX				
PF	14-MAY-2001; 2001WO-US15567.			
XX				
PR	12-MAY-2000; 2000US-204039P.			
XX				
PR	27-JUN-2000; 2000US-214591P.			
PR	14-MAY-2001; 2001US-0214591.			
XX				
PA	(AMGE-) AMGEN INC.			
XX				
XX	Theill LE, Yu G;			
XX				
DR	WPI; 2002-066686/09.			
XX				
XX	Inhibiting activity of B cell maturation protein and/or transmembrane			
XX	activator and intracellular cyclophilin ligand interactor, by			
PT	administering a binding partner for APRIL, a tumor necrosis factor			
PT	family ligand			
XX				
PS	Disclosure; Fig 10A; 94pp; English.			
XX				
XX	The invention relates to a method for inhibiting TACI (transmembrane			
CC	activator and intracellular CAML interactor) and/or B cell maturation			
CC	protein (BCMA) activity in a mammal. The method comprises administering			
CC	a specific binding partner for APRIL (GRO), a tumour necrosis factor-TNFR			
CC	family ligand), having the consensus region of TACI, BCMA, or the TACI			
CC	BCMA extracellular consensus sequence, but not the extracellular region			
CC	of TACI or BCMA. The method is useful for inhibiting activity of TACI			
CC	and/or BCMA in a mammal which is useful for treating B-cell or T-cell			
CC	lymphoproliferative disorders, one or more solid tumours such as lung,			
CC	gastrointestinal, pancreatic or prostatic tumour. APRIL, BCMA and TACI			
CC	antagonists are useful for treating inflammation and immune function			

CC apoptosis, viral infections, inflammatory response, such as rheumatoid
 CC arthritis, inflammatory bowel disease or septic shock. BCMA is useful for
 CC identifying compounds that modulate NF- κ B expression and thus for drug
 CC designing.

Sequence 184 AA;
 40.4%; Score 201; DB 21; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3, 4e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSNTPTLCORYC 34
 8 CSQNEYFDSLHACIPCOLRCSNTPTLCORYC 41

Db

RESULT 9
 ID AAY94001 standard; Protein; 184 AA.
 AC AAY94001;
 XX
 XX 20-OCT-2000 (first entry)

DE A human BCMA protein, a B cell protein related to TACI.
 KW Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
 KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
 KW TNF4 activity; antibody production; autoimmune disease; amyloidosis;
 KW systemic lupus erythematosus; myasthenia gravis; multiple myeloma;
 KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
 KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
 KW renal neoplasia; multiple myeloma; lymphoma; light chain neurotoxicity;
 KW immune response; immunosuppression; graft rejection; joint pain;
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
 KW renal artery stenosis; occlusion; cholesterol; renal emboli.

OS Homo sapiens.
 XX
 XX
 XX WO200040716-A2.
 XX
 XX 13-JUL-2000.
 XX
 XX 07-JAN-2000; 2000WO-US00396.
 XX
 XX 07-JAN-1999; 99US-0226533.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Gross JA, Xu W, Madden K, Yee DP,
 DR WPI: 2000-452538/39.
 DR N-PSDB; AAA58559.
 XX
 XX Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
 PT renal disease, graft versus host disease, and inflammation, comprises
 PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide -
 XX
 XX Disclosure; Page 152; 175pp; English.

The present sequence represents a human BCMA protein, a B cell protein
 related to transmembrane activator and CAML-interactor (TACI) receptor.
 TACI is a tumour necrosis factor (TNF) receptor. The extracellular
 domain of BR43x2 (an isoform of TACI) receptor or BCMA (a related B cell
 protein) receptor contain a cysteine rich domain, and are used for
 inhibiting ztnf4 activity. Ztnf4 is a TNF ligand, and are used for
 for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated
 with activated or resting B lymphocytes, effector cells, or with
 antibody production. The antibody production is associated with an
 autoimmune disease selected from systemic lupus erythematosus, myasthenia
 gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity
 and BR43x2, TACI or BCMA receptor-ligand engagement is associated with

CC asthma, bronchitis, emphysema, end stage renal failure,
 CC glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy,
 CC amyloidosis, moderating immune response, immunosuppression, graft
 CC rejection, graft versus host disease, inflammation, insulin dependent
 CC diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
 CC septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies, or
 CC agonists or antagonists can be used to treat hypertension, renal artery
 CC stenosis, or occlusion, and cholesterol or renal emboli.

Sequence 184 AA;
 40.4%; Score 201; DB 21; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3, 4e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSNTPTLCORYC 34
 8 CSQNEYFDSLHACIPCOLRCSNTPTLCORYC 41

Db

RESULT 10
 ID AAE09241 standard; Protein; 184 AA.
 AC AAE09241;
 XX
 XX 19-NOV-2001 (first entry)

DE Human BCMA protein.
 KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
 KW TNFR; TACI; BCMA; therapy; cancer; leukemia; myeloma; lymphoma;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
 KW psoriasis.

OS Homo sapiens.
 XX
 XX
 XX WO200160397-A1.
 XX
 XX 23-AUG-2001.
 XX
 XX 28-NOV-2000; 2000WO-US32378.
 XX
 XX 16-FEB-2000; 2000US-018938.
 XX
 XX 22-AUG-2000; 2000US-0226986.
 XX
 XX (GENTH) GENTTECH INC.
 XX
 XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Picti RM,
 PI Yan M;
 PI WPI: 2001-541628/60.
 DR N-PSDB; AAD15902.
 DR
 XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
 PT activity, for treating autoimmune disorders and cancer, comprises
 PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
 PT antagonists -
 XX
 XX Example 2; Fig 2; 160pp; English.

The invention relates to methods of using one or more agonists or
 antagonists to modulate the activity of the members of TNF (tumour
 necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
 e.g. TACI or BCMA. The method is useful for treating pathological
 conditions or diseases associated with increased TALL-1 and APRIL
 expression or activity. TALL-1 and APRIL antagonists are used to
 block the interaction between APRIL and TALL-1 with TACI or BCMA.
 They are useful for treating a mammal suffering from cancer such
 as leukemia, lymphoma, myeloma, cancers of lung, colon and
 autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
 psoriasis and lupus erythematosus. The present sequence is human

Tue Jan 7 10:36:45 2003

CC BCM protein.
XX
SQ Sequence 184 AA;
Query Match 40.4%; Score 201; DB 22; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.4e-10; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0;
QY 1 CSQNEYFDSLHACIPQLRCSSTPPLTCQRYC 34
DB 8 CSQNEYFDSLHACIPQLRCSSTPPLTCQRYC 41
RESULT 11
AAE00506
ID AAE00506 standard; Protein; 184 AA.
XX
AC AAE00506;
XX
DT 31-JUL-2001 (first entry)
XX
DE Human B cell maturation protein (BCMA).
XX
KW Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
KW B-cell lympho-proliferative disorder; HIV; human immunodeficiency virus; TNF;
KW organ transplantation; HIV; human immunodeficiency virus; TNF;
KW tumour necrosis factor; BCMA; B cell maturation protein.
XX
OS Homo sapiens.
XX
PN WO200124811-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27579.
XX
PR 06-OCT-1999; 99US-0157933.
PR 11-FEB-2000; 2000US-0181807.
PR 30-JUN-2000; 2000US-0215688.
XX
PA (BIOJ) BIOGEN INC.
PA (APOT-) APOTECH R & D SA.
XX
PI Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
PI WPI: 2001-266242/27.
DR N-PSDB; AAD03844.
XX
PT Treating a mammal for a condition associated with undesired cell
PT proliferation such as cancer or carcinoma, comprises administering a
PT composition comprising A Proliferation Inducing Ligand Receptor
PT (APRIL-R) antagonist.
XX
PS Claim 3; Fig 3A; 85pp; English.
XX
XX The invention relates to a method of treating a mammal for a condition
XX associated with undesired cell proliferation such as cancer or
XX carcinoma. The method involves administering a composition comprising
XX A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as
XX B cell maturation protein (BCM or BCMA) antagonist that antagonises the
XX interaction between APRIL and its cognate receptor(s). This method is
XX useful for treating undesired cell proliferation such as cancer or
XX carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
XX prostate carcinoma, and other carcinomas whose proliferation is modulated
XX by APRIL. It is also useful for treating autoimmune diseases (Grave's
XX disease, systemic lupus erythematosus-SLE; hypertension, cardiovascular
XX disease, renal disorders, B-cell lympho-proliferative disorders,
XX immunosuppressive diseases, organ transplantation inflammation and
XX human immunodeficiency virus (HIV), and for treating, suppressing or
XX altering an immune response involving a signalling pathway between

CC APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
CC The present sequence is human APRIL-R also referred as BCMA or
CC BCM protein.
XX
SQ Sequence 184 AA;
Query Match 40.4%; Score 201; DB 22; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.4e-10; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0;
QY 1 CSQNEYFDSLHACIPQLRCSSTPPLTCQRYC 34
DB 8 CSQNEYFDSLHACIPQLRCSSTPPLTCQRYC 41
RESULT 12
AAB60698
ID AAB60698 standard; Protein; 184 AA.
XX
AC AAB60698;
XX
DT 22-MAY-2001 (first entry)
XX
DE Human BAFF receptor (BAFF-R).
XX
KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
KW immune-related disorder; B-cell growth inhibitor; BCMA;
KW B-cell maturation inhibitor; immunoglobulin production inhibitor;
KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
KW renal disorder; immunosuppressive disorder; HIV infection;
KW organ transplantation; anti-inflammatory; systemic lupus erythematosus;
KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
KW lymphoma; gene therapy; cancer; tumour.
XX
OS Homo sapiens.
XX
PN WO200112812-A2.
XX
PD 22-FEB-2001.
XX
PF 16-AUG-2000; 2000WO-US22507.
XX
PR 17-AUG-1999; 99US-0149378.
PR 11-FEB-2000; 2000US-0181864.
PR 18-FEB-2000; 2000US-0183536.
XX
PA (BIOJ) BIOGEN INC.
PA (APOT-) APOTECH R & D SA.
XX
PI Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
PI Thompson J;
XX
DR WPI: 2001-202866/20.
DR N-PSDB; AAF59998.
XX
PT Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
PT lympho-proliferative disorder by administering BAFF-receptor
PT polypeptide, chimeric molecule comprising receptor or anti-BAFF-R
PT antibody homolog.
XX
PS Claim 20; Fig 1; 59pp; English.
XX
XX The invention relates to the use of a BAFF receptor (BAFF-R, also known
XX as BCMA) protein, or a BAFF-R fusion protein as an agent for the
XX treatment of a variety of immune-related disorders. BAFF-R is a member of
XX the TNF (tumour necrosis factor) family, acting as an immunoregulatory
XX agent, and also plays a role in the development of hypertension and
XX related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
XX specific antibodies can be used for inhibiting B-cell growth, dendritic
XX cell-induced B-cell growth and maturation, and immunoglobulin production,
XX and in the treatment of autoimmune disorders, B-cell lymphoproliferative
XX disorders, hypertension and renal disorders. The BAFF-R proteins may also

CC be used in the treatment of immunosuppressive disorders and HIV
CC infection, and in patients undergoing organ transplantation. The BAPF-R
CC proteins or BAPF-R specific antibodies may be used for treating,
CC suppressing or altering an immune response involving a signalling pathway
CC between BAPF-R and BAPF, thereby inhibiting inflammation. Since BAPF-R
CC inhibits B-cell growth and maturation it is useful for treating diseases
CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
CC human BAPF-R may be used in gene therapy to treat tumours, lymphomas,
CC autoimmune disorders and inherited B-cell-associated disorders. The
CC present sequence represents human BAPF-R.

XX Sequence 184 AA;

Query Match 40.4%; Score 201; DB 22; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.4e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34
DB 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 41

RESULT 13

AAV71979
ID AAV71979 standard; Protein, 184 AA.

XX AAV71979;

DT 28-MAR-2001 (first entry)

XX Human B cell maturation factor (BCMA) protein.

XX Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALI-1;
KW Tumour necrosis factor and Apol-related Leucocyte expressed Ligand 1;
KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
KW haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;
KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 1..62
PI /label= Extracellular_domain

PN WO200068378-A1.

PD 16-NOV-2000.

PF 05-MAY-2000; 2000WO-US12266.

PR 06-MAY-1999; 99US-0132892.

PR 01-MAY-2000; 2000US-0201012.

PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.

PI Shu HS;

DR WPI; 2001-016094/02.

DR N-PsDB; AAD02125.

PT Isolated TALI-1 protein is used to identify compounds that regulate B

PT lymphocyte proliferation, used to treat B lymphocyte associated

PT autoimmune disorders -

PS Claim 37; Page 104-105; 112pp; English.
XX The present invention relates to Tumour necrosis factor (TNF) and
XX Apol-related Leucocyte expressed Ligand 1 (TALI-1) nucleic acid
CC

CC molecules, proteins (including homologues), and their antibodies. The
CC invention in particular relates to methods for regulating the
CC interaction between TALI-1 and TALI-1 receptors (BCMA referred as B cell
CC maturation factor) to regulate monocyte, macrophage and B lymphocyte
CC mediated immune responses. TALI-1 protein is useful for identifying
CC compounds that regulate B lymphocyte proliferation. It is also useful for
CC treating B lymphocyte associated autoimmune disorders like rheumatoid
CC arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes
CC mellitus, multiple sclerosis, myasthenia gravis, Grave's disease,
CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura,
CC Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever,
CC post-streptococcal glomerulonephritis or polyarteritis nodosa.
CC The TALI-1 protein and its corresponding nucleic acid sequence are also
CC useful in diagnostic assays.
CC The present sequence is a human B cell maturation factor (BCMA)
CC protein. It is the receptor for TALI-1 protein. BCMA gene is
CC located on chromosome 16. In human tissues, BCMA is expressed by
CC spleen and lymph nodes but not by brain, muscle, heart, lung, kidney,
CC pancreas, testis and placenta. BCMA mRNA is absent in the pro-B
CC lymphocyte stage but its expression increases with B lymphocyte
CC maturation.

SQ Sequence 184 AA;

Query Match 40.4%; Score 201; DB 22; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.4e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34
DB 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 41

RESULT 14

ABB81487
ID ABB81487 standard; Protein, 184 AA.

XX ABB81487;

DT 02-SEP-2002 (first entry)

XX Human BCMA receptor related protein SEQ ID NO:7.

XX Human; Znf712; tumour necrosis factor receptor; cytostatic;
KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
KW neuroprotective; antirheumatic; antiarthritic; antiashmatic;
KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
KW light chain neuropathy; hypertension; large vessel disease;
KW graft-versus host disease; graft rejection; Cron's disease.

XX Homo sapiens.

XX WO200238766-A2.

PD 16-MAY-2002.

PF 05-NOV-2001; 2001WO-US47018.

PR 07-NOV-2000; 2000US-246449P.

PR 20-DEC-2000; 2000US-257131P.

PR 28-JUN-2001; 2001US-301715P.

PR 29-AUG-2001; 2001US-315565P.

PA (ZYMO) ZYMOGENETICS INC.
XX Gross JA, Xu W, Henne RM, Grant FJ;
XX WPI; 2002-508212/54.
DR

Tue Jan 7 10:36:45 2003

XX Novel isolated human tumor necrosis factor receptor polypeptide, termed
PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end
PT stage renal failure or renal disease and lymphoma -
XX
XX
XX Disclosure; Page 135-136; 154pp; English.
XX
XX The present invention describes a human tumor necrosis factor receptor
CC designated ztnfr12 (I). (I) has cytostatic, immunosuppressive,
CC dermatological, anti-inflammatory, neuroprotective, antidiabetic,
CC antirheumatic, antiarthritic, antischismatic, nephrotropic and hypotensive
CC activities, and can be used in gene therapy; (I) can be used for
CC inhibiting, in a mammal, the activity of a ligand that binds ztnfr12
CC (e.g. ZTNF4), for treating disorders and diseases associated with B
CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
CC inhibiting the proliferation of tumour cells. (I) is useful for treating
CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
CC leukaemia, nephritis, and pyelonephritis, and for treating renal
CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
CC ankylosis, hypertension, large vessel diseases, graft-versus host
CC disease, graft rejection and Crohn's disease. (I) is useful for
CC modulating the immune system, for regulating B cell responses and
CC development for modulating development of other cells, antibody
CC production and cytokine production, and for modulating T and B cell
CC communication. The present sequence represents a protein which is
CC given in the exemplification of the present invention.

XX Sequence 184 AA;
SQ
Query Match 40.4%; Score 201; DB 23; Length 184;
Best Local Similarity 100.0%; Pred No. 3 4e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSQNEFYDLSLLHACIPCOLRCSNTPTLCQRYC 34
DB 8 CSQNEFYDLSLLHACIPCOLRCSNTPTLCQRYC 41

RESULT 15
AAB60700
ID AAB60700 standard; Protein; 157 AA.
AC AAB60700;
DT 22-MAY-2001 (first entry)
DE Human BAFF receptor (BAFF-R) sequence encoded by A plasmid pJST535.
XX Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
KW immune-related disorder; B-cell growth inhibitor; BCMA;
KW B-cell maturation inhibitor; immunoglobulin production inhibitor;
KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
KW renal disorder; immunosuppressive disorder; HIV infection;
KW organ transplantation; anti-inflammatory; systemic lupus erythematosus;
KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
KW lymphoma; gene therapy; cancer; tumour; plasmid pJST535.
XX Homo sapiens.
OS
XX WO200112812-A2.
XX
XX 22-FEB-2001.
XX
XX 16-AUG-2000; 2000WO-US22507.
XX
XX 17-AUG-1999; 99US-0149378.
XX 11-FEB-2000; 2000US-0181684.
XX 18-FEB-2000; 2000US-0183536.
XX

PA (BIOJ) BIOGEN INC.
PA (APOT-) APOTTECH R & D SA.
XX Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
PI Thompson J;
XX WPI; 2001-202866/20.
DR N-PSDB; AAF60000.
XX
XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
PT lympho-proliferative disorder by administering BAFF-receptor
PT polypeptide, chimeric molecule comprising receptor or anti-BAFF-R
PT antibody homolog -
XX
XX Example 1; Fig 3; 59pp; English.
XX
XX The invention relates to the use of a BAFF receptor (BAFF-R, also known
CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the
CC treatment of a variety of immune-related disorders. BAFF-R is a member of
CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
CC agent, and also plays a role in the development of hypertension and
CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
CC specific antibodies can be used for inhibiting B-cell growth, dendritic
CC cell-induced B-cell growth and maturation, and immunoglobulin production,
CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
CC disorders, hypertension and renal disorders. The BAFF-R proteins may also
CC be used in the treatment of immunosuppressive disorders and HIV
CC infection, and in patients undergoing organ transplantation. The BAFF-R
CC proteins or BAFF-R specific antibodies may be used for treating
CC suppressing or altering an immune response involving a signalling pathway
CC between BAFF-R and BAFF thereby inhibiting inflammation. Since BAFF-R
CC inhibits B-cell growth and maturation it is useful for treating diseases
CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
CC autoimmune disorders and inherited B-cell-associated disorders. The
CC present sequence represents a human BAFF-R protein sequence as encoded
CC by plasmid pJST535. However, this BAFF-R protein sequence is 27 amino
CC acids shorter than that given in AAB60696.
XX
XX Sequence 157 AA;
SQ
Query Match 32.0%; Score 159.5; DB 22; Length 157;
Best Local Similarity 90.6%; Pred. No. 1.1e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 3 QNEFYDLSLLHACIPCOLRCSNTPTLCQRYC 34
DB 7 QNEFYDLSLLHACIPCOLRCSNTPTLCQRYC 35
Search completed: January 7, 2003, 09:37:26
Job time : 29.0301 secs

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Tue Jan 7 10:36:47 2003

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OM protein - protein search, using sw model
Run on: January 7, 2003, 09:35:04 ; Search time 11.5714 Seconds
(without alignments)
672.941 Million cell updates/sec

Title: US-09-855-158-13
Perfect score: 498
Sequence: 1 CSQNEVFDLLHACIPCOLR.....SEYFDSLLHACPPATCQPYC 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	201	40.4	184	2 S43486	B-cell maturation
2	94.5	19.0	223	2 B38346	ultra-high-sulfur
3	94.5	19.0	230	2 A38346	ultra-high-sulfur
4	92.5	18.6	169	1 S18946	ultra-high-sulfur
5	91.5	18.4	186	2 A45910	ultra-high-sulfur
6	89	17.9	1574	2 T13954	MEGF6 protein - ra
7	87	17.5	1680	2 A43434	furin (EC 3.4.21.7
8	86.5	17.4	1548	2 S34583	serine proteinase
9	86	17.3	188	2 J65547	high sulfur prote
10	83	16.7	131	1 KRSH3	keratin high-sulfu
11	83	16.7	175	2 S37649	high-sulfur kerati
12	82	16.5	126	2 I46489	cysteine-rich hair
13	82	16.5	526	2 JC6133	deubiquitinating e
14	81	16.3	2823	2 T23064	hypothetical prote
15	81	16.3	2823	2 F87908	protein T22A3.8 [i
16	81	16.3	3102	2 T43291	laminin alpha chain
17	80.5	16.2	151	2 S60314	hair keratin cyste
18	80.5	16.2	937	2 I53282	gene PAC84 protein
19	80.5	16.2	1101	2 T16840	hypothetical prote
20	80.5	16.2	1798	2 S53869	laminin beta-2 cha
21	79.5	16.1	3075	2 S14458	laminin alpha-1 ch
22	79.5	16.0	965	2 S62935	hypothetical prote
23	79.5	16.0	1077	2 T41146	probable cysteine-
24	79.5	16.0	1077	2 T41146	hemocytin - silkwo
25	79.5	16.0	3133	2 S52093	Notch homolog Motc
26	78.5	15.9	861	2 A48925	hypothetical prote
27	78.5	15.8	201	2 D71190	hypothetical prote
28	78.5	15.8	294	2 T23682	hypothetical prote
29	78	15.7	572	2 T29880	hypothetical prote
	78	15.7	1188	2 D86236	protein F14N23.5 [

30	77.5	15.6	132	1 KRGT3J	keratin high-sulfu
31	77.5	15.6	177	2 S37650	high-sulfur kerati
32	77	15.5	162	2 I47107	keratin high-sulfu
33	77	15.5	172	1 KRSHHA	zonadhesin - mouse
34	77	15.5	5376	2 T42215	PAGE4A - mouse (fr
35	76.5	15.4	1513	2 I52527	hypothetical prote
36	76.5	15.4	1513	2 T23681	transcription adap
37	76.5	15.4	2414	2 A54277	high-sulfur wool m
38	76	15.3	172	2 I47106	high-sulfur wool m
39	76	15.3	182	2 I47105	furin (EC 3.4.21.7
40	76	15.3	1299	2 T43251	transcription coac
41	76	15.3	2440	2 S39182	CREB-binding prote
42	76	15.3	2441	2 S39181	otogelin - mouse
43	76	15.3	2910	2 T42214	hypothetical prote
44	75.5	15.2	654	2 T30136	adhesive ligand ep
45	75.5	15.2	1713	2 A55347	

ALIGNMENTS

RESULT 1
S43486
B-cell maturation factor - human
N;Alternate names: BCM protein; BCMA protein; BEL protein
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence revision 27-Jan-1995 #text_change 21-Jul-2000
C;Accession: S43486; S31208; S36661
R;Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
Nucleic Acids Res. 22, 1147-1154, 1994
A;Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bidirec
A;Reference number: S43486; MUID:94218235; PMID:8165126
A;Accession: S43486
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-184 <LA2>
A;Cross-references: EMBL:Z29574; NID:9471244; PIDN:CAA82690.1; PID:9471245
R;Laabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
EMBO J. 11, 3897-3904, 1992
A;Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16
A;Reference number: S31208; MUID:93010984; PMID:1396583
A;Accession: S31208
A;Molecule type: mRNA
A;Residues: 1-184 <LA2>
A;Cross-references: EMBL:Z14954; NID:929407; PIDN:CAA78679.1; PID:929408
A;Accession: S36661
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 4-184 <LA3>
A;Cross-references: EMBL:Z14955
C;Genetics:
A;Gene: GDB:BCMA
A;Cross-references: GDB:135977; OMIM:109545
A;Map position: 16p13.1-16p13.1
A;Introns: 44/1; 93/1
C;Superfamily: human B-cell maturation factor

Query Match 40.4%; Score 201; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 8.1e-11;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CSQNEVFDLLHACIPCOLRCSSNTPPLTCQRYC 34
Db 8 CSQNEVFDLLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 2
B38346
ultra-high-sulfur keratin 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change 24-Sep-1999
C;Accession: A38660; B38346
R;Wood, L.; Mills, M.; Hatzenbuehler, N.; Vogel, G.

us-09-855-158-13.rpr

Tue Jan 7 10:36:47 2003

```
RESULT 6
MEG6 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C:Accession: T13954
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: Z14126; MUID:98360089; PMID:9691030
A:Accession: T13954
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1574 <NAK>
A:Cross-references: EMBL:AB011532; NID:93449293; PIDN:BAA32462.1; PID:g3449294
A:Experimental source: strain Sprague-Dawley; brain
C:Keywords: hydrolyase; serine proteinase
C:Gene: MEG6

Query Match 17.9%; Score 89; DB 2; Length 1574;
Best Local Similarity 29.4%; Pred. No. 1.8; Indels 38; Gaps 8;
Matches 30; Conservative 9; Mismatches 38; FDSLLHACPC 47

QY 1 CSQNEYFDSLLHACIPCOL-----RCSNTPLT-----CQRYCCEY-----FDSLLHACPC 47
Db 966 CSAGAPCDVATGSCI-CPAGRWCPCAQSCPLTFLGLNCSQICTCFNGASCDSVTCQC-- 1022
QY 48 LRCSP-----PTCQYCCFHSEYFDSLLHACPPA-----TCQPYC 81
Db 1023 -HCAPGMWGPTC-----LOACPGLYGNKQCHSC 1050

RESULT 7
A43434
furin (EC 3.4.21.75) 2 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 04-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 31-Mar-2000
C:Accession: A43433
R:Roebroek, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, E.
J. Biol. Chem. 267, 17208-17215, 1992
A:Title: Cloning and functional expression of dfurin2, a subtilisin-like proprotein proc
A:Reference number: A43434; MUID:92381036; PMID:1512259
A:Accession: A43434
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1680 <ROE>
A:Cross-references: GB:M94375; NID:9157461; PID:9157462
A:Note: sequence extracted from NCBI backbone (NCBIN:111933, NCBIIP:111934)
C:Gene: Furin
C:Superfamily: keratin high-sulfur matrix protein IIIA
C:Keywords: hair

Query Match 17.5%; Score 87; DB 2; Length 1680;
Best Local Similarity 25.0%; Pred. No. 2.9; Indels 50; Gaps 9;
Matches 31; Conservative 12; Mismatches 50;

QY 1 CSQNEYFDSLLHACIPCOLRCSNTPLTTCQ-----RYC--CEYFDSLLH-----ACP--- 46
Db 1051 CPDGYFENSRRNRTVCPEPNCAS-----CODHPEYCTSCDH-HLVNHEHKYCSACFLDT 1103
QY 47 -----CLRCSPTTCQY--CFHSEYF--DLSLLHACPPA-----TC 77
Db 1104 YETEDNKAFCFHCATCNGFTDQDITCRSSRYAWQNKCLISCPDGFYADKKRLECMPC 1163
QY 78 QPYC 81
Db 1164 QEGC 1167
```

```
RESULT 8
S34583
serine proteinase (EC 3.4.21.-) PC6B - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S34583
R:Nakagawa, T.; Murakami, K.; Nakayama, K.
FEBS Lett. 327, 165-171, 1993
A:Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a t
A:Reference number: S34583; MUID:93327934; PMID:8335106
A:Accession: S34583
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1548 <NAK>
A:Cross-references: GB:D17583; NID:9407344; PIDN:BAA04507.1; PID:d1005033; PID:g440374
A:Keywords: hydrolase; serine proteinase
C:Keywords: hydrolase; serine proteinase

Query Match 17.4%; Score 85.5; DB 2; Length 1548;
Best Local Similarity 22.1%; Pred. No. 3; Indels 53; Gaps 3;
Matches 29; Conservative 6; Mismatches 42

QY 1 CSQNEYFDSLLHACIPCOLRCSNTPLTTCQRYCCEYFDSLL----- 42
Db 1152 CAAYVWDEGSHRCOPCHKKCRSGPSEDQCYTCPRFTLLNTTCVKECPGYHTDKDS 1211
QY 43 -----HACPLRCSP-----PTCQYCCFHSEYFDSLLHACPC----- 73
Db 1212 QQCVLCHSCTRCPEGPHSMQCLSCRPGWFLGKELLCQDRDGYGEGTSGRCEKCDKSK 1271
QY 74 -----PATCQ 78
Db 1272 SCRGPRPTDQ 1282

RESULT 9
JC6547
high sulfur protein B2E - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000
C:Accession: JC6547
R:Mitsu, S.; Ohuchi, A.; Adachi-Yamada, T.; Hotta, M.; Tauboi, R.; Ogawa, H.
Gene 208, 123-129, 1998
A:Title: Structure and hair follicle-specific expression of genes encoding the rat high s
A:Reference number: JC6547; MUID:98201805; PMID:9524245
A:Accession: JC6547
A:Molecule type: DNA
A:Residues: 1-188 <MIT>
A:Cross-references: DBJ:AB003753; NID:93046870; PIDN:BAA25573.1; PID:g3046871
A:Comment: This protein is a cysteine-rich, keratin associated protein.
C:Genetics:
C:Gene: b2E
C:Superfamily: keratin high-sulfur matrix protein IIIA
C:Keywords: hair

Query Match 17.3%; Score 86; DB 2; Length 188;
Best Local Similarity 22.5%; Pred. No. 0.73; Indels 62; Gaps 7;
Matches 29; Conservative 10; Mismatches 28;

QY 1 CSQNEYFDSLLHACIP-----COLRCSNTPLTTCQ-----R 32
Db 69 CSQSS-----CCQPSCCCTSCCQPTCCQNS---SCOTSCCGTSGQGGSGATSCRV 118
QY 33 YC---CEYFDSLLHACPLCRSPPTC-----QYCCFHSEYFDSLLHAC 72
Db 119 WCRPDVRVETGLPPCCVWCTPPTCCOLHHAQASCCRPSCYCGSCCRPA---CCCHCC 174
QY 73 PATCQPYC 81
Db 175 EPSCRPSC 183
```

RESULT 10
 KRSH3A3
 Keratin high-sulfur matrix protein IIIA3 - sheep
 N/Alternate names: M2.6 protein
 C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C/Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 16-Aug-1996
 C/Accession: A02840
 R/Swift: 7.5; Haylett, T.
 A/Title: Studies on the high-sulfur proteins of reduced merino wool. Amino acid sequence
 A/Reference number: A90269; MUID:74022242; PMID:4584026
 A/Accession: A02840
 A/Molecule type: protein
 A/Residues: 131 <SWA>
 A/Experimental: 131
 C/Comment: Wool and hair consist of microfibrils embedded in a rigid matrix of other proteins.
 C/Superfamily: keratin high-sulfur matrix protein IIIA
 C/Keywords: duplication, hair

Query Match
 Best Local Similarity 16.7%; Score 83; DB 1; Length 131;
 Matches 26; Conservative 12; Mismatches 35; Indels 30; Gaps 6;

QY 1 CSQNEFYDSLHACIPQQR---CSSNTPPLT-----COR-YCCSEYFDSLHA 44
 DB 18 CLOPRYRD-----PCCRPVSCQVSRPVTFRCTRPICPCRRPVCDDPCSLQEGC 71
 QY 45 CCLCRSPPTQY-----CCPHSEYFDSLHACP---PATCOP 79
 DB 72 CRPTCCFNSQAVVCRRCMAITCCQPVSVCCPCRCRPTSCOP 114

RESULT 11
 S37649
 high-sulfur keratin - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
 C/Accession: S37649
 R/Zhumbadava, B.D.; Genjig, L.V.; Gazaryan, K.G.
 A/Title: Cloning and structural characterization of human hair sulfur-rich keratin genes
 A/Reference number: S37649
 A/Accession: S37649
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 175 <ZHU>
 A/Cross-references: EMBL:X63338; NID:9311881; PTDN:CAA44938.1; PID:9311882
 C/Superfamily: keratin high-sulfur matrix protein IIIA

Query Match
 Best Local Similarity 16.7%; Score 83; DB 2; Length 175;
 Matches 22; Conservative 6; Mismatches 24; Indels 16; Gaps 5;

QY 17 COLCSSNTPPLTCORYCCSEYFDSLHACPCRLCSPPTQ---YCCF-HSEYFDSLHACP 73
 DB 25 CQPCSCRTS---CQPCSCB-----TSC---CQPCSCRTSFCQFLASQVLDQLSCCQ 71
 QY 74 PATCOPYC 81
 DB 72 PSCCETSC 79

RESULT 12
 146489
 cysteine-rich hair keratin associated protein - rabbit
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 24-Sep-1999
 C/Accession: I46489; S49201
 R/Powell, B.C.; Arthur, J.; Nesci, A.
 A/Title: Characterization of a gene encoding a cysteine-rich keratin associated protein
 A/Reference number: I46489; MUID:95228955; PMID:7536172
 A/Accession: I46489

A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-126 <POK>
 A/Cross-references: EMBL:X80035; NID:9510540; PTDN:CAA56339.1; PID:9510541
 C/Genetics:
 A/Gene: KAP4L
 C/Superfamily: ultra-high-sulfur keratin

Query Match
 Best Local Similarity 16.5%; Score 82; DB 2; Length 126;
 Matches 23; Conservative 6; Mismatches 23; Indels 24; Gaps 6;

QY 14 CIP--COLCSSNTPPLTCORYCCSEYFDSLHACPCRLCSPPTQ-----YCCPHSEYF 65
 DB 26 CRPCCCRPPQCCQ---PSCCRPTC-----ISSC---CRPCCQSVCCOPTCRPSCYI 72
 QY 66 DSLHACPPATCOPYC 81
 DB 73 SS---CCRPCCCRPTC 85

RESULT 13
 J06133
 deubiquitinating enzyme - mouse
 N/Alternate names: DOB-1 protein
 C/Species: Mus musculus (house mouse)
 C/Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 05-Nov-1999
 C/Accession: J06133
 R/Zhu, Y.; Cai, H.; M.; Papa, F.R.; Hochstrasser, M.; D'Andrea, A.D.
 A/Title: DOB-1, a deubiquitinating enzyme with growth-suppressing activity.
 A/Reference number: J06133; MUID:96194957; PMID:8622927
 A/Accession: J06133
 A/Molecule type: mRNA
 A/Residues: 1-526 <ZHU>
 A/Cross-references: GB:U41636; NID:91302629; PTDN:AGC52532.1; PID:91302630
 C/Comment: This enzyme is the first enzyme of the ubiquitin system directly implicated
 A/Genetic: dub-1
 C/Genetic: dub-1

Query Match
 Best Local Similarity 16.5%; Score 82; DB 2; Length 526;
 Matches 19; Conservative 8; Mismatches 18; Indels 8; Gaps 2;

QY 19 IACSSNTPPLTCORYCCSEYFDSLHACPCRLCSPPTQYCCPHSEYFDSLHA 71
 DB 66 LQCLTHRPPL-----ADVWLQSHSQC--CSPECKLCAMEALVTQSLHS 110

RESULT 14
 T23064
 hypothetical protein T22A3.8 - Caenorhabditis elegans (fragment)
 C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
 C/Accession: T23064; T25096
 R/Barron, K.
 A/Title: The EMBL Data Library, October 1997
 A/Reference number: T23064
 A/Accession: T23064
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-2823 <MTL>
 A/Cross-references: EMBL:AL008585; PTDN:CAA15432.1; GSPDB:GN00019; CESP:T22A3.8
 R/McMurry, A.
 A/Title: The EMBL Data Library, October 1996
 A/Reference number: T25096
 A/Accession: T25096
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-2823 <MTL>
 A/Cross-references: EMBL:Z81125; PTDN:CAB03385.1; GSPDB:GN00019; CESP:T22A3.8

US-09-855-158-13.rpt

Tue Jan 7 10:36:47 2003

A:Experimental source: clone T22A3
C:Genetics:
A:Gene: CESP:T22A3.8
A:Map position: 1
A:Introns: 45/1; 282/2; 312/3; 416/2; 1255/3; 1329/3; 1418/3; 1776/2; 1988/2; 2760/2
C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

Query Match 16.3%; Score 81; DB 2; Length 2823;
Best Local Similarity 27.7%; Pred. No. 14;
Matches 26; Conservative 10; Mismatches 32; Indels 26; Gaps 7;
QY 1 CSQNEYFDSLHACIPCOLRCSNTPL---TCQRYCCEYFDSLHACPLRC-----SPP 53
Db 873 CSDGFEDPLTGKIEC--TCNGNIDPMGIGNC-----DS--ETGKCLKICGHTIGD 920
QY 54 TCQYCCFHFSEYFDSLHACPPATC-----QPYC 81
Db 921 SCESCKEH-HWGNALHTCKPCGCHTQGA VNPQC 953

RESULT 15
protein T22A3.8 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-Aug-2001
C:Accession: F87908
R:anonymus, The C. elegans Sequencing Consortium.
S:PubMed, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: F87908
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2823 <STO>
A:Cross-references: GB:chr_1; PIDN:CAAL5432.1; PID:g3924779; GSPDB:GN00019; CESP:T22A3.8
A:Accession: E87908
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2823 <ST2>
A:Cross-references: GB:chr_1; PIDN:CAB03385.1; PID:g3924881; GSPDB:GN00019; CESP:T22A3.8
C:Genetics:
A:Gene: T22A3.8
A:Map position: 1
C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

Query Match 16.3%; Score 81; DB 2; Length 2823;
Best Local Similarity 27.7%; Pred. No. 14;
Matches 26; Conservative 10; Mismatches 32; Indels 26; Gaps 7;
QY 1 CSQNEYFDSLHACIPCOLRCSNTPL---TCQRYCCEYFDSLHACPLRC-----SPP 53
Db 873 CSDGFEDPLTGKIEC--TCNGNIDPMGIGNC-----DS--ETGKCLKICGHTIGD 920
QY 54 TCQYCCFHFSEYFDSLHACPPATC-----QPYC 81
Db 921 SCESCKEH-HWGNALHTCKPCGCHTQGA VNPQC 953

Search completed: January 7, 2003, 09:41:10
Job time : 13.5714 secs

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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:31:59 ; Search time 6.09023 Seconds
(without alignments)
551.635 Million cell updates/sec

Title: US-09-855-158-13
Perfect score: 498
Sequence: 1 CSQNEYFDLLHACIPQCLR.....SEYFDSLLHACPPATCQPYC 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	201	40.4	184	1	Q02223
2	136	27.3	185	1	Q88472
3	98	19.7	249	1	Q9235
4	93	18.7	293	1	Q4836
5	92.5	18.6	169	1	P26371
6	91	18.3	194	1	Q75690
7	87	17.5	1680	1	P30432
8	86.5	17.4	1877	1	Q04532
9	83	16.7	131	1	P02441
10	82	16.5	526	1	Q61068
11	81	16.3	1587	1	Q9966
12	80.5	16.2	1937	1	Q63415
13	80.5	16.1	3075	1	P25391
14	80	16.0	965	1	P53971
15	79.5	16.0	3133	1	P98092
16	79.5	15.9	1696	1	Q94315
17	79	15.6	132	1	P02442
18	77.5	15.6	139	1	Q43609
19	77.5	15.6	171	1	P02438
20	77	15.5	5376	1	Q08759
21	77	15.4	2414	1	Q09472
22	76.5	15.4	2441	1	P45481
23	76	15.3	2441	1	Q16787
24	75.5	15.2	1713	1	Q9r0b6
25	75	15.1	1581	1	P11047
26	75	15.1	1609	1	Q28065
27	74.5	15.0	610	1	P07942
28	74	14.9	1786	1	Q92793
29	74	14.9	2442	1	Q9qkv9
30	73.5	14.8	313	1	Q61292
31	73.5	14.8	1799	1	Q91xv9
32	72.5	14.6	969	1	P29122
33	72.5	14.6	1592	1	Q98930

P07204 homo sapien
P98167 bos taurus
P08069 homo sapien
Q03376 chironomus
Q61789 mus musculus
P98164 homo sapien
P19214 plasmodium
P80321 medicago sc
P07851 ascaris suu
Q92832 homo sapien
Q00174 drosophila
Q41065 pisum sativ

ALIGNMENTS

RESULT 1	ID	TRI7_HUMAN	STANDARD	PRT	184 AA
AC	Q02223				
DT	01-JUL-1993	(Rel. 26, Created)			
DT	01-JUL-1993	(Rel. 26, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 17 (B-cell maturation protein).				
DE	TNFRSF17 OR BCMA OR BCM.				
GN	Homo sapiens (Human).				
OS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OC	NCBI_TaxID=9606;				
OX	[1]				
RC	SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION.				
RC	Tissue=Peripheral blood leukocytes, and Lymph node;				
RC	MEDLINE=93010984; PubMed=1396583;				
RA	Laabi Y, Gras M.P., Carbonnel F., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;				
RA	"A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma.";				
RL	EMBO J. 11:3897-3904(1992).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=94218235; PubMed=8165126;				
RA	Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;				
RT	"The BCMA gene preferentially expressed during B lymphoid maturation, is bidirectionally transcribed.";				
RL	Nucleic Acids Res. 22:1147-1154(1994).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=9425270; PubMed=10493829;				
RA	Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R., Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L., Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S., Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;				
RT	"Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";				
RL	Genomics 60:295-308(1999).				
RN	[4]				
RP	SEQUENCE FROM N.A., AND VARIANT THR-153.				
RP	MEDLINE=21419161; PubMed=11528522;				
RA	Kawasaki A., Tsuchiya N., Fukazawa N., Tokunaga K.;				
RT	"Presence of four major haplotypes in human BCMA gene: lack of association with systemic lupus erythematosus and rheumatoid arthritis.";				
RL	Genes Immun. 2:276-279(2001).				
RN	[5]				
RP	FUNCTION.				
RP	MEDLINE=20363816; PubMed=10903733;				
RA	Hatzoglou A., Rousset J., Bourgeade M.-F., Rogier E., Madry C., Inoue J., Devereux O., Tsapis A.;				
RT	"TNF receptor family member BCMA (B cell maturation) associates with TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38				

RT mitogen-activated protein kinase.";
 RL J. Immunol. 165:1322-1330(2000).
 RN [6]
 RP FUNCTION
 RX MEDLINE=20259066; PubMed=10981128;
 RA Gross J.A., Johnston J., Mukri S., Enselman R., Dillon S.R.,
 RA Madden K., Xu W., Parrish-Novak J., Foster D., Lotton-Dav C.,
 RA Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H.,
 RA Harrison K., Kandevoel W., Clegg C.H.,
 RT "TACI and BCMA are receptors for a TNF homologue implicated in B-cell
 RT autoimmune disease.";
 RL Nature 404:995-999(2000).
 RN [7]
 RP FUNCTION, AND INTERACTION WITH APRIL AND BAFF.
 RX MEDLINE=21170294; PubMed=10973284;
 RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
 RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
 RA Boyle W.J., Sarosi I., Heu H., Senaldi G., Theill L.E.,
 RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
 RT humoral immunity.";
 RL Nat. Immunol. 1:252-256(2000).
 RN [8]
 RP INTERACTION WITH TRAF5 AND TRAF6.
 RX MEDLINE=20381353; PubMed=10908663;
 RA Shu H.-B., Johnson H.,
 RT "B-cell maturation protein is a receptor for the tumor necrosis factor
 RT family member TALL-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
 CC -1- FUNCTION: Receptor for TNFSF13B/Byls/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK.
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane
 CC and perinuclear Golgi-like structures.
 CC -1- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
 CC cells or monocytes.
 CC -1- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS
 CC CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;P13)
 CC WHICH INVOLVES BCMA AND IL2.
 CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
 CC -----
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 CC -----
 DR EMBL: Z14934; CAU78679.1; -
 DR EMBL: Z28575; CA82691.1; -
 DR EMBL: Z28574; CA82690.1; -
 DR EMBL: U05742; AAB67251.1; -
 DR EMBL: AB052772; BAB60895.1; -
 DR PIR: S31208; S31208.
 DR PIR: S31209; S31209.
 DR Genew; HGNC:11913; TNFRSF17.
 DR MM; 109545; -
 KW Receptor; Immune response; Proto-oncogene; Signal-anchor;
 KW Transmembrane; Chromosomal translocation; Polymorphism;
 KW EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 1 54
 FT TRANSMEM 55 77
 FT SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT REPEAT 78 184
 FT SITE 3 4
 FT BREAKPOINT FOR TRANSLOCATION TO FORM
 FT INTERLEUKIN 2/BCM ONCOGENE.
 FT BY SIMILARITY.
 FT DISULFID 8 21
 FT DISULFID 24 37
 FT DISULFID 28 41
 FT VARIANT 153 153
 FT A->T.
 FT /FTID=VAR_012234.
 SQ SEQUENCE 184 AA; 20138 MW; 277AF1E2767D932 CRC64;

Query Match 40.4%; Score 201; DB 1; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4-2e-13;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 CSNFFPSLHACTPOLRCSSWTPPLTCORC 34
 Db 8 CSNFFPSLHACTPOLRCSSWTPPLTCORC 41
 RESULT 2
 TR17 MOUSE STANDARD; PRT; 185 AA.
 ID TR17 MOUSE
 AC O88472;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 17 (B-cell
 DE maturation protein).
 GN TNFRSF17 OR BCMA OR BCM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=BAIB/C; TISSUE=spleen
 RX MEDLINE=99061155; PubMed=9846698;
 RA Madry C., Laabli Y., Callebaut I., Roussel J., Hatzoglou A.,
 RA Le Contat M., Morron J.P., Berger R., Tsapis A.,
 RT "The characterization of murine BCMA gene defines it as a new member
 RT of the tumor necrosis factor receptor superfamily.";
 RL Int. Immunol. 10:1693-1702(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Colon
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi S., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochava H.,
 RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schmitt L.M., Strubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Oikido T., Furuno M., Kono H., Baldarelli R., Baisn G.,
 RA Blake J., Boffelli D., Bojunga N., Carimni P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann W., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons F., Marchionni L., Mashima U., Mazzarelli J., Mombere P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlschki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: Receptor for TNFSF13B/Byls/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK (By similarity).
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Detected in spleen, thymus, bone marrow and
 CC heart and at lower levels in kidney and lung.
 CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
 CC -----
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DR EMBL; AF061505; AAC23799.1;
DR EMBL; AF061505; AAC23799.1;
DR EMBL; AK020247; BAB32038.1;
DR MGD; MG1:1343050; Tnfrrsf17.
DR MGD; MG1:1343050; Tnfrrsf17.
KW Receptor; Immune response; Signal-anchor; Transmembrane;
Alternative splicing.

DOMAIN	1	49	EXTRACELLULAR (POTENTIAL)
FT	50	70	SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
FT			(POTENTIAL)
FT			CYTOPLASMIC (POTENTIAL)
FT	71	185	TNFR-CYS.
DOMAIN	4	36	BY SIMILARITY.
REPEAT	5	18	BY SIMILARITY.
DISULFID	21	32	BY SIMILARITY.
DISULFID	25	36	BY SIMILARITY.
FT	87	91	MISSING (IN ISOFORM 2).
VARSPIC			
SEQUENCE	185 AA;	20442 MW;	8606352B4FD26A8E CRC64;
SO			

Query Match	27.3%;	Score 136;	DB 1;	Length 185;
Best Local Similarity	70.6%;	Pred. No. 9.1e-07;		
Matches	24;	Conservative	2;	Mismatches 6;
Indels				
Gaps				

RESULT 3	
T13X MOUSE	
ID T13X MOUSE STANDARD; PRT; 249 AA.	
AC Q9ET35; Q9DBZ3;	
DT 15-JUN-2002 (Rel. 41, Created)	
DT 15-JUN-2002 (Rel. 41, Last sequence update)	
DT 15-JUN-2002 (Rel. 41, Last annotation date)	
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane	

DE activator and CAML interactor.1.
GN TNFRSF13B OR TACI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Spleen.
RC MEDLINE=21177254; PubMed=10891172;
RX MEDLINE=21177254; PubMed=10891172; Ashkenazi A.

RA Yan M., Marsters S.A., Griewal I.S., Wang H.; *Immunity* 1999, 10: 1-11.

RA Ditt V.M.; *Cell* 1998, 94: 189-192.

RT "Identification of a receptor for BlyS demonstrates a crucial role in humoral immunity."; *Cell* 1999, 97: 127-137.

RT humoral immunity."; *Nat Immunol.* 1:37-41(2000).

PL

12] SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Lung;
RC MEDLINE=21085660; PubMed=11217851;
RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arawaka T., Haraoka A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Komachi Y., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bonin H., Kakawa T., Saito R.,
RA Kadota K., Matsuda H.A., Asamura-Goto, C., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland Y., Nikaide I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Maruyama Y., Niki K., Tomita M., Wagner L., Washio T.,
RA Schumi L., Stadel F., Suzuki R., Tomita M., Baldarelli R., Barsh G.,
RA Sakai Y., Baffelli D., Bejunga N., Carninci P., de Bonaldo M.F.,
RA Blakesley R., Bickel S., Bickel S., Fujita M., Gariboldi M.,
RA Blakesley M.J., Bult C., Fletcher C., Fujita A., Kamiya M., Lee N.H.,
RA Guertinch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
PA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Storch K.-F.,
PA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,

RESULT 4	STANDARD;	PRT;	293 AA.
1	133X_HUMAN		
2	133X_HUMAN		
3	014836;		
4	15-JUN-2002 (Rel. 41, Created)		
5	15-JUN-2002 (Rel. 41, Last sequence update)		
6	15-JUN-2002 (Rel. 41, Last annotation update)		
7	Tumor necrosis factor receptor superfamily member 13B (Transmembrane		
8	acid, type I and CAML interactor).		
9	TNFRSF13B OR TNCT.		
10	Homo sapiens (human)		
11	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
12	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
13	NCBI_TaxId=9606;		
14	(1)		
15	SEQUENCE FROM N.A.		
16	TISSUE=B-cell;		
17	MEDLINE=97458245; PubMed=9311921;		
18	von Buelow G.-U., Bram R.J.;		
19	"NF-AT activation induced by a CAML-interacting member of the tumor		
20	necrosis factor receptor superfamily.";		
21	Science 278:138-141(1997).		
22	(2)		
23	SEQUENCE FROM N.A.		
24	TISSUE=Blood;		
25	Straussberg R.;		
26	Submitted (APR-2002) to the EMBL/Genbank/DBJ database.		
27	(3)		
28	FUNCTION		
29	MEDLINE=20519647; PubMed=10956646;		
30	Wu Y., Bressette D., Carrell J.A., Kaufman T., Feng P., Taylor K.,		
31	Gan Y., Cho Y.H., Garcia A.D., Goliatz E., Dinke D., Lafleur D.,		
32	Migone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J.,		
33	Olsen H.S., Kanakaraj P., Moore P.A., Baker K.P.;		
34	"Tumor necrosis factor (TNF) receptor superfamily member TNCT is a		
35	high affinity receptor for TNF family members APRIL and BLYS.";		
36	J. Biol. Chem. 275:35478-35485(2000).		
37	(4)		
38	FUNCTION.		
39	MEDLINE=21170294; PubMed=10973284;		
40	Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,		
41	McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo Y., Stolina M.,		
42	Boyle W.J., Sarsosi I., Hsu H., Senaldi G., Theill L.E.;		
43	"APRIL and TNF-1 and receptors BCMA and TNCT: system for regulating		
44	humoral immunity".		
45	Nat. Immunol. 1:252-256(2000).		
46	(1) FUNCTION: Receptor for TNFRSF13/APRIL and TNFRSF13B/TNAIL/BAFF/BLYS		
47	that binds both ligands with similar high affinity. Mediates		
48	calcineurin-dependent activation of NF-AT, as well as activation		
49	of NF-kappa-B and AP-1. Involved in the stimulation of B- and T- cell function and the regulation of humoral immunity.		
50	(1) SUBUNIT: Binds TRAF2, TRAF3 and TRAF6. Binds the NH2-terminal domain of CAML with its C-terminus.		
51	(1) TISSUE SPECIFICITY: Type II membrane protein.		
52	Intestine and peripheral blood leukocytes. Expressed in resting B- cells and activated T-cells, but not in resting T-cells.		
53	(1) SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.		
54	(1) CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.		
55	-----		
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62	or send an email to license@isb-sib.ch).		
63	-----		
64	EMBL; AF023614; AAC51790.1; -		
65	EMBL; BC028072; AAH28072.1; -		
66	Genew; HGNC:18153; TNFRSF13B.		
67	MM; 604907; -		

```

DR InterPro: IPRO01368; TNFR_C6.
DR PROSITE: PS00652; TNFR_NGFR_1; 1. FALSE NEG.
DR PROSITE: PS005050; TNFR_NGFR_2; 2. FALSE NEG.
KW Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;
KW Domain.
FT DOMAIN 1 165 EXTRACELLULAR (POTENTIAL),
FT TRANSMEM 166 186 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
(POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 187 293
FT REPEAT 187 293 TNFR-CYS 1.
FT REPEAT 70 104 TNFR-CYS 2.
FT DISULFID 34 47 BY SIMILARITY.
FT DISULFID 50 62 BY SIMILARITY.
FT DISULFID 54 66 BY SIMILARITY.
FT DISULFID 71 86 BY SIMILARITY.
FT DISULFID 89 100 BY SIMILARITY.
FT DISULFID 93 104 BY SIMILARITY.
FT CARBOHYD 128 128 N-LINKED (GLCNAC..) (POTENTIAL).
FT CONFLICT 251 251 P - S L (IN REF. 2).
SQ SEQUENCE 293 AA; 31816 MW; 411799FDE17A5EB CRC64;

Query Match 18.7%; Score 93; DB 1; Length 293;
Best Local Similarity 28.4%; Pred. No. 0.017;
Matches 21; Conservative 13; Mismatches 22; Indels 18; Gaps
5;

Oy 1 CSQNEVDSILHACIPQLRCSSNPPTCCQRCY-----C-----EYFDSILHACPQLRCS 51
Db 34 CPBEQYWDPLFLTGNSCKTICNHQS-QRTCAACAFRLSCRKQEGKPYDHLR--DCISCA 90
Oy 52 -----PPTCCQYCC 59
Db 91 SIGQGHKQCAVFC 104

RESULT 5
KRUAA_HUMAN STRAND: PRT; 169 AA.
ID KRUAA_HUMAN STRAND: PRT; 169 AA.
AC P26371;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Keratin, ultra high-sulfur matrix protein A (UHS keratin A) (UHS
DE Kera).
GN KRN1 OR UHSK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxId:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=follicle;
RX MEDLINE=9115951; PubMed=1703541;
RA "Keratin P.J., Powell B.C., Rogers G.E.;
RA "Structure and expression of genes for a class of cysteine-rich
RA proteins of the cuticle layers of differentiating wool and hair
RA follicles."
RL J. Cell Biol. 111:2587-2600 (1990).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE=99148005; PubMed=10023043;
RA Perez C, Anril J, Gerst C, Bernard B.A., Egly J.-M.;
RA "Genomic organization and promoter characterization of two human UHS
RA keratin genes."
RL Gene 227:137-146 (1999).
CC -1- FUNCTION: THE KERATIN PRODUCTS OF MAMMALIAN EPIDERMAL DERIVATIVES
CC SUCH AS WOOL AND HAIR CONSIST OF MICROFIBRILS EMBEDDED IN A RIGID
CC MATRIX OF OTHER PROTEINS. THE MATRIX PROTEINS INCLUDE THE HIGH-
CC SULFUR AND HIGH-TYROSINE KERATINS, HAVING MOLECULAR WEIGHTS OF
CC 6-20 KDa, WHEREAS THE MICROFIBRILS CONTAIN THE LARGER, LOW-SULFUR
CC KERATINS (40-56 KDa).
CC -1- TISSUE SPECIFICITY: CUTICLE LAYERS OF DIFFERENTIATING
CC HAIR FOLLICLES.
CC -1- DEVELOPMENTAL STAGE: AT A LATE STAGE OF FIBER DIFFERENTIATION.

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us-09-855-158-13.rsp

Tue Jan 7 10:36:48 2003

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CC  -!- DOMAIN: MAINLY COMPOSED OF CYS-RICH (CR), GLY-RICH (GR) AND SER-
CC  RICH (SR) REPEATS.
CC  -!- SIMILARITY: BELONGS TO THE UHS KERATIN FAMILY.
CC  -----
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CC  -----
CC  EMBL; X55293; CAA39005.1; -.
CC  DR EMBL; AJ006693; CAA07189.1; -.
CC  DR HSSP; P01064; 1P12.
CC  DR GSWP; HGNC:6409; KRNL.
CC  DR MIM; 148021; -.
CC  KW Keratin Repeat; Multigene family.
CC  SQ SEQUENCE 169 AA; 16276 MW; 219B14FEEB49D4AB CRC64;

Query Match 18.6%; Score 92.5; DB 1; Length 169;
Best Local Similarity 30.0%; Pred. No. 0.012;
Matches 27; Conservative

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPLTCQRYCCYFVDSLHAC-PCLR-----CS 51
DB 77 CSQ-----CSCCKPC-CSSGCGSSCCQCKPCYSCQSCCKPCCSSGRGSSCCQ 127
QY 52 PPTQYCCFHSEYFDSLHACPPATCPYC 81
DB 128 SSCCKPCCSSGCGSS-----CCQSCCKPCC 154

RESULT 6
KRUB HUMAN STANDARD; PRT; 194 AA.
ID KRUB_HUMAN STANDARD; PRT; 194 AA.
AC O75690;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Keratin, ultra high-sulfur matrix protein B (UHS keratin B) (UHS
DE Kerb).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=99148005; PubMed=10023043;
RA Perez C., Auriol J., Gerst C., Bernard B.A., Egly J.-M.;
RA "Genomic organization and promoter characterization of two human UHS
RA keratin genes."
RT Gene 227:137-148 (1999).
CC -!- FUNCTION: THE KERATIN PRODUCTS OF MAMMALIAN EPIDERMAL DERIVATIVES
CC SUCH AS WOOL AND HAIR CONSIST OF MICROFIBRILS EMBEDDED IN A RIGID
CC MATRIX OF OTHER PROTEINS. THE MATRIX PROTEINS INCLUDE THE HIGH-
CC SULFUR AND HIGH-TYROSINE KERATINS, HAVING MOLECULAR WEIGHTS OF
CC 6-20 kDa, WHEREAS THE MICROFIBRILS CONTAIN THE LARGER, LOW-SULFUR
CC KERATINS, (40-56 kDa).
CC -!- TISSUE SPECIFICITY: CUTICLE LAYERS OF DIFFERENTIATING
CC HAIR FOLLICLES.
CC -!- DOMAIN MAINLY COMPOSED OF CYS-RICH (CR), GLY-RICH (GR) AND SER-
CC RICH (SR) REPEATS.
CC -!- SIMILARITY: BELONGS TO THE UHS KERATIN FAMILY.
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DR EMBL; AJ006692; CAA07188.1; -.
DR HSSP; P01055; 1BBI.
KW Keratin; Repeat; Multigene family.
SQ SEQUENCE 194 AA; 18094 MW; 8607B2AE906FE44A CRC64;

Query Match 18.3%; Score 91; DB 1; Length 194;
Best Local Similarity 31.7%; Pred. No. 0.019;
Matches 26; Conservative

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPLTCQRYCCYFVDSLHACPCRCSPPT-CQYCC 59
DB 121 CSQSS-----CCKPCS-CSSGCGSSCCQSCCK-----PC-CSQSSCKPCC 160
QY 60 FHSEYFDSLHACPPATCPYC 81
DB 161 CSQSGCGSS-----CCQSCCKPCC 179

RESULT 7
FUR2_DROME STANDARD; PRT; 1680 AA.
ID FUR2_DROME STANDARD; PRT; 1680 AA.
AC F0432;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Furin-like protease 2 precursor (EC 3.4.21.75) (Furin 2).
DE FUR2.
GN Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
OX [1]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=92381036; PubMed=1512259;
RA Roelcke A.J.M., Creemers J.W.M., Pauli I.G.L., Kurzik-Dumke U.,
RA Rentrop M., Gateff E.A.F., Leunissen J.A.M., van de Ven W.J.;
RA "Cloning and functional expression of Dfurin2, a subtilisin-like
RA proprotein processing enzyme of Drosophila melanogaster with multiple
RA repeats of a cysteine motif."
RT J. Biol. Chem. 267:17208-17215 (1992).
CC -!- FUNCTION: FURIN IS LIKELY TO REPRESENT THE UBQUITOUS ENDOPEPTIDASE
CC ACTIVITY WITHIN CONSTITUTIVE SECRETORY PATHWAYS AND CAPABLE OF
CC CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF (BY SIMILARITY).
CC CC
CC -!- CATALYTIC ACTIVITY: Release of mature proteins from their
CC propeptides by cleavage of Arg-Xaa-Yaa-Arg-|-Zaa bonds, where Xaa
CC can be any amino acid and Yaa is Arg or Lys. Releases albumin,
CC complement component C3 and von Willebrand factor from their
CC respective precursors.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8. FURIN SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M94375; AAA28551.1; -.
CC DR FUR; A43434; A43434.
CC DR HSSP; Q99405; 1MPT.
CC DR MEROPS; S08.049; Fur2.
CC DR Flybase; FBgn004598; Fur2.
CC DR InterPro; IPR000561; EGF-like.
CC DR InterPro; IPR002174; Furin-like.
CC DR InterPro; IPR002884; P-domain.
CC DR InterPro; IPR000209; Peptidase_S8.
CC DR Pfam; PF01483; P; PARTIAL.
CC DR PRINTS; PR00723; SUBTILISIN.
CC DR ProDom; PD000717; P-domain; 1.
CC DR SMART; SM00181; EGF; 1.

```

DR SMART: SM00261; FU; 10.
DR PROSITE; PS00136; SUBTILASE ASP; 1.
DR PROSITE; PS00137; SUBTILASE HIS; 1.
DR PROSITE; PS00138; SUBTILASE SER; 1.
KW Multigene family; Zymogen; Repeat
FT SIGNAL 1
FT PROPEP 1 319
FT CHAIN 320 1680
FT ACT_SITE 418 418
FT ACT_SITE 457 457
FT ACT_SITE 638 638
FT DOMAIN 962 1444
FT REPEAT 962 1007
FT REPEAT 1008 1057
FT REPEAT 1058 1104
FT REPEAT 1105 1153
FT REPEAT 1154 1205
FT REPEAT 1206 1254
FT REPEAT 1255 1299
FT REPEAT 1300 1346
FT REPEAT 1347 1393
FT REPEAT 1394 1444
FT TRANSMEM 1508 1532
FT DOMAIN 1533 1680
FT CARBOHYD 3 3
FT CARBOHYD 109 109
FT CARBOHYD 130 130
FT CARBOHYD 203 203
FT CARBOHYD 443 443
FT CARBOHYD 481 481
FT CARBOHYD 928 928
FT CARBOHYD 1061 1061
FT CARBOHYD 1182 1182
FT CARBOHYD 1275 1275
FT CARBOHYD 1278 1278
FT CARBOHYD 1440 1440
FT SEQUENCE 1680 AA; 183599 MW; 0A93CE8770A8E293 CRC64;

Query Match 17.5%; Score 87; DB 1; Length 1680;
Best Local Similarity 25.0%; Pred. No. 0.3; 31; Indels 50; Gaps 9
Matches 31; Conservative 12; Mismatches 31; Indels 50; Gaps 9

QY 1 CSQNEVYDSLLHACIPQCLRCSSNTPPLTCQ---RYC-CBYFDSLH-----ACP-- 46
Db 1051 CPDGFENSRNRTCTVPCPEPCAS-----CDHPREYCTSCDH-ILVMEHKVCYSACPLDT 1103
QY 47 -----CLRCSPPTCYC--CFHSEYF--DSLHACPPA-----TC 77
Db 1104 YETEDNKCACFGHSTCATCATNGPTDPCDICTCRSSRYAMONKCLISCDGFAVDKRLKCMPC 1163

QY 78 QPYC 81
Db 1164 QEGC 1167

RESULT 8
PCK5_MOUSE
ID_PCK5_MOUSE STANDARD; PRT; 1877 AA.
AC PP04557; 062040; STANFORD; PRT; 1877 AA.
DT 01-FEB-1995 (Rel. 31, Created)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DB Proprietary convertase subunit/lin/lexin type 5 precursor (EC 3.4.21.-)
DE (Proprietary convertase PCS) (Subtilisin/lexin-like protease PCS)
DE (Convertase PCS) (PC6) (Subtilisin-like proprotein convertase 6)
DE (SPC6).
GN PCSK5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]

SEQUENCE OF 330-1877 FROM N.A. (ISOFORM PCSB)
RC STRAIN=ICR; TISSUE=Intestine;
RX MEDLINE=93327934; PubMed=8335106;
RA Nakagawa T., Murakami K., Nakayama K.;
RT "Identification of an isoform with an extremely large Cys-rich region
RT of PC6, a Kex2-like processing endoprotease.";
RL FEBS Lett. 327:165-171(1993).
[2]
RN PCSB
RP SEQUENCE FROM N.A. (ISOFORM PCSA).
RC TISSUE=Brain, and Intestine;
RX MEDLINE=93224489; PubMed=8468318;
RA Nakagawa K., Hosaka M., Torii S., Watanabe T., Murakami K.,
NAKAYAMA K.;
RT "Identification and functional expression of a new member of the
RT mammalian kex2-like processing endoprotease family: its striking
RT structural similarity to PACE4.";
RL J. Biochem. 113:132-135(1993).
[3]
RN PCSA
RP SEQUENCE FROM N.A. (ISOFORM PCSA).
RC TISSUE=Adrenal cortex;
RX MEDLINE=93342056; PubMed=8341687;
RA Lussan J., Vleau D., Hamelin U., Day R., Chretien M., Seidah N.G.;
RT "CNA structure of the mouse and rat subtilisin/kexin-like PCs: a
RT candidate proprotein convertase expressed in endocrine and
RT nonendocrine cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
[4]
RN PCSE
RP PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.
RC MEDLINE=97103178; PubMed=8947550;
RA De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,
Bendayan M., Seidah N.G.;
RT "The isoforms of proprotease convertase PC5 are sorted to different
RT subcellular compartments.";
RL J. Cell Biol. 135:1261-1275(1996).
[5]
RN PCSE
RP DEVELOPMENTAL EXPRESSION.
RC MEDLINE=86293359; PubMed=8698813;
RA Constant D.B., Galfon M., Robertson E.J.,
RT "SPC4, SPCE, and the novel protease SPC7 are coexpressed with bone
RT morphogenetic proteins at distinct sites during embryogenesis.";
RL J. Cell Biol. 134:181-191(1996).
[6]
RN PCSE
RP DEVELOPMENTAL EXPRESSION.
RC MEDLINE=97436919; PubMed=9291583;
RA Rancourt S.L., Rancourt D.E.;
RT "Murine subtilisin-like proteinase SPCE is expressed during embryonic
RT implantation, somitogenesis, and skeletal formation.";
RL Dev. Genet. 21:75-81(1997).
-1- FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPEPTASE ACTIVITY
CC WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE
CC OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF. MAY BE RESPONSIBLE
CC FOR THE MATURATION OF GASTROINTESTINAL PEPTIDES. MAY BE INVOLVED
CC IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA THE ACTIVATION
CC OF GROWTH FACTORS.
-1- CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
CC PROPOTETES BY CLEAVAGE OF ARG-XAA-YAA-ARG-|-ZAA BONDS, WHERE XAA
CC CAN BE ANY AMINO ACID AND YAA IS ARG OR IYS.
-1- SUBCELLULAR LOCATION: PCSA IS SECRETED THROUGH THE REGULATED
CC SECRETORY PATHWAY. PCSE IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO
CC A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH
CC EARLY ENDOSOMES.
-1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS: PCSE/LONG (SHOWN HERE)
CC AND PCSE/SHORT. ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- TISSUE SPECIFICITY: PCSE IS EXPRESSED IN MOST TISSUES BUT IS MOST
CC ABUNDANT IN THE INTSTINE AND ADRENALS. PCSEB IS EXPRESSED IN THE
CC INTESTINS, ADRENALS AND LUNG BUT NOT IN THE BRAIN.
-1- DEVELOPMENTAL STAGE: WEAKLY EXPRESSED THROUGHOUT THE EMBRYO,
CC EXCEPT IN THE DEVELOPING NERVOUS SYSTEM, THE RIBS AND THE LIVER,
CC BUT MARKEDLY UPREGULATED AT DISCRETE SITES DURING DEVELOPMENT. AT
CC BE.5, PROMINENT EXPRESSION OBSERVED IN DIFFERENTIATED DECIDUA. AT
CC ET.5, INTENSE EXPRESSION IN EXTRAMEMBRYONIC ENDODERM, ANIONIC AND
CC NASCENT MESODERM. AT 8.5, ABUNDANT EXPRESSION IN SOMITERS AND YOLK
CC SAC FOLLOWED BY A CONFINATION TO DERMATOTOME COMPARTMENT. BETWEEN

Db 72 CRPITCPTSCQAVCPCCWATTCCQPVSCQCCPRTSCOP 114

RESULT 10

UBPW_MOUSE STANDARD; PRT; 526 AA.

061068: DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Ubiquitin carboxyl-terminal hydrolase DUB-1 (EC 3.1.2.15) (Ubiquitin thiolesterase DUB-1) (Ubiquitin-specific processing protease DUB-1) (Deubiquitinating enzyme 1).

GN DUB1 OR DUB-1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

[1]

SEQUENCE FROM N.A.

RP MEDLINE=96194957; Pubmed=8622927;

RA Zhu Y., Carroll M., Papa F.R., Hochstrasser M., D'Andrea A.D.;

RT "DUB-1, a deubiquitinating enzyme with growth-suppressing activity.";

RL Proc. Natl. Acad. Sci. U.S.A. 93:3275-3279(1996).

CC -1- FUNCTION: HAS GROWTH-SUPPRESSING ACTIVITY, INDUCES ARREST IN G1

CC -1- PHASE UPON CONTROLLED EXPRESSION.

CC -1- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O =

CC -1- ubiquitin + a thiol.

CC -1- INDUCTION: BY INTERLEUKIN-3.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C19.

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CC EMBL: U41636; AAC52532.1; -

DR MEMOPS: C19.031; DUB1.

DR MGD: MGI:107699; DUB1.

DR InterPro: IPR001394; UCH-2.

DR Pfam: PF00442; UCH-1; 1.

DR Pfam: PF00443; UCH-2; 1.

DR PROSITE: PS00972; UCH_2_1; 1.

DR PROSITE: PS00973; UCH_2_2; 1.

DR PROSITE: PS50235; UCH_2_3; 1.

RT Ubi conjugation pathway; Hydrolyase; Thiol protease; Multigene family.

FW ACT_SITE 60

FW ACT_SITE 298

FW ACT_SITE 307

SQ SEQUENCE 526 AA; 59073 MW; 263AA7B579694EA CRC64;

Query Match 15.5%; Score 82; DB 1; Length 526;

Best Local Similarity 36.8%; Pred. No. 0.33;

Matches 19; Conservative 8; Mismatches 18; Indels 8; Gaps 2;

OY 19 LRCSNPPLTCQRYCCYFSLHLACGCLRCSPPTQVCCPFHSEYDLSLHA 71

Db 66 LGCTHTPPL-----ADYMLSGEHSQIC--CSPEGKGLCMKMLVYQSLHS 110

RESULT 11

LMG3_HUMAN STANDARD; PRT; 1587 AA.

AC Q9Y6N6;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Laminin gamma-3 chain precursor (Laminin 12 gamma 3).

LN LAMC3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_TaxID=9606;

[1]

SEQUENCE FROM N.A.

RP TISSUE=Placenta;

RA MEDLINE=99242614; Pubmed=10225960;

RA Koch M., Olson P.F., Albus A., Jin W., Hunter D.D., Brunken W.J.,

RT "Characterization and expression of the laminin gamma3 chain: a novel, non-basement membrane-associated, laminin chain.";

RL J. Cell Biol. 145:605-618(1999).

CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin is thought to mediate the attachment, migration, and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.

CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three different polypeptide chains (alpha, beta, gamma), which are bound to each other by disulfide bonds into a cross-shaped molecule comprising one long and three short arms with globules at each end.

CC THE GAMMA-3 CHAIN IS A SUBUNIT OF LAMININ-12.

CC -1- SUBCELLULAR LOCATION: Extracellular.

CC -1- TISSUE SPECIFICITY: Broadly expressed in: skin, heart, lung, and the reproductive tracts.

CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

CC -1- DOMAIN: DOMAIN IV IS GLOBULAR.

CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).

CC -1- SIMILARITY: CONTAINS 11 LAMININ EGF-LIKE DOMAINS.

CC -1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.

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CC EMBL: AF041835; AAD36991.1; -

DR HSSP: P02468; LTLB.

DR GeneW: HGNC:6494; LAMC3.

DR MIM: 604349; -

DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR001886; Lamnt.

DR InterPro: IPR000034; Laminin.B.

DR InterPro: IPR002049; Laminin.B.

DR Pfam: PF00052; laminin_B_1.

DR Pfam: PF00053; laminin_EGF_10.

DR Pfam: PF00055; laminin_Nterm_1.

DR PRINTS: PR00011; EGF/LAMININ.

DR ProDom: PD003031; Laminin.B.

DR ProDom: PD003082; Lamnt; 1.

DR SMART: SM00180; EGF_Lam; 10.

DR SMART: SM00001; EGF_Like; 1.

DR SMART: SM00136; Lamnt; 1.

DR SMART: SM00136; Lamnt; 1.

DR PROSITE: PS00022; EGF_1; 7.

DR PROSITE: PS01186; EGF_2; 2.

DR PROSITE: PS01248; LAMININ TYPE EGF; 10.

KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;

KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.

FT SIGNAL 1

FT CHAIN 19

FT DOMAIN 20 1587

FT DOMAIN 20 270

FT DOMAIN 271 326

FT DOMAIN 327 382

FT DOMAIN 383 426

FT DOMAIN 430 473

FT DOMAIN 480 489

FT DOMAIN 490 672

FT DOMAIN 673 706

FT LAMININ GAMMA-3 CHAIN

FT LAMININ N-TERMINAL (DOMAIN VI).

FT LAMININ EGF-LIKE 1.

FT LAMININ EGF-LIKE 2.

FT LAMININ EGF-LIKE 3.

FT LAMININ EGF-LIKE 4 (N-TERMINAL).

FT LAMININ EGF-LIKE 5 (C-TERMINAL).

FT LAMININ DOMAIN IV.

FT LAMININ EGF-Like 5 (C-TERMINAL).

UU

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI TaxID=9606;
 RX SEQUENCE FROM N.A.
 MEDLINE=95213013; PubMed=7698745;
 RA Mewer U.M., Gerecke D.R., Durkin M.E., Kurtz K.S., Mattei M.G.,
 Champlaud M.F., Burgess R.E., Albrechtsen R.;
 RT "human beta 2 chain of laminin (formerly S chain): cDNA cloning,
 RT chromosomal localization, and expression in carcinomas";
 RT Genomics 24:243-252(1994).
 RN [2]
 RE SEQUENCE FROM N.A.
 RX MEDLINE=95316263; PubMed=7795887;
 RA Iivanainen A., Vuolteenaho R., Sainio K., Eddy R., Shows T.B.,
 RT "The human laminin beta 2 chain (S-laminin): structure, expression in
 RT fetal tissues and chromosomal assignment of the LAMB2 gene";
 RL Matrix Biol. 14:489-497(1995).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration, and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 CC different polypeptide chains (alpha, beta, gamma), which are bound
 CC to each other by disulfide bonds into a cross-shaped molecule
 CC comprising one long and three short arms with globules at each
 CC end.
 CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4
 CC (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
 CC COMPONENT) S-LAMININ IS CONCENTRATED IN THE SYNAPTIC
 CC CLEFT OF THE NEUROMUSCULAR JUNCTION.
 CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
 CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
 CC -1- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.
 CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VII).
 CC -1- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; Z68155; CA932279.1; -;
 DR EMBL; Z68156; CA932279.1; JOINED.
 DR EMBL; X79683; CA56130.1; -;
 DR EMBL; S77512; AAB34682.2; -;
 DR HSBP; P02468; IKLO.
 DR Genew; HGNC:6487; LAMB2.
 DR MIM; 150325; -;
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001886; LamNT.
 DR InterPro; IPR02049; Laminin_EGF.
 DR Pfam; PF00053; laminin_EGF_13.
 DR Pfam; PF00055; laminin_Nterm_1.
 DR PRINTS; PRO0011; EGF/LAMININ.
 DR ProDom; PD002082; LamNT; 1.
 DR SMART; SM00180; EGF_Lam; 11.
 DR SMART; SM00136; LamNT; 1.
 DR PROSITE; PS00022; EGF_1; 10.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01248; LAMININ TYPE EGF; 12.
 KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
 KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
 FT SIGNAL 1 32 POTENTIAL.
 FT CHAIN 33 1798 LAMININ BETA-2 CHAIN.
 FT DOMAIN 33 280 LAMININ N-TERMINAL (DOMAIN VI).
 FT DOMAIN 283 346 LAMININ EGF-LIKE 1.

FT DOMAIN 347 409 LAMININ EGF-LIKE 2.
 FT DOMAIN 410 469 LAMININ EGF-LIKE 3.
 FT DOMAIN 521 521 LAMININ EGF-LIKE 4.
 FT DOMAIN 522 552 LAMININ EGF-LIKE 5 (INCOMPLETE).
 FT DOMAIN 553 781 LAMININ DOMAIN IV.
 FT DOMAIN 783 830 LAMININ EGF-LIKE 6.
 FT DOMAIN 831 876 LAMININ EGF-LIKE 7.
 FT DOMAIN 877 926 LAMININ EGF-LIKE 8.
 FT DOMAIN 927 985 LAMININ EGF-LIKE 9.
 FT DOMAIN 986 1037 LAMININ EGF-LIKE 10.
 FT DOMAIN 1038 1094 LAMININ EGF-LIKE 11.
 FT DOMAIN 1095 1142 LAMININ EGF-LIKE 12.
 FT DOMAIN 1143 1189 LAMININ EGF-LIKE 13.
 FT DOMAIN 1190 1409 DOMAIN II.
 FT DOMAIN 1410 1442 DOMAIN ALPHA.
 FT DOMAIN 1443 1798 DOMAIN 1.
 FT DOMAIN 1453 1526 COILED COIL (POTENTIAL).
 FT DOMAIN 1472 1526 COILED COIL (POTENTIAL).
 FT DOMAIN 1577 1790 COILED COIL (POTENTIAL).
 FT DOMAIN 283 292 BY SIMILARITY.
 FT DISULFID 285 310 BY SIMILARITY.
 FT DISULFID 312 321 BY SIMILARITY.
 FT DISULFID 324 344 BY SIMILARITY.
 FT DISULFID 347 356 BY SIMILARITY.
 FT DISULFID 349 374 BY SIMILARITY.
 FT DISULFID 377 386 BY SIMILARITY.
 FT DISULFID 389 407 BY SIMILARITY.
 FT DISULFID 410 423 BY SIMILARITY.
 FT DISULFID 412 438 BY SIMILARITY.
 FT DISULFID 440 449 BY SIMILARITY.
 FT DISULFID 452 467 BY SIMILARITY.
 FT DISULFID 470 484 BY SIMILARITY.
 FT DISULFID 472 491 BY SIMILARITY.
 FT DISULFID 492 502 BY SIMILARITY.
 FT DISULFID 503 519 BY SIMILARITY.
 FT DISULFID 519 521 BY SIMILARITY.
 FT DISULFID 783 795 BY SIMILARITY.
 FT DISULFID 804 813 BY SIMILARITY.
 FT DISULFID 813 828 BY SIMILARITY.
 FT DISULFID 831 850 BY SIMILARITY.
 FT DISULFID 850 861 BY SIMILARITY.
 FT DISULFID 864 874 BY SIMILARITY.
 FT DISULFID 877 886 BY SIMILARITY.
 FT DISULFID 879 893 BY SIMILARITY.
 FT DISULFID 896 905 BY SIMILARITY.
 FT DISULFID 908 924 BY SIMILARITY.
 FT DISULFID 927 943 BY SIMILARITY.
 FT DISULFID 929 954 BY SIMILARITY.
 FT DISULFID 956 965 BY SIMILARITY.
 FT DISULFID 968 983 BY SIMILARITY.
 FT DISULFID 986 1000 BY SIMILARITY.
 FT DISULFID 988 1007 BY SIMILARITY.
 FT DISULFID 1010 1019 BY SIMILARITY.
 FT DISULFID 1022 1035 BY SIMILARITY.
 FT DISULFID 1095 1107 BY SIMILARITY.
 FT DISULFID 1097 1114 BY SIMILARITY.
 FT DISULFID 1116 1125 BY SIMILARITY.
 FT DISULFID 1128 1140 BY SIMILARITY.
 FT DISULFID 1143 1155 BY SIMILARITY.
 FT DISULFID 1145 1162 BY SIMILARITY.
 FT DISULFID 1164 1173 BY SIMILARITY.
 FT DISULFID 1176 1187 BY SIMILARITY.
 FT DISULFID 1190 1199 INTERCHAIN (PROBABLE).
 FT DISULFID 1193 1193 INTERCHAIN (PROBABLE).
 FT DISULFID 1197 1797 INTERCHAIN (PROBABLE).
 FT CARBOHYD 248 248 N-LINKED (GLCNAC).
 FT CARBOHYD 368 368 N-LINKED (GLCNAC).
 FT CARBOHYD 1085 1085 N-LINKED (GLCNAC).
 FT CARBOHYD 1249 1249 N-LINKED (GLCNAC).
 FT CARBOHYD 1348 1348 N-LINKED (GLCNAC).
 FT CARBOHYD 1348 1348 N-LINKED (GLCNAC).
 FT CARBOHYD 1499 1499 N-LINKED (GLCNAC).

us-09-855-158-13-rsp

Tue Jan 7 10:36:48 2003

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FT CONFLICT 914 914 R -> G (IN REF. 2).
FT CONFLICT 1179 1179 G -> A (IN REF. 2).
SQ SEQUENCE 1798 AA; 196079 MW; 9555CF5B24850CB7 CRC64;

Query Match
Best Local Similarity 16.2%; Score 80.5; DB 1; Length 1798;
Matches 29; Conservative 7; Mismatches 31; Indels 41; Gaps 8;

QY 1 CSQNEYFDSLL-----HACIP-----COL-RCSNPPPTTCQRYCC 35
DB 943 CHQDEYSQIVCHCRAGYGLRCEACPHFGDPSRPGRCOLCEGNDPMDPD--AC 1000
QY 36 EYFDSLHACPLRC-----SPPTCQVC--CFHSEYFDSLHACPPATC 77
DB 1001 D-----PHTGQCLRLHHTGPHCAKCPGFGQAARSCRC---TC 1040

RESULT 14
ID LAM1 HUMAN STANDARD; PRT: 3075 AA.
AC P2539; 1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-MAY-1992 (Rel. 41, Last annotation update)
DE 15-JUN-2002 (Rel. 41, Last sequence update)
DE Laminin alpha-1 chain precursor (Laminin A chain).
GN LAM1 OR LAMA (Human)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=9133420; PubMed=1714537;
RX MEDLINE=91264789; PubMed=2049067;
RA Nissinen M., Vuolteenaho R., Boot-Handford R., Kallunki P.,
RA Tryggsaen K.;
RT "Primary structure of the human laminin A chain. Limited expression
RT in human tissues."
RL Biochem. J. 276:369-379 (1991).
RN [3]
RP SEQUENCE OF 1-2628 FROM N.A.
RX MEDLINE=89280632; PubMed=2733383;
RA Olsen D., Nagayoshi T., Fazio M., Peltonen J., Jaakkola S.,
RA Sanborn D., Sasaki T., Kuivaniemi H., Chu M.L., Deutzmann R.,
RA Timpl R., Utto J.;
RT "Human laminin: cloning and sequence analysis of cDNAs encoding A, B1
RT and B2 chains, and expression of the corresponding genes in human
RT skin and cultured cells."
RL Lab. Invest. 60:772-782 (1989).
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration, and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end. THE ALPHA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMININ) AND
CC LAMININ-3 (S-LAMININ).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
CC COMPONENT).
CC -!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -!- DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR.
CC -!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC -!- SIMILARITY: CONTAINS 17 LAMININ EGF-LIKE DOMAINS.

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CC CC -!- SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.
CC CC -!- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
CC CC -----
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CC CC -----
CC CC EMBL; X58531; CAA41418.1; -.
CC CC PIR; S14458; S14458.
CC CC HSSP; Q60675; 1QOU.
CC CC Genew; HGNC:6481; LAM1.
CC CC MIM; 150320; -.
CC CC InterPro; IPR000561; EGF-like.
CC CC InterPro; IPR001886; LamNT.
CC CC InterPro; IPR000034; Laminin_B.
CC CC InterPro; IPR002049; Laminin_EGF.
CC CC InterPro; IPR001791; Laminin_G.
CC CC Pfam; PF00052; laminin_B; 2.
CC CC Pfam; PF00053; laminin_EGF; 15.
CC CC Pfam; PF00054; laminin_G; 5.
CC CC Pfam; PF00055; laminin_Nterm; 1.
CC CC PRINTS; PR00011; EGF-LAMININ.
CC CC ProDom; PD002082; LamNT; 1.
CC CC ProDom; PD003031; Laminin_B; 2.
CC CC SMART; SM00180; EGF_Lam; 14.
CC CC SMART; SM00001; EGF_Like; 1.
CC CC SMART; SM00281; LamB; 2.
CC CC SMART; SM00282; LamG; 5.
CC CC SMART; SM00136; LamNT; 1.
CC CC PROSITE; PS00022; EGF_1; 11.
CC CC PROSITE; PS01186; EGF_2; 2.
CC CC PROSITE; PS01248; LAMININ TYPE EGF; 15.
CC CC PROSITE; PS50025; LAM G DOMAIN; 5.
CC CC Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
CC CC Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
CC CC POTENTIAL.
CC CC SIGNAL 1 17
CC CC CHAIN 18 3075
CC CC LAMININ N-TERMINAL (DOMAIN VI).
CC CC LAMININ EGF-LIKE 1.
CC CC LAMININ EGF-LIKE 2.
CC CC LAMININ EGF-LIKE 3.
CC CC LAMININ EGF-LIKE 4.
CC CC LAMININ EGF-LIKE 5 (N-TERMINAL).
CC CC LAMININ DOMAIN IV 1 (DOMAIN IV B).
CC CC LAMININ EGF-LIKE 5 (C-TERMINAL).
CC CC LAMININ EGF-LIKE 6.
CC CC LAMININ EGF-LIKE 7.
CC CC LAMININ EGF-LIKE 8.
CC CC LAMININ EGF-LIKE 9.
CC CC LAMININ EGF-LIKE 10.
CC CC LAMININ EGF-LIKE 11.
CC CC LAMININ EGF-LIKE 12.
CC CC LAMININ EGF-LIKE 13.
CC CC LAMININ EGF-LIKE 14 (N-TERMINAL).
CC CC LAMININ DOMAIN IV 2 (DOMAIN IV A).
CC CC LAMININ EGF-LIKE 14 (C-TERMINAL).
CC CC LAMININ EGF-LIKE 15.
CC CC LAMININ EGF-LIKE 16.
CC CC LAMININ EGF-LIKE 17.
CC CC LAMININ EGF-LIKE 1.
CC CC LAMININ G-LIKE 1.
CC CC LAMININ G-LIKE 2.
CC CC LAMININ G-LIKE 3.
CC CC LAMININ G-LIKE 4.
CC CC LAMININ G-LIKE 5.
CC CC COILED COIL (POTENTIAL).
CC CC COILED COIL (POTENTIAL).
CC CC COILED COIL (POTENTIAL).
CC CC CELL ATTACHMENT SITE.
CC CC SITE

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FT DISULFID 270 279 BY SIMILARITY.
 FT DISULFID 272 290 BY SIMILARITY.
 FT DISULFID 292 301 BY SIMILARITY.
 FT DISULFID 297 305 POTENTIAL.
 FT DISULFID 304 324 BY SIMILARITY.
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 FT DISULFID 772 788 BY SIMILARITY.
 FT DISULFID 791 806 BY SIMILARITY.
 FT DISULFID 793 816 BY SIMILARITY.
 FT DISULFID 819 828 BY SIMILARITY.
 FT DISULFID 831 846 BY SIMILARITY.
 FT DISULFID 849 863 BY SIMILARITY.
 FT DISULFID 851 870 BY SIMILARITY.
 FT DISULFID 873 882 BY SIMILARITY.
 FT DISULFID 885 899 BY SIMILARITY.
 FT DISULFID 902 914 BY SIMILARITY.
 FT DISULFID 904 921 BY SIMILARITY.
 FT DISULFID 923 932 BY SIMILARITY.
 FT DISULFID 935 948 BY SIMILARITY.
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 FT DISULFID 998 1007 BY SIMILARITY.
 FT DISULFID 1000 1014 BY SIMILARITY.
 FT DISULFID 1016 1025 BY SIMILARITY.
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 FT DISULFID 1044 1056 BY SIMILARITY.
 FT DISULFID 1064 1063 BY SIMILARITY.
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 FT DISULFID 1077 1087 BY SIMILARITY.
 FT DISULFID 1403 1412 BY SIMILARITY.
 FT DISULFID 1405 1419 BY SIMILARITY.
 FT DISULFID 1422 1431 BY SIMILARITY.
 FT DISULFID 1434 1449 BY SIMILARITY.
 FT DISULFID 1452 1466 BY SIMILARITY.
 FT DISULFID 1454 1476 BY SIMILARITY.
 FT DISULFID 1479 1488 BY SIMILARITY.
 FT DISULFID 1481 1506 BY SIMILARITY.
 FT DISULFID 1509 1521 BY SIMILARITY.
 FT DISULFID 1511 1528 BY SIMILARITY.
 FT DISULFID 1530 1539 BY SIMILARITY.
 FT DISULFID 1542 1553 BY SIMILARITY.
 FT DISULFID 1556 1566 INTERCHAIN (PROBABLE).
 FT DISULFID 1560 INTERCHAIN (PROBABLE).
 FT CARBOHYD 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 555 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 665 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 763 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 926 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 952 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1045 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1407 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1579 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1596 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1678 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1689 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1698 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1717 N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 16.1%; Score 80; DB 1; Length 3075;
 Best Local Similarity 23.4%; Pred. No. 2.4;
 Matches 29; Conservative 10; Mismatches 37; Indels 48; Gaps 8;
 QY 1 CSONEYFSPSLT-HACIPCO-----LRCSNTPPLTCORVCC-- 36
 DB 831 CADGYGNPTVPSSCVPDCSGNVDPSEAGHCDVTSGBCKLGNITDGAHCR-CADGF 889
 QY 37 YEDSL---LHACPC-----LACSP-PTCOVC--CFHSEYFDSLHACP 73
 DB 890 YGDVATKNCACACCHVKSHSAVCHLEFGLCDCKRNVTGQCCDGLHGYGLDSGHCR 949
 QY 74 PATC 77
 DB 950 PCNC 953
 RESULT 15
 YNC3_YEAST STANDARD; PRT; 965 AA.
 ID YNC3_YEAST
 AC P53971;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical 108.5 kDa protein in UME3-HDA1 intergenic region.
 GN YNL023C OR N2812.
 OS Saccharomyces cerevisiae (Baker's Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Duestenhoelt A., Floeth M., Fritz C., Heuss-Neitzel D.,
 RA Hilbert H., Moestl D.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA Andre B., Iragui Housaani I., Urrestarazu L.A., Vissers S.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: TO DROSOPHILA SHUTTLE CRAFT PROTEIN (STC) AND HUMAN
 CC NFX1.
 CC -1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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 CC -----
 CC EMBL; Z71299; CA95885.1; --
 CC SGD; S0004966; INL023C.
 DR InterPro; IPR001374; R3H.
 DR InterPro; IPR000967; Znf_NFX1.
 DR Pfam; PF01422; zf-NFX1; 5.
 DR Pfam; PF01424; R3H; 1.
 DR SMART; SM00393; R3H; 1.
 DR SMART; SM00184; R3H; 1.
 DR SMART; SM00438; Znf_NFX; 7.
 DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE; PS00089; ZF_RING_2; 1.
 KW Hypothetical protein; zinc-finger; Repeat.
 FT ZN FING 68 644 7 X APPROXIMATE REPEATS, CYS-RICH.
 FT DOMAIN 150 185 1.
 FT REPEAT 206 251 2.
 FT REPEAT 273 330 3.
 FT REPEAT 352 390 4.
 FT REPEAT 458 497 5.
 FT REPEAT 575 610 6.

us-09-855-158-13.rsp

Tue Jan 7 10:36:48 2003

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FT REPEAT 611 644 7. 121C57BB07C6FA9D CRC64;
SQ SEQUENCE 965 AA; 108494 MW; 121C57BB07C6FA9D CRC64;

Query Match 16.0%; Score 79.5; DB 1; Length 965;
Best Local Similarity 29.6%; Pred. No. 0.98; 26; Indels 37; Gaps 7;
Matches 29; Conservative 6; Mismatches 26; Indels 37; Gaps 7;

QY 12 HACT-PCQLRCSNTPLTCORYC-----CEYFDSLHACPC-----LRCSP--P 53
Db 456 HICLKPCNLTSCGIH--KCQRKCHPGKCPCLSDSNDLVCPGNTVVVPAPVRCGTKLP 513

QY 54 TCQYCCF-----HSEYFDSLHACPPAT 76
Db 514 TCNHPCKVVRGESCQHKMPHTCH--SLDVSCPCT 549
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Search completed: January 7, 2003, 09:38:07
Job time : 8.05023 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:34:29 ; Search time 22.9398 Seconds
(without alignments)
727.547 Million cell updates/sec

Title: US-09-855-158-13
Perfect score: 498
Sequence: 1 CSQNEYFSLHACIPCLR.....SEYFDSLHACPPATCPYC 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 21:
1: sp.archaea:
2: sp.bacteria:
3: sp.fungi:
4: sp.human:
5: sp.invertebrate:
6: sp.mammal:
7: sp.mhc:
8: sp.organelle:
9: sp.phage:
10: sp.plant:
11: sp.podent:
12: sp.virus:
13: sp.vertebrate:
14: sp.unclassified:
15: sp.virus:
16: sp.bacteriaph:
17: sp.archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.5	20.2	1792	13	O57484
2	94.5	19.0	223	11	Q62220
3	94.5	19.0	230	11	Q64507
4	93.5	18.8	195	11	Q9D141
5	92.5	18.6	169	4	Q14564
6	92.5	18.6	227	11	Q9D225
7	91.5	18.4	136	4	Q9BYR5
8	91.5	18.4	186	4	Q9BYR2
9	91.5	18.4	186	11	Q64526
10	91.5	18.4	191	11	Q9D3H7
11	89	17.9	159	4	Q9BYG3
12	88	17.7	1574	11	Q88281
13	88	17.7	166	4	Q9BYR3
14	87.5	17.6	154	4	Q9BYQ2
15	87.5	17.6	174	4	Q9BYQ4
16	87.5	17.6	193	4	Q9BYQ5

17	87	17.5	159	4	Q9BYQ0
18	87	17.5	165	11	Q9D7P3
19	87	17.5	195	11	Q9D0X9
20	87	17.5	1376	5	Q8SZS2
21	87	17.5	1673	5	Q24301
22	86	17.3	188	11	O70148
23	86	17.3	2112	5	Q8WPL0
24	85.5	17.2	154	4	Q9BYP9
25	85.5	17.2	177	11	Q9D644
26	85.5	17.2	189	11	Q9D5Z7
27	85	17.1	202	11	Q91W93
28	85	17.1	325	10	Q94HS1
29	84.5	17.0	767	13	Q9DGR2
30	84	16.9	195	4	Q9BYO6
31	84	16.9	201	4	Q9BQ66
32	84	16.9	210	4	Q9BYR0
33	84	16.9	1671	5	Q9NJV5
34	83.5	16.8	110	5	Q9BIR2
35	83.5	16.8	130	11	Q9Z287
36	83.5	16.8	191	4	Q9BYQ8
37	83	16.7	175	4	Q97628
38	82	16.5	98	4	Q9BYR8
39	82	16.5	126	6	Q28707
40	82	16.5	167	11	Q9D122
41	82	16.5	168	11	Q9D732
42	81.5	16.4	85	11	O70555
43	81.5	16.4	429	13	Q91650
44	81	16.3	353	5	Q9VW81
45	81	16.3	353	5	Q8SZS8

ALIGNMENTS

RESULT 1

O57484 PRELIMINARY; PRT; 1792 AA.
ID O57484
AC O57484
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE Laminin beta 2-like chain.
DE Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93015947; PubMed=1400373;
RA O'Rear J.J.;
RT "A novel laminin B1 chain variant in avian eye."
RL J. Biol. Chem. 267:20555-20557(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98205634; PubMed=9550264;
RA Liu J. Swadlow S., Xie W., Brewton R.G., Mayne R.;
RT "Primary structure and expression of a chicken laminin beta chain: evidence for four beta chains in birds."
RL Matrix Biol. 16:471-481(1998).
DE EMBL; AF038555; AAB92586.1; --
DR HSSR; P02468; I150;
DR InterPro; IPR002106; RRNA_ligaseII.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001886; LamNT.
DR Pfam; PF00053; laminin_EGF; 13.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGF_LAMININ.
DR SMART; SM00180; EGF Lam; 13.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00339; AA TRNA LIGASE II_2; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_10.

DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
 KM EGF-like domain; Glycoprotein; Laminin EGF-like domain; Repeat.
 SQ SEQUENCE 1792 AA; 195723 MW; 4A4CB8E0206FA600 CRC64;

Query Match 20.2%; Score 100.5; DB 13; Length 1792;
 Best Local Similarity 32.0%; Pred. No. 0.00059;
 Matches 32; Conservative 8; Mismatches 35; Indels 25; Gaps 6;

QY 1 CSQNEFYDLSLHACIPQALRCSSNTPTLCQRYCCYFPSLHACPLRCSPPTQYCCF 49
 DB 1017 CGPGYGDARHSC---RRCSCNTLTGTDPTNGPQCCQCDQRSQGHCLPHVEGQSCDR 1072
 QY 50 CSP-----PTQYCCYFPSLHACPPATQPYC 81
 DB 1073 CSPHFMNLGSGGCEPACHPQH--SLSPACNPTQCCSC 1110

RESULT 2
 ID Q62220 PRELIMINARY; PRT; 223 AA.

AC Q62220;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Serine 2 ultra high sulfur protein.
 GN KRTAP5-4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=91065960; PubMed=2250030;
 RA Wood L., Mills M., Hatzenbuehler N., Vogel G.;
 RT "Serine-rich ultra high sulfur protein gene expression in murine hair
 and skin during the hair cycle."
 RL J. Biol. Chem. 265:21375-21380(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=91154184; PubMed=1840598;
 RA Wood L., Mills M., Hatzenbuehler N., Vogel G.;
 RT "Additions and Corrections: Serine-rich ultra high sulfur protein gene
 expression in murine hair and skin during the hair cycle."
 RL J. Biol. Chem. 266:4024-4024(1991).
 DR EMBL; M37760; AAA40107.1; -.
 DR HSSP; P01064; IP12.
 DR MGD; MG1:1354758; Krtap5-4.
 DR InterPro; IPR001450; 4Fe4S_ferredoxin.
 DR InterPro; IPR001007; VWF_C.
 DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; UNKNOWN_2.
 DR PROSITE; PS01208; VWF_C; UNKNOWN_2.
 SQ SEQUENCE 223 AA; 21442 MW; C65BDB9FD08C59A CRC64;

Query Match 19.0%; Score 94.5; DB 11; Length 223;
 Best Local Similarity 29.6%; Pred. No. 0.00052;
 Matches 24; Conservative 3; Mismatches 27; Indels 27; Gaps 5;

QY 1 CSQNEFYDLSLHACIPQALRCSSNTPTLCQRYCCYFPSLHACPLRCSPPTQYCCF 60
 DB 150 CCQSS-----CCKPFC--CSSGCGSSCCQSSCK-----PCC-QSSCKPCC 189
 QY 61 HSEYFDSLHACPPATQPYC 81
 DB 190 QSS-----CCKPCCQSSC 203

RESULT 3
 ID Q64507 PRELIMINARY; PRT; 230 AA.
 AC Q64507;

DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Serine 1 ultra high sulfur protein.
 GN KRTAP5-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=91065960; PubMed=2250030;
 RA Wood L., Mills M., Hatzenbuehler N., Vogel G.;
 RT "Serine-rich ultra high sulfur protein gene expression in murine hair
 and skin during the hair cycle."
 RL J. Biol. Chem. 265:21375-21380(1990).
 DR EMBL; M37759; AAA40106.1; -.
 DR HSSP; P01064; IP12.
 DR MGD; MG1:1354732; Krtap5-1.
 DR InterPro; IPR001450; 4Fe4S_ferredoxin.
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR001305; DnaJ_CXXCXXG.
 DR InterPro; IPR001007; VWF_C.
 DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; UNKNOWN_1.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; UNKNOWN_1.
 DR PROSITE; PS00637; DnaJ_CXXCXXG; UNKNOWN_1.
 DR PROSITE; PS01208; VWF_C; UNKNOWN_3.
 SQ SEQUENCE 230 AA; 21781 MW; 6CC50B1B2137C23 CRC64;

Query Match 19.0%; Score 94.5; DB 11; Length 230;
 Best Local Similarity 29.6%; Pred. No. 0.00053;
 Matches 24; Conservative 3; Mismatches 27; Indels 27; Gaps 5;

QY 1 CSQNEFYDLSLHACIPQALRCSSNTPTLCQRYCCYFPSLHACPLRCSPPTQYCCF 60
 DB 149 CCQSS-----CCKPFC--CSSGCGSSCCQSSCK-----PCC-QSSCKPCC 188
 QY 61 HSEYFDSLHACPPATQPYC 81
 DB 189 QSS-----CCKPCCQSSC 202

RESULT 4
 ID Q6D141 PRELIMINARY; PRT; 195 AA.

AC Q6D141;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE 18 days embryo cDNA, RIKEN full-length enriched library,
 DE clone1110030N11, full insert sequence.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRIO;
 RX MEDLINE=C57BL/6J; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Koehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schram L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazarelli J., Momberts P.,

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SCALP;
 RA Rogers M.A., Langbein L., Winter H., Ehmann C., Korn B., Schweizer J.;
 RT "Characterization of a cluster of human high/ultrahigh keratin
 RT associated proteins on chromosome 17q12-21."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ406934; CAC27573.1; -
 DR InterPro; IPR002494; Keratin_B2.
 DR InterPro; IPR001368; TNFR_C6.
 DR Pfam; PF01500; Keratin_B2.1.
 DR PROSITE; PS00652; TNFR_NGFR.1; UNKNOWN_1.
 SQ SEQUENCE 136 AA; 14402 MW; 51E514863925E02E CRC64;

Query Match 18.4%; Score 91.5; DB 4; Length 136;
 Best Local Similarity 29.7%; Pred. No. 0.00079;
 Matches 27; Conservative 5; Mismatches 38; Indels 21; Gaps 5;

QY 10 LILACIP--COLRC-----SSNTPLTQRYCYCEYFDSLILAC--PCLR---C 50
 DB 17 LENCRRPSCCQYTCRTCTCCRRPSCVSSCCRPCCQSVCCQPTCCSPCCQYTCRTCTCC 76
 QY 51 SPPTCYCCFHSFYFDSLILACPPATCOPYC 81
 DB 77 RPSCVSSCFRRPCCQSV--CCQPTCCRPSC 105

RESULT 8

Q9BYR2 PRELIMINARY; PRT; 186 AA.

AC Q9BYR2;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Keratin associated protein 4.5.

GN KRTAB4.5;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SCALP;
 RA Rogers M.A., Langbein L., Winter H., Ehmann C., Korn B., Schweizer J.;
 RT "Characterization of a cluster of human high/ultrahigh keratin
 RT associated proteins on chromosome 17q12-21."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ406937; CAC27576.1; -
 DR InterPro; IPR002494; Keratin_B2.
 DR InterPro; IPR001304; Keratin_C.
 DR InterPro; IPR001368; TNFR_C6.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF01500; Keratin_B2.1.
 DR PROSITE; PS00615; C_TYR_PLECTIN.1; UNKNOWN_1.
 DR PROSITE; PS00652; TNFR_NGFR.1; UNKNOWN_1.
 DR PROSITE; PS01208; VWF_C; UNKNOWN_2.
 SQ SEQUENCE 186 AA; 19916 MW; 034D9C7343D4F63A CRC64;

Query Match 18.4%; Score 91.5; DB 4; Length 186;
 Best Local Similarity 30.5%; Pred. No. 0.001;
 Matches 25; Conservative 6; Mismatches 28; Indels 23; Gaps 6;

QY 10 LILACIP--COLRCSSNT--PPLTCQRYCYCEYFDSLILACPPCLRCSPPTC-----QYCC 59
 DB 17 LENCRRPSCCQYTCRTCTCCRRPSCVSSCCRPCCQSVCCQPTCCSPCCQYTCRTCTCC 71
 QY 60 FHSFYFDSLILACPPATCOPYC 81
 DB 72 ESS-----CCRPPCCRRSC 85

RESULT 9

Q64526

ID Q64526 PRELIMINARY; PRT; 186 AA.
 AC Q64526;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Ultra-high sulphur keratin.
 GN KRTAP9-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89140394; PubMed=2465353;
 RA McNab A.R., Wood L., Theriault N., Gierman T., Vogel G.;
 RT "An ultra-high sulfur keratin gene is expressed specifically during
 RT hair growth."
 RL J. Invest. Dermatol. 92:263-266(1989).
 CC 1. SIMILARITY: TO THE PLANT THIONIN FAMILY.
 DR EMBL; M27685; AA81560.1; -
 DR MGd; MG1305997; Krtap9-1.
 DR InterPro; IPR002494; Keratin_B2.
 DR InterPro; IPR001010; Thionin.
 DR InterPro; IPR001368; TNFR_C6.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF01500; Keratin_B2.1.
 DR PROSITE; PS00271; THIONIN.1.
 DR PROSITE; PS00652; TNFR_NGFR.1; UNKNOWN_1.
 DR PROSITE; PS01208; VWF_C; UNKNOWN_1.
 SQ SEQUENCE 186 AA; 19658 MW; 61D6BFDAB72CFEB4 CRC64;

Query Match 18.4%; Score 91.5; DB 11; Length 186;
 Best Local Similarity 34.7%; Pred. No. 0.001; 24; Indels 19; Gaps 6;
 Matches 25; Conservative 4; Mismatches 19;

QY 14 CIP--COLRC--SSNTPLTQRYCYCEYFDSLILAC--PCLRCSPPTCYCCFHSFYFDSLIL 69
 DB 85 CQPCQPSCCQSCCQPCRRSCCQPCRCISCCQPC--CRPSCQSSC----- 132
 QY 70 HACPATCOPYC 81
 DB 133 --CRPC--CQPC 141

RESULT 10

Q9D3H7 PRELIMINARY; PRT; 191 AA.

AC Q9D3H7;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE 10 days neonate head cDNA, RIKEN full-length enriched library,
 DE clone:5530401.02, full insert sequence.

OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=HEAD;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Komoto H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Strabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bona M.F.,
 RA Brownstein M.J., Bule C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann W., Hume D.A., Kamiya M., Lee N.H.,

RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA	Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA	Hayashizaki Y.,
RA	"Functional annotation of a full-length mouse cDNA collection.";
RL	Nature 409:685-690(2001).
RL	EMBL; AK017437; BAB30743.1; -
DR	InterPro; IPRO02494; Keratin_B2.
DR	InterPro; IPRO01010; Thionin.
DR	InterPro; IPRO01368; TNFR C6.
DR	InterPro; IPRO01007; VWF C.
DR	Pfam; PF01500; Keratin_B2; 1.
DR	PROSITE; PS00271; THIONIN; UNKNOWN_1.
DR	PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR	PROSITE; PS01208; VWF; UNKNOWN_1.
DR	SEQUENCE 191 AA; 20068 MW; 522B841DC9A8A9D5 CRC64;
SO	

Query Match	18.4%	Score 91.5	DB 11	Length 191;
Best Local Similarity	32.9%	Pred. NO. 0.0011		
Matches	23	Mismatches	21	Indels
		Conservative		
QY	16	PCQLRGSSNTP---	PLTCORYCCYCFDPSLLHACPCURCSPPTCQ-YCCFHSEYFDSLHA	71
Db	63	PCVSSCCRTPCQPCCVSSCCQ-----	PC--CFSCCCQSCQPS-----	C 103
QY	72	CPATCPYC	81	
Db	104	CPSCCPSC	113	

RESULT 11	Q9BYQ3	PRELIMINARY;	PRT; 159 AA.
ID	Q9BYQ3		
AC	Q9BYQ3.1		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DI	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-OCT-2001 (TREMBLrel. 18, Last annotation update)		
DI	01-OCT-2001 (TREMBLrel. 18, Last annotation update)		
DE	keratin associated protein 9.3.		
DE	KRTA9.3		
GN	KRTA9.3		
OS	Homo sapiens (Human)		
OS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OC			
OX	NFBL_TaxID=9606;		
LN	1		
RR	SEQUENCE FROM N.A.		
RC	TSISSUS=SCALP;		
EA	Rothers M.A., Langbein L., Winter H., Ehmann C., Korn B., Schweizer J.;		
PA	"Characterization of a cluster of human high/ ultrahigh keratin		
RT	associated proteins on chromosome 17q12-21.";		
RL	Submitted (Oct-2000) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL: AJ406947; CAC27586.1; -		
DR	InterPro: IPR002494; Keratin B2.		
DR	InterPro: IPR001368; TNFR c6.		
DR	Pfam: PF01500; Keratin B2.1.		
DR	PROSITE: PS00652; TNFR NGFR 1.		
SO	SEQUENCE 159 AA; 16853 MW; 375CC1B52BECDE68 CRC64;		
SO	UNKNOWN 1.		

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Query Match      17.9%  Score 89;  DB 4;  Length 159;
Best Local Similarity 29.5%  Pred. NO. 0.0018;
Matches 26;  Conservative 4;  Mismatches 20;  Indels 38;  Gaps 7;

QY  10  LUHACIP-CQLRC-----SNTPLTCQYCCFEYDSLTHAC--PCLRCGPP 53
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB  1  MTHCCSPCCQPTTCRTTQKQPTTTCSTB--CCQPSCC-----VSSCCQPC--CHPT 50
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY  54  TQYCCFSEHYEDSLTHACPPATCQPYC 81
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB  51  CCNTCC-----CRITCCQPIC 66
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

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RESULT 12

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088281      PRELIMINARY;      PRT; 1574 AA.
ID
AC Q88381
Q88381,      SEQUENCE FROM N.A.
01-NOV-1998 (TREMBLrel. 08, Created)
DT DT
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DT DE
DT MEGP6.
GN MEGP6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC
FN NCBI_TaxID=10116;
RX
RN [1]
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE=98360089; PubMed=9693030;
RA Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
RT "Identification of high-molecular-weight proteins with multiple EGF-
RT like motifs by motif-trap screening.";
RL Genomics 51:27-34(1998).
DR EMBL; AB011532; BAA32462.1; -.
DR HSPF; P00736; IAPQ.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR Pfam; PF00009; EGF; 24.
DR SMART; SM00179; EGF_Ca. 4.
DR SMART; SM00001; EGF-like. 19.
DR PROSITE; PS00010; ASX_HYDROXYL; 5.
DR PROSITE; PS00022; EGF_1; UNKNOWN_23.
DR PROSITE; PS01186; EGF_2; 23.
DR PROSITE; PS01187; EGF_Ca; 5.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
KW SEQUENCE 1574 AA; 165445 MW; 2B48533D8F77F6E7 CRC64.
SO

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Query Match      17.9%; Score 89; DB 11; Length 1574;
Best Local Similarity 29.4%; Pred. No. 0.014;
Matches 30; Conservative 9; Mismatches 25; Indels 38; Gaps 8;

Qy 1 CSQNEYFDSLHLHACIPCOL-----RCSSNTPPLT---CQRYCCEV----FDSLHLHACPC 47
Db 966 CSAGAPCDVATGSGI-CPAGRWGPRCAQSCPPPLTFGLNCSQICTCFNGASCDSVTGQC-- 1022

Qy 48 LRCSP-----PTCQYCCPHSEYFDSLHLHACPPA-----TCQPYC 81
Db 1023 -HCAFGWGWGPTC-----LQACPPGPLYGNKCQHSK 1050

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RESULT 13
Q9BYR3
ID Q9BYR3 PRELIMINARY; PRT; 166 AA.
AC Q9BYR3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Keratin associated protein 4.4.
GN KRTAP4.4.
OS Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=SCALP;
RC Rogers M.A.; Langbein L.; Winter H.; Etmann C.; Korn B.; Schweizer J.;
RT "Characterization of a cluster of human high/ ultrahigh keratin
RT associated proteins on chromosome 17q12-21";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AJ406936; CAC27575.1; -
DR InterPro; IPR002494; Keratin_B2.
DR InterPro; IPR001368; TNFR_c6.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PF01500; Keratin_B2; 1.

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DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS01208; VMEC; UNKNOWN_1.
SQ SEQUENCE 166 AA; 18023 MW; C373D121611A7115 CRC64;

Query Match 17.7%; Score 88; DB 4; Length 166;
Best Local Similarity 28.4%; Pred. No. 0.0025;
Matches 25; Conservative 4; Mismatches 29; Indels 30; Gaps 5;

QY 10 LTHACIP-COLRC-----SSNTPLTCQRYCEYFDSLHACPLR--CSP 53
DB 17 LENCRCPSYCCCTCCRTCCRPSCVSCCPCCQTTCCR--TTCCPSCVSSCCRPQ 74

QY 54 TCQYCCFHSYFDSLHACPPATCQPYC 81
DB 75 CCQSV-----CQPTCCRPQC 90

RESULT 14
Q9BYQ2 PRELIMINARY; PRT; 154 AA.

AC Q9BYQ2; 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Keratin associated protein 9.4.
GN KRTAP9.4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SCALP;
RA Rogers M.A., Langbein L., Winter H., Ehmann C., Korn B., Schweizer J.;
RT "Characterization of a cluster of human high/ultrahigh keratin
RT Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ406946; CAC27585.1;
DR InterPro; IPR002494; Keratin_B2.
DR Pfam; PF01500; Keratin_B2; 1.
SQ SEQUENCE 154 AA; 16454 MW; 2EAF682E16165105 CRC64;

Query Match 17.6%; Score 87.5; DB 4; Length 154;
Best Local Similarity 26.4%; Pred. No. 0.0027;
Matches 29; Conservative 10; Mismatches 30; Indels 41; Gaps 8;

QY 1 CSQNEYFD--SLHACIP-----COLRC-----SSNTPLTCQRYCEYFDS--- 40
DB 56 CCQNTCCQPTCVSCCPSCSTPCQPTCCGSSCDSGSCAPVYCRRTC--YPTVTVCL 113

QY 41 ---LHAC-----PCLRCSPPTCQYCFHSEYFDSLHACPPATCQPYC 81
DB 114 PGLNCGSCSNCCQPC--CRPACERTTCRP-----TCVSSCCQPC 153

RESULT 15
Q9BYQ4 PRELIMINARY; PRT; 174 AA.

AC Q9BYQ4; 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Keratin associated protein 9.2.
GN KRTAP9.2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SCALP;
RA Rogers M.A., Langbein L., Winter H., Ehmann C., Korn B., Schweizer J.;
RT "Characterization of a cluster of human high/ ultrahigh keratin

RT associated proteins on chromosome 17q12-21."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ406946; CAC27585.1;
DR InterPro; IPR002494; Keratin_B2.
DR Pfam; PF01500; Keratin_B2; 1.
SQ SEQUENCE 174 AA; 18261 MW; 2C378CFB0AA9F24D CRC64;

Query Match 17.6%; Score 87.5; DB 4; Length 174;
Best Local Similarity 28.6%; Pred. No. 0.003;
Matches 26; Conservative 4; Mismatches 22; Indels 39; Gaps 7;

QY 10 LTHACIP-COLRCSSNT-----PPLT-----CORYCEYFDSLHAC--PCLRC 50
DB 1 MTHCCPCCQPTCCRTCCRTCCCKKPTTVTTCSTSCCQPAAC-----VSSCCQPC--C 52

QY 51 SPPTCQYCFHSEYFDSLHACPPATCQPYC 81
DB 53 RPTSCQNTC-----CRTCCQPTC 71

Search completed: January 7, 2003, 09:40:07
Job time : 24.9398 secs

us-09-855-158-13.ra1

Tue Jan 7 10:36:46 2003

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:35:14 ; Search time 9.94737 Seconds
(without alignments)
239.587 Million cell updates/sec

Title: US-09-855-158-13
Perfect score: 498
Sequence: 1 CSQNYFDSLLHACIPCOLR.....SEYFDSLLHACPPATCPYC 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgm2_6/ptodata/1/iaa/5A COMB.pcp.*
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3: /cgm2_6/ptodata/1/iaa/6A COMB.pcp.*
4: /cgm2_6/ptodata/1/iaa/6B COMB.pcp.*
5: /cgm2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
6: /cgm2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	93	18.7	166	2	US-08-810-572A-6
2	93	18.7	166	4	US-09-290-333-6
3	93	18.7	293	4	US-08-810-572A-2
4	93	18.7	293	4	US-09-290-333-2
5	82	16.5	508	4	US-09-019-095A-8
6	82	16.5	521	4	US-09-019-095A-22
7	82	16.5	526	4	US-09-019-095A-2
8	80	16.1	3075	2	US-08-460-309-5
9	80	16.1	3075	2	US-08-125-077-5
10	80	16.1	5405	4	US-08-718-388-9
11	79	15.9	320	4	US-09-183-861-22
12	79	15.9	320	4	US-09-183-861-55
13	79	15.9	320	4	US-09-022-765-22
14	79	15.9	320	4	US-09-022-765-55
15	78	15.7	545	4	US-09-019-095A-38
16	78	15.7	109	2	US-08-527-044-2
17	78	15.7	109	3	US-09-013-780-2
18	77.5	15.6	139	3	US-08-965-903B-20
19	77.5	15.6	139	4	US-09-370-398-4
20	76.5	15.4	2414	1	US-08-227-535-2
21	76.5	15.4	2414	1	PCT-US95-04682-2
22	76	15.3	2441	1	US-08-861-739-2
23	76	15.3	2441	3	US-08-861-739-2
24	76	15.3	2441	4	US-08-814-247A-8
25	76	15.3	2442	4	US-08-814-247A-10
26	75.5	15.2	156	3	US-08-800-982-30
27	75.5	15.2	156	5	PCT-US94-10261A-30

28	75.5	15.2	1713	3	US-08-600-982-24
29	75.5	15.2	1713	5	PCT-US94-10261A-24
30	75	15.1	219	1	US-08-152-019A-31
31	75	15.1	219	2	US-08-460-309-18
32	75	15.1	219	2	US-08-125-077-18
33	75	15.1	430	3	US-08-997-897-2
34	75	15.1	430	3	US-09-156-836B-2
35	73.5	14.8	435	4	US-09-561-989-10
36	73	14.7	689	4	US-09-177-249-2
37	73	14.7	689	4	US-09-061-769A-2
38	72.5	14.6	969	2	US-08-284-941-2
39	72.5	14.6	969	2	US-08-447-642-2
40	72.5	14.6	969	4	US-09-236-503-2
41	72.5	14.6	969	5	PCT-US93-02147A-2
42	72	14.5	275	1	US-08-312-870-7
43	72	14.5	366	4	US-08-857-076-103
44	72	14.5	446	1	US-08-307-444A-5
45	72	14.5	446	1	US-08-587-389-5

ALIGNMENTS

RESULT 1
US-08-810-572A-6
; Sequence 6, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESS: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq. David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-343-1684
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-810-572A-6
Query Match 18.7%; Score 93; DB 2; Length 166;
Best Local Similarity 28.4%; Pred. No. 0.037;

ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

```

ZIP: 07806
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Passport Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/290,333
FILING DATE: 12-Apr-1999
CLASSIFICATION: Unknown>

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ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684

TELEFAX: 2 ID NO: 2;
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 293 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 SEQUENCE DESCRIPTION: SEQ ID
 NO: 200-333-2

[illegible]

```

RESULT 5
US-09-019-095A-8
; Sequence 8, Application US/09019095A
; Patent No. 6287858
; GENERAL INFORMATION:
; APPLICANT: D'Andrea, Alan D.
; INVENTOR: Zhu, Yuan
; TITLE OF INVENTION: Deubiquitinating Enzymes That Regulate
; FILE OF INVENTION: Cell Growth
; FILE REFERENCE: DFCI-435p2A2
; CURRENT APPLICATION NUMBER: US/09/019,095A
; CURRENT FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: PCT/US96/12884
; PRIOR FILING DATE: 1996-08-07
; PRIOR APPLICATION NUMBER: US 60/002,066
; PRIOR FILING DATE: 1995-08-09
; PRIOR APPLICATION NUMBER: US 60/019,787
; PRIOR FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 508
; TYPE: 'PRT'

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; ORGANISM: Murine
; US-09-019-095A-8
;
Query Match      16.5%; Score 82; DB 4; Length 508;
Best Local Similarity 35.8%; Pred. No. 1.2; 18; Indels 8;
Matches 19; Conservative
;
QY 19 LRCSNTPPLTCQRYCCYFDSLHACPLRCSPPTCCYCCFHSEYFDSLHA 71
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; 55 LQCLTHIPPL-----ADYMLSQEHSQTC--CSPEGCKLCAMEALVTQSLHLS 99
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
;
RESULT 6
US-09-019-095A-22
; Sequence 22, Application US/09019095A
; Patent No. 6287858
; GENERAL INFORMATION:
; APPLICANT: D'Andrea, Alan D.
; TITLE OF INVENTION: Deubiquitinating Enzymes That Regulate
; FILE OF INVENTION: Cell Growth
; FILE REFERENCE: DFCI-4352A2
; CURRENT APPLICATION NUMBER: US/09/019,095A
; CURRENT FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: PCT/US96/12884
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: US 60/002,066
; PRIOR FILING DATE: 1995-08-09
; PRIOR APPLICATION NUMBER: US 60/019,787
; PRIOR FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Murine
; US-09-019-095A-22
;
Query Match      16.5%; Score 82; DB 4; Length 521;
Best Local Similarity 35.8%; Pred. No. 1.2; 18; Indels 8;
Matches 19; Conservative
;
QY 19 LRCSNTPPLTCQRYCCYFDSLHACPLRCSPPTCCYCCFHSEYFDSLHA 71
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; DB 61 LQCLTHIPPL-----ADYMLSQEHSQTC--CSPEGCKLCAMEALVTQSLHLS 105
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
;
RESULT 7
US-09-019-095A-2
; Sequence 22, Application US/09019095A
; Patent No. 6287858
; GENERAL INFORMATION:
; APPLICANT: D'Andrea, Alan D.
; TITLE OF INVENTION: Deubiquitinating Enzymes That Regulate
; FILE OF INVENTION: Cell Growth
; FILE REFERENCE: DFCI-4352A2
; CURRENT APPLICATION NUMBER: US/09/019,095A
; CURRENT FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: PCT/US96/12884
; PRIOR FILING DATE: 1996-08-07
; PRIOR APPLICATION NUMBER: US 60/002,066
; PRIOR FILING DATE: 1995-08-09
; PRIOR APPLICATION NUMBER: US 60/019,787
; PRIOR FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Murine
; US-09-019-095A-2

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us-09-855-158-13.ra1

Page 4

Query Match 16.5%; Score 82; DB 4; Length 526;
Best Local Similarity 35.8%; Pred. No. 1.2; Indels 8; Gaps 2;
Matches 19; Conservative 8; Mismatches 18;

QY 19 LRCSSNTPPLTCORVCEYFDSLHACPLRCSPPTCOYCFHSEYFDSLHAC 71
DB 66 LQCLHTHPPL-----ADVYLSEHSGTC--CSPECKCKAMEALVTQSLHLS 110

RESULT 8

US-08-460-309-5
; Sequence 5, Application US/08460309
; Patent No. 5837496
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leivo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; TITLE OF INVENTION: Fragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,309
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,077
; FILING DATE: 22-SEP-1993
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,319
; FILING DATE: 30-JAN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/919,951
; FILING DATE: 27-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9721
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3075 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-460-309-5

Query Match 16.1%; Score 80; DB 2; Length 3075;

Best Local Similarity 23.4%; Pred. No. 10;

Matches 29; Conservative 10; Mismatches 37; Indels 48; Gaps 8;

QY 1 CSQNEVFDL--HACIPCO-----LRCSSNTPPLTCORVCE-- 36

DB 831 CADGYGNPTVPBESCVPCDCSGNVDPSEAGHDSVTGECIKLGNTDGAHCR--CADGF 889

QY 37 YFDSL-----LHACPC-----LRCSP--PTCOYC--CFHSEYFDSLHACP 73

DB 890 YGDAVTKNCRACECHVKGSHSAVCHLETLGLCDCKPNVTGQCDQCLHGYGLDSHGCR 949

QY 74 PATC 77

DB 950 PCNC 953

RESULT 9

US-08-125-077-5
; Sequence 5, Application US/08125077
; Patent No. 5872231
; Patent No. 5840863
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leivo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; TITLE OF INVENTION: Fragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/125,077
; FILING DATE: 22-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,319
; FILING DATE: 30-JAN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/919,951
; FILING DATE: 27-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9721
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3075 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-125-077-5

Query Match 16.1%; Score 80; DB 2; Length 3075;

Best Local Similarity 23.4%; Pred. No. 10;

Matches 29; Conservative 10; Mismatches 37; Indels 48; Gaps 8;

QY 1 CSQNEVFDL--HACIPCO-----LRCSSNTPPLTCORVCE-- 36

DB 831 CADGYGNPTVPBESCVPCDCSGNVDPSEAGHDSVTGECIKLGNTDGAHCR--CADGF 889

QY 37 YFDSL-----LHACPC-----LRCSP--PTCOYC--CFHSEYFDSLHACP 73

DB 890 YGDAVTKNCRACECHVKGSHSAVCHLETLGLCDCKPNVTGQCDQCLHGYGLDSHGCR 949

QY 74 PATC 77

DB 950 PCNC 953

RESULT 10
US-08-718-388-9

us-09-855-158-13.ra1

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```

; Sequence 9, Application US/08718388
; Patent No. 6271362
; GENERAL INFORMATION:
; APPLICANT: MORIKAWA, MINORU
; APPLICANT: HARADA, NAOKI
; TITLE OF INVENTION: GENE ENCODING IgG FC REGION-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,388
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 0230-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5405 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-718-388-9

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Query Match 16.1%; Score 80; DB 4; Length 5405;
Best Local Similarity 25.4%; Pred. No. 17;
Matches 29; Conservative 12; Mismatches 48; Gaps 10;

QY 1 CSQNEYFDSLHACI-PCQRCSSNTPPLTCQRYCCEYFDSLHACPC-----LRCS 51
DB 2733 CPQNGHYE-----LCADTCSLGSALSAPLQCPDCAE-----GCQDSGFLYNGOACV 2781

QY 52 PPTCQYC-CFHS-EYFD---SL-----HACPPA-TCQP 79
DB 2782 P--IQCGYHNGAYPEPTVLIDNCRCQCTCHAGKVVVQCEHSCRFPGQVCQP 2833

```

```

RESULT 11
US-09-183-861-22
; Sequence 22, Application US/09183861
; Patent No. 6365165
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk

```

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/183,861
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 09/022,765
; APPLICATION NUMBER: 12-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.420C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 320 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-183-861-22

Query Match 15.9%; Score 79; DB 4; Length 320;
Best Local Similarity 27.5%; Pred. No. 1.5;
Matches 25; Conservative 11; Mismatches 23; Indels 32; Gaps 7;

QY 13 ACIPCO-----LRCSN---TPPLTCQRYCCEYFDSLHACPCLRCSPT- 54
DB 105 ACVRCQEPNCFSCDSANKCTCAPNYVLTPLLTCTSPVAC-----NIEH---CMQCDPQT 157

QY 55 --COYCC--FHSEYFDSLH--ACPPATCQ 78
DB 158 SRQECVSPYVDSYDGLCGLSDACSVNCK 188

RESULT 12
US-09-183-861-55
; Sequence 55, Application US/09183861
; Patent No. 6365165
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/183,861
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/022,765
; FILING DATE: 12-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.420C3

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-183-861-55

Query Match 15.9%; Score 79; DB 4; Length 320;
Best Local Similarity 27.5%; Pred. No. 1.5;
Matches 25; Conservative 11; Mismatches 23; Indels 32; Gaps 7;

OY 13 ACIPQ-----LRCSN---TPPLTCQRYCCYFDSLHACPCIRCSPT- 54
DB 105 ACVRCQEPNCFSCDSANKCTQCAPNYLTPPLTCSPVAC---NIEH---CMQCDPQTP 157
OY 55 --CQYCC--FHSEYFDSLH--ACPPATQ 78
DB 158 SRCQECVSPYVDSYDGLCRSLDACSVPNCK 188

RESULT 13
US-09-022-765-22
Sequence 22, Application US/09022765
Patent No. 6375955

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, David C.
APPLICANT: Skeiky, Yasar A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,765
FILING DATE: 12-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-765-22

Query Match 15.9%; Score 79; DB 4; Length 320;
Best Local Similarity 27.5%; Pred. No. 1.5;
Matches 25; Conservative 11; Mismatches 23; Indels 32; Gaps 7;

OY 13 ACIPQ-----LRCSN---TPPLTCQRYCCYFDSLHACPCIRCSPT- 54
DB 105 ACVRCQEPNCFSCDSANKCTQCAPNYLTPPLTCSPVAC---NIEH---CMQCDPQTP 157
OY 55 --CQYCC--FHSEYFDSLH--ACPPATQ 78
DB 158 SRCQECVSPYVDSYDGLCRSLDACSVPNCK 188

RESULT 14
US-09-022-765-55
Sequence 55, Application US/09022765
Patent No. 6375955

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, David C.
APPLICANT: Skeiky, Yasar A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,765
FILING DATE: 12-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-022-765-55

Query Match 15.9%; Score 79; DB 4; Length 320;
Best Local Similarity 27.5%; Pred. No. 1.5;
Matches 25; Conservative 11; Mismatches 23; Indels 32; Gaps 7;

OY 13 ACIPQ-----LRCSN---TPPLTCQRYCCYFDSLHACPCIRCSPT- 54
DB 105 ACVRCQEPNCFSCDSANKCTQCAPNYLTPPLTCSPVAC---NIEH---CMQCDPQTP 157
OY 55 --CQYCC--FHSEYFDSLH--ACPPATQ 78
DB 158 SRCQECVSPYVDSYDGLCRSLDACSVPNCK 188

RESULT 15
US-09-019-095A-38

Sequence 38, Application US/09019095A
Patent No. 6287858

GENERAL INFORMATION:
APPLICANT: D'Andrea, Alan D.

us-09-855-158-13.ra1

Tue Jan 7 10:36:46 2003

```

; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: Deubiquitinating Enzymes That Regulate
; TITLE OF INVENTION: Cell Growth
; FILE REFERENCE: DFCI-435p2A2
; CURRENT APPLICATION NUMBER: US/09/019,095A
; CURRENT FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: PCT/US96/12884
; PRIOR FILING DATE: 1996-08-07
; PRIOR APPLICATION NUMBER: US 60/002,066
; PRIOR FILING DATE: 1995-08-09
; PRIOR APPLICATION NUMBER: US 60/019,787
; PRIOR FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 545
; TYPE: PRT
; ORGANISM: murine
; US-09-019-095A-38

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Query Match 15.9%; Score 79; DB 4; Length 545;
Best Local Similarity 34.0%; Pred. No. 2.4;
Matches 18; Conservative 9; Mismatches 18; Indels 8; Gaps 2;

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QY 19 LRCSSNTPTLCQRYCCEYFDSLHACPCILRCSPPTCQYCCFHSYFDSLHA 71
DB 66 LQCLHTPTPL-----ADYMLSQEYSQTC--CSPEGCKMCAMEAHVTQSLLHS 110

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Search completed: January 7, 2003, 09:42:05
Job time : 11.9474 secs

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us-09-855-158-13.rapb

Tue Jan 7 10:36:46 2003

GenCore version 5.1.3
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OM protein - protein search, using sw model
Run on: January 7, 2003, 09:40:20 ; Search time 6.09023 Seconds
(without alignments)
252.055 Million cell updates/sec

Title: US-09-855-158-13
Perfect score: 498
Sequence: 1 CSQNEYFDSLHACIPCOLR.....SEYFDSLHACPPATCQPYC 81

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 117078 seqs, 18951520 residues
Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
11: /cgn2_6/ptodata/1/pubaa/US10_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	498	100.0	81	10	US-09-854-864-13
2	230.5	46.3	207	9	US-10-077-438-3
3	220.5	46.3	207	9	US-10-077-137-3
4	201.5	40.5	283	10	US-09-854-864-9
5	201	40.4	34	10	US-09-854-864-7
6	201	40.4	51	10	US-09-854-864-6
7	201	40.4	58	10	US-09-854-864-21
8	201	40.4	181	10	US-09-854-864-5
9	201	40.4	184	9	US-10-077-438-1
10	201	40.4	184	9	US-10-077-438-7
11	201	40.4	184	9	US-10-077-137-1
12	201	40.4	184	9	US-10-077-137-7
13	139.5	30.7	117	10	US-09-854-864-12
14	136	28.0	281	10	US-09-854-864-10
15	105	27.3	185	10	US-09-854-864-11
16	105	21.1	167	10	US-09-854-864-16
17	93	18.7	166	10	US-09-854-864-15
18	93	18.7	291	9	US-09-779-050A-43
19	93	18.7	293	9	US-09-779-050A-42

93	18.7	293	9	US-10-084-971-2	Sequence 2, Appl
93	18.7	293	10	US-09-879-919-22	Sequence 22, Appl
93	18.7	293	10	US-09-854-864-14	Sequence 14, Appl
93	18.7	293	10	US-09-961-376-2	Sequence 2, Appl
93	18.7	297	10	US-09-854-864-18	Sequence 18, Appl
91.5	18.4	231	10	US-09-864-761-37946	Sequence 37946, A
89.5	18.0	134	10	US-09-864-761-39564	Sequence 39564, A
84.5	17.0	270	10	US-09-764-855-145	Sequence 145, Appl
83	16.7	93	10	US-09-864-761-46675	Sequence 46675, A
82	16.3	230	10	US-09-874-062-3	Sequence 3, Appl
81	16.3	1587	10	US-09-845-583-10	Sequence 10, Appl
80.5	16.2	198	10	US-09-864-761-39864	Sequence 39864, A
80.5	16.2	1798	10	US-09-938-275-9	Sequence 9, Appl
80	16.1	3075	10	US-09-938-275-5	Sequence 5, Appl
80	16.1	5405	9	US-10-025-380-1116	Sequence 1116, Ap
80	16.1	5405	10	US-09-922-217-1116	Sequence 20, Appl
79	15.9	59	10	US-09-854-864-20	Sequence 22, Appl
79	15.9	320	9	US-09-991-496-22	Sequence 55, Appl
79	15.9	320	9	US-09-991-496-55	Sequence 22, Appl
79	15.9	320	10	US-09-874-923-22	Sequence 55, Appl
79	15.9	320	10	US-09-874-923-55	Sequence 121, App
79	15.9	709	9	US-09-991-496-121	Sequence 121, App
79	15.9	709	10	US-09-874-923-121	Sequence 121, App
78	15.7	70	10	US-09-864-761-44312	Sequence 44312, A
76	15.3	191	9	US-09-950-933A-66	Sequence 66, Appl
76	15.3	2441	12	US-10-109-886-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-854-864-13
Sequence 13, Application US/09854864
Patent No. US20030081296A1
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
FILE REFERENCE: A686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 81
TYPE: PRT
ORGANISM: Consensus
US-09-854-864-13

Query Match	100.0%	Score 498	DB 10	Length 81
Best Local Similarity	100.0%	Pred. No. 1.5e-35		
Matches 81	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY 1 CSQNEYFDSLHACIPCOLRCSNTPLTCQRYCCEYFDSLHACPCLRCSPTCOYCCF 60
Db 1 CSQNEYFDSLHACIPCOLRCSNTPLTCQRYCCEYFDSLHACPCLRCSPTCOYCCF 60

QY 61 HSEYFDSLHACPPATCQPYC 81
Db 61 HSEYFDSLHACPPATCQPYC 81

RESULT 2
US-10-077-438-3
Sequence 3, Application US/10077438
Patent No. US20020165156A1
GENERAL INFORMATION:

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/ APPLICANT: Mackay, Fabienne
/ APPLICANT: Browning, Jeffrey
/ APPLICANT: Ambrose, Christine
/ APPLICANT: Tschopp, Jurg
/ APPLICANT: Schneider, Pascal
/ APPLICANT: Thompson, Jeffrey
/ APPLICANT: Biogen, Inc.
/ APPLICANT: Apotech R&D S.A.
/ TITLE OF INVENTION: Baff Receptor (BCMA), An
/ TITLE OF INVENTION: Immunoregulatory Agent
/ FILE REFERENCE: A080PCT
/ CURRENT APPLICATION NUMBER: US/10/077,438
/ CURRENT FILING DATE: 2002-02-18
/ PRIOR APPLICATION NUMBER: 60/149,378
/ PRIOR FILING DATE: 1999-08-17
/ PRIOR APPLICATION NUMBER: 60/181,684
/ PRIOR FILING DATE: 2000-02-11
/ PRIOR APPLICATION NUMBER: 60/183,536
/ PRIOR FILING DATE: 2000-02-18
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 207
/ TYPE: PRT
/ ORGANISM: homo sapien
US-10-077-438-3

Query Match          46.3%; Score 230.5; DB 9; Length 207;
Best Local Similarity 57.8%; Pred. No. 5.7e-13;
Matches 48; Conservative 0; Mismatches 4; Indels 31; Gaps 4;
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QY 1 CSQNEYPDSLHACIPCOLRCSSNTPLTCQRYCCEYPFDSLHAC-PC-LRCSPTQCYC 58
DB 46 CSQNEYPDSLHACIPCOLRCSSNTPLTC-----LHACIPCOLRCSSNT----- 90
QY 59 CFHSEYFDSLHACPPATCQPYC 81
DB 91 -----PPLTCQRYC 99
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RESULT 3
US-10-077-137-3
/ Sequence 3, Application US/10077137
/ Patent No. US20020172674A1
/ GENERAL INFORMATION:
/ APPLICANT: Mackay, Fabienne
/ APPLICANT: Browning, Jeffrey
/ APPLICANT: Ambrose, Christine
/ APPLICANT: Tschopp, Jurg
/ APPLICANT: Schneider, Pascal
/ APPLICANT: Thompson, Jeffrey
/ APPLICANT: Biogen, Inc.
/ APPLICANT: Apotech R&D S.A.
/ TITLE OF INVENTION: Baff Receptor (BCMA), An
/ TITLE OF INVENTION: Immunoregulatory Agent
/ FILE REFERENCE: A080PCT
/ CURRENT APPLICATION NUMBER: US/10/077,137
/ CURRENT FILING DATE: 2001-02-15
/ PRIOR APPLICATION NUMBER: 60/149,378
/ PRIOR FILING DATE: 1999-08-17
/ PRIOR APPLICATION NUMBER: 60/181,684
/ PRIOR FILING DATE: 2000-02-11
/ PRIOR APPLICATION NUMBER: 60/183,536
/ PRIOR FILING DATE: 2000-02-18
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 207
/ TYPE: PRT
/ ORGANISM: homo sapien
US-10-077-137-3
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Query Match 46.3%; Score 230.5; DB 9; Length 207;

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Best Local Similarity 57.8%; Pred. No. 5.7e-13;
Matches 48; Conservative 0; Mismatches 4; Indels 31; Gaps 4;

QY 1 CSQNEYPDSLHACIPCOLRCSSNTPLTCQRYCCEYPFDSLHAC-PC-LRCSPTQCYC 58
DB 46 CSQNEYPDSLHACIPCOLRCSSNTPLTC-----LHACIPCOLRCSSNT----- 90
QY 59 CFHSEYFDSLHACPPATCQPYC 81
DB 91 -----PPLTCQRYC 99
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RESULT 4
US-09-854-864-9
/ Sequence 9, Application US/09854864
/ Patent No. US20020081296A1
/ GENERAL INFORMATION:
/ APPLICANT: THEILL, LARS EYDE
/ APPLICANT: YU, GANG
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
/ TITLE OF INVENTION: BLYS/Ap-3, AND TACI
/ FILE REFERENCE: A-686B
/ CURRENT APPLICATION NUMBER: US/09/854,864
/ CURRENT FILING DATE: 2001-09-11
/ PRIOR APPLICATION NUMBER: US 60/204,039
/ PRIOR FILING DATE: 2000-05-12
/ PRIOR APPLICATION NUMBER: US 60/214,591
/ PRIOR FILING DATE: 2000-06-27
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 9
/ LENGTH: 283
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-854-864-9
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Query Match 40.5%; Score 201.5; DB 10; Length 283;
Best Local Similarity 60.6%; Pred. No. 1.9e-10;
Matches 40; Conservative 2; Mismatches 9; Indels 15; Gaps 3;

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QY 1 CSQNEYPDSLHACIPCOLRCSSNTPLTCQRYC-CEYFDSL-----LHACPC 47
DB 5 CSQNEYPDSLHACIPCOLRCSSNTPLTCQRYCNASVTNSVGTNAGGGGDKHTCP- 63
QY 48 LRCSPP 53
DB 64 -PCPAP 68
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RESULT 5
US-09-854-864-7
/ Sequence 7, Application US/09854864
/ Patent No. US20020081296A1
/ GENERAL INFORMATION:
/ APPLICANT: THEILL, LARS EYDE
/ APPLICANT: YU, GANG
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
/ TITLE OF INVENTION: BLYS/Ap-3, AND TACI
/ FILE REFERENCE: A-686B
/ CURRENT APPLICATION NUMBER: US/09/854,864
/ CURRENT FILING DATE: 2001-09-11
/ PRIOR APPLICATION NUMBER: US 60/204,039
/ PRIOR FILING DATE: 2000-05-12
/ PRIOR APPLICATION NUMBER: US 60/214,591
/ PRIOR FILING DATE: 2000-06-27
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 7
/ LENGTH: 34
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-854-864-7
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Query Match          40.4%; Score 201; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSTNPPLTCORYC 34
Db 1 CSQNEYFDSLHACIPCOLRCSSTNPPLTCORYC 34

RESULT 6
US-09-854-864-6
; Sequence 6, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-6

Query Match          40.4%; Score 201; DB 10; Length 51;
Best Local Similarity 100.0%; Pred. No. 5.1e-11;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSTNPPLTCORYC 34
Db 5 CSQNEYFDSLHACIPCOLRCSSTNPPLTCORYC 38

RESULT 7
US-09-854-864-21
; Sequence 21, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-21

Query Match          40.4%; Score 201; DB 10; Length 58;
Best Local Similarity 100.0%; Pred. No. 5.6e-11;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSTNPPLTCORYC 34
Db 1 CSQNEYFDSLHACIPCOLRCSSTNPPLTCORYC 34

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RESULT 8
US-09-854-864-5
; Sequence 5, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5

Query Match          40.4%; Score 201; DB 10; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSTNPPLTCORYC 34
Db 5 CSQNEYFDSLHACIPCOLRCSSTNPPLTCORYC 38

RESULT 9
US-10-077-438-1
; Sequence 1, Application US/10077438
; Patent No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoep, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: AG80PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-1

Query Match          40.4%; Score 201; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSTNPPLTCORYC 34

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Db      8 CSQNEYPDSLHACIPCOLRCSSNTPLTCORYC 41

RESULT 10
US-10-077-438-7
; Sequence 7, Application US/10077438
; Patent No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Teschopp, Jurig
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-7

Query Match      40.4%; Score 201; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CSQNEYPDSLHACIPCOLRCSSNTPLTCORYC 34
Db      8 CSQNEYPDSLHACIPCOLRCSSNTPLTCORYC 41

RESULT 11
US-10-077-137-1
; Sequence 1, Application US/10077137
; Patent No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Teschopp, Jurig
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT

; ORGANISM: homo sapien

Query Match      40.4%; Score 201; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CSQNEYPDSLHACIPCOLRCSSNTPLTCORYC 34
Db      8 CSQNEYPDSLHACIPCOLRCSSNTPLTCORYC 41

RESULT 12
US-10-077-137-7
; Sequence 7, Application US/10077137
; Patent No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Teschopp, Jurig
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-7

Query Match      40.4%; Score 201; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CSQNEYPDSLHACIPCOLRCSSNTPLTCORYC 34
Db      8 CSQNEYPDSLHACIPCOLRCSSNTPLTCORYC 41

RESULT 13
US-09-854-864-12
; Sequence 12, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
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us-09-855-158-13.rapb

Tue Jan 7 10:36:46 2003

Query Match 27.3%; Score 136; DB 10; Length 185;
Best Local Similarity 70.6%; Pred. No. 3.8e-05;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;
QY 1 CSOREYFDSLHACIPCOLRCSSNTPLTCORYC 34
DB 5 CFHSEYFDSLHACKPCHLRCSN--PPATCOPYC 36
Search completed: January 7, 2003, 09:54:54
Job time : 6.09023 secs

TYPE: PRT
ORGANISM: human-murine Consensus
US-09-854-864-12
Query Match 30.7%; Score 153; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 9.9e-07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 35 CEYFDSLHACPLRCSPPTCOYC 58
DB 4 CEYFDSLHACPLRCSPPTCOYC 27

RESULT 14
US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10

Query Match 28.0%; Score 139.5; DB 10; Length 281;
Best Local Similarity 45.5%; Pred. No. 2.7e-05;
Matches 30; Conservative 3; Mismatches 16; Indels 17; Gaps 3;
QY 1 CSOREYFDSLHACIPCOLRCSSNTPLTCORYCCEYFDSL--HACPC 47
DB 5 CFHSEYFDSLHACKPCHLRCSN--PPATCOPYDPSVTSVKVGTGGGDKHTCP- 61
QY 48 LRCSP 53
DB 62 -PCPAP 66

RESULT 15
US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 7, 2003, 09:38:19 ; Search time 10.5564 Seconds
(without alignments)
543.836 Million cell updates/sec

Title: US-09-855-158-13
Perfect score: 498
Sequence: 1 CSQNEVFDLLHACIPCOLR.....SEVFDLLHACIPATCPQYC 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262191 seqs, 70875818 residues

Total number of hits satisfying chosen parameters: 262191

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New.*

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- 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	201	40.4	34	6	US-10-281-053-11
3	201	40.4	184	1	PCT-US02-34376-6
4	201	40.4	184	1	PCT-US02-06001-39
5	201	40.4	184	5	US-09-848-271-2
6	201	40.4	184	6	US-10-281-053-6
7	201	40.4	184	6	US-10-087-080-39
8	100.5	20.2	334	6	US-10-258-368-8
9	100.5	20.2	366	6	US-10-258-368-6
10	93	18.7	166	6	US-10-293-816-6
11	93	18.7	233	6	US-10-268-951-22
12	93	18.7	233	6	US-10-258-368-1
13	93	18.7	233	6	US-10-293-816-2
14	93	18.7	301	6	US-10-258-368-12
15	93	18.7	404	6	US-10-258-368-15
16	91.5	17.4	231	6	US-10-203-138A-15078
17	86.5	17.4	158	6	US-10-180-903-2
18	83.5	16.8	120	6	US-10-276-774-2647
19	83	16.7	93	6	US-10-203-138A-14491
20	81	16.3	1396	5	US-09-724-676A-75263
21	81	16.3	1396	5	US-08-724-676A-75263
22	81	16.3	1408	5	US-08-724-676A-75262
23	81	16.3	1408	5	US-08-724-676A-75262
24	81	16.3	1575	5	US-09-724-676A-75261
25	81	16.3	1575	5	US-09-724-676A-75261
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31	80.5	16.2	1351	5	US-09-724-676A-74761	Sequence 74761, A
32	80.5	16.2	1351	5	US-09-724-676A-74771	Sequence 74771, A
33	80.5	16.2	1351	5	US-09-724-676A-74772	Sequence 74772, A
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37	80.5	16.2	1351	5	US-09-724-676A-74772	Sequence 74772, A
38	80.5	16.2	1609	5	US-09-724-676A-74756	Sequence 74756, A
39	80.5	16.2	1609	5	US-09-724-676A-74767	Sequence 74767, A
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42	80.5	16.2	1610	5	US-09-724-676A-74757	Sequence 74757, A
43	80.5	16.2	1610	5	US-09-724-676A-74768	Sequence 74768, A
44	80.5	16.2	1610	5	US-09-724-676A-74757	Sequence 74757, A
45	80.5	16.2	1610	5	US-09-724-676A-74768	Sequence 74768, A

ALIGNMENTS

RESULT 1
PCT-US02-34376-11
Sequence 11, Application PC/TUS0234376
GENERAL INFORMATION:
APPLICANT: Zhang, Gongyi
APPLICANT: Shu, Hong-Bing
APPLICANT: Liu, Yingfang
APPLICANT: Xu, Lianguo
TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
TITLE OF INVENTION: Modified Proteins and Methods Related Thereof
FILE REFERENCE: 2879-86-PCT
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 60/345,106
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 60/348,962
PRIOR FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: 60/354,966
PRIOR FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: 60/403,364
PRIOR FILING DATE: 2002-08-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patent in version 3.1
SEQ ID NO 11
LENGTH: 34
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-34376-11
Query Match 40.4%; Score 201; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.1e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CSQNEVFDLLHACIPCOLRCSNTPLTCQRYC 34
RESULT 2
US-10-281-053-11
Sequence 11, Application US/10281053
GENERAL INFORMATION:
APPLICANT: Zhang, Gongyi
APPLICANT: Shu, Hong-Bing
APPLICANT: Liu, Yingfang
APPLICANT: Xu, Lianguo
TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
TITLE OF INVENTION: Modified Proteins and Methods Related Thereof
FILE REFERENCE: 2879-86

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/ CURRENT APPLICATION NUMBER: US/10/281,053
/ CURRENT FILING DATE: 2002-10-24
/ PRIOR APPLICATION NUMBER: 60/345,106
/ PRIOR FILING DATE: 2001-10-24
/ PRIOR APPLICATION NUMBER: 60/348,962
/ PRIOR FILING DATE: 2002-01-14
/ PRIOR APPLICATION NUMBER: 60/354,966
/ PRIOR FILING DATE: 2002-02-07
/ PRIOR APPLICATION NUMBER: 60/403,364
/ PRIOR FILING DATE: 2002-08-13
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 11
/ LENGTH: 34
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-281-053-11
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Query Match 40.4%; Score 201; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.1e-12;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
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RESULT 3
PCT-US02-34376-6
/ Sequence 6, Application PC/TUS0234376
/ GENERAL INFORMATION:
/ APPLICANT: Zhang, Gongyi
/ APPLICANT: Shu, Hong-Bing
/ APPLICANT: Liu, Yingfang
/ APPLICANT: Xu, Liangguo
/ TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
/ FILE REFERENCE: 2879-86-PCT
/ CURRENT FILING DATE: 2002-10-24
/ PRIOR APPLICATION NUMBER: 60/345,106
/ PRIOR FILING DATE: 2001-10-24
/ PRIOR APPLICATION NUMBER: 60/348,962
/ PRIOR FILING DATE: 2002-01-14
/ PRIOR APPLICATION NUMBER: 60/354,966
/ PRIOR FILING DATE: 2002-02-07
/ PRIOR APPLICATION NUMBER: 60/403,364
/ PRIOR FILING DATE: 2002-08-13
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 6
/ LENGTH: 184
/ TYPE: PRT
/ ORGANISM: Homo sapiens
PCT-US02-34376-6
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Best Local Similarity 100.0%; Pred. No. 9.3e-12;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 8 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 41
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RESULT 4
PCT-US02-06001-39
/ Sequence 39, Application PC/TUS0206001
/ GENERAL INFORMATION:
/ APPLICANT: Mack, David H.
/ APPLICANT: Markowitz, Sanford David
/ APPLICANT: Eos Biotechnology, Inc.
/ APPLICANT: Case Western Reserve University
```

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/ TITLE OF INVENTION: Novel Methods of Diagnosis of Metastatic Colorectal
/ TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
/ FILE REFERENCE: 018501-000840PC
/ CURRENT APPLICATION NUMBER: PCT/US02/06001
/ CURRENT FILING DATE: 2002-12-20
/ PRIOR APPLICATION NUMBER: US 60/272,206
/ PRIOR FILING DATE: 2001-02-27
/ PRIOR APPLICATION NUMBER: US 60/281,149
/ PRIOR FILING DATE: 2001-04-02
/ PRIOR APPLICATION NUMBER: US 60/284,555
/ PRIOR FILING DATE: 2001-04-17
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 39
/ LENGTH: 184
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE: tumor necrosis factor receptor superfamily, member
/ OTHER INFORMATION: 17 (TNFRSF17)
PCT-US02-06001-39
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Query Match 40.4%; Score 201; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 9.3e-12;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
Db 8 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 41
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RESULT 5
US-09-848-271-2
/ Sequence 2, Application US/09848271
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Steven
/ APPLICANT: Ruben, Kevin
/ TITLE OF INVENTION: Human Tumor Necrosis Factor TR18 and Methods Based Thereon
/ FILE REFERENCE: P5526
/ CURRENT FILING DATE: 2001-05-04
/ PRIOR APPLICATION NUMBER: US/09/848,271
/ CURRENT FILING DATE: 2001-05-04
/ PRIOR APPLICATION NUMBER: 60/254,931
/ PRIOR FILING DATE: 2000-12-13
/ PRIOR APPLICATION NUMBER: 60/236,038
/ PRIOR FILING DATE: 2000-09-28
/ PRIOR APPLICATION NUMBER: 60/201,852
/ PRIOR FILING DATE: 2000-05-04
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 2
/ LENGTH: 184
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-848-271-2
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Best Local Similarity 100.0%; Pred. No. 9.3e-12;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 8 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 41
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RESULT 6
US-10-281-053-6
/ Sequence 6, Application US/10281053
/ GENERAL INFORMATION:
/ APPLICANT: Zhang, Gongyi
/ APPLICANT: Shu, Hong-Bing
/ APPLICANT: Liu, Yingfang
/ APPLICANT: Xu, Liangguo
```



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; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/10/293,816
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-816-6
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Best Local Similarity 28.4%; Pred. No. 0.07;
Matches 21; Conservative 13; Mismatches 22; Indels 18; Gaps 5;
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RESULT 11
US-10-268-951-22
; Sequence 22, Application US/10268951
; GENERAL INFORMATION:
; APPLICANT: IN, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P2
; CURRENT APPLICATION NUMBER: US/10/268,951
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 10/082,260
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/879,919
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/328,401
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/293,812
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-21
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-268-951-22
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Query Match 18.7%; Score 93; DB 6; Length 293;
Best Local Similarity 28.4%; Pred. No. 0.1;
Matches 21; Conservative 13; Mismatches 22; Indels 18; Gaps 5;
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QY 52 -----PPTQYCC 59
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Db 91 SICGQHPKQCAVFC 104
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RESULT 12
US-10-258-368-1
; Sequence 1, Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; APPLICANT: Rennett, Paul
; TITLE OF INVENTION: TacI As As Anti-Tumor Agent
; FILE REFERENCE: BIO0130 NP of PCT/US01/40626
; CURRENT APPLICATION NUMBER: US/10/258,368
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US9N 60/199,946
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-1
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Query Match 18.7%; Score 93; DB 6; Length 293;
Best Local Similarity 28.4%; Pred. No. 0.1;
Matches 21; Conservative 13; Mismatches 22; Indels 18; Gaps 5;
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QY 52 -----PPTQYCC 59
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Db 91 SICGQHPKQCAVFC 104
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RESULT 13
US-10-293-816-2
; Sequence 2, Application US/10293816
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: Von Bulow, Goetz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/10/293,816
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-816-2
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Query Match 18.7%; Score 93; DB 6; Length 293;
Best Local Similarity 28.4%; Pred. No. 0.1;
Matches 21; Conservative 13; Mismatches 22; Indels 18; Gaps 5;
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

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Run on: January 7, 2003, 09:31:39 ; Search time 59.4937 Seconds
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Title: US-09-855-158-15

Perfect score: 909

Sequence: 1 MSGLRGRGGRSRVDQBER.....SPALPGLKSLADQVALVYST 166

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	909	100.0	166	23 AAE15494	Human TACI extrace
3	909	100.0	265	22 AAE09244	Human TACI splice
4	909	100.0	293	19 AAW75783	Human lymphocyte s
5	909	100.0	293	21 AAB36312	Human neutrokin-a
6	909	100.0	293	21 AAY94000	A transmembrane ac
7	909	100.0	293	22 AAE09240	Human TACI protein
8	909	100.0	293	22 AAY71914	Human tumour necro
9	909	100.0	293	23 AAU99512	Human TACI-IgG Fc
10	909	100.0	293	23 ABB81488	Human TACI recepto

11	909	100.0	293	23 AAO14130	Human transmembran
12	909	100.0	293	23 AAW75408	Tumour necrosis fa
13	909	100.0	293	23 AAE15493	Human transmembran
14	909	100.0	293	23 AAU09900	Human AGP-3 relate
15	904	99.4	312	23 AAO14135	Protein of N-termi
16	904	99.4	397	23 AAE15498	Human TACI-immunog
17	894.5	98.4	291	23 AAU10949	Human AGP-3 recept
18	881	96.9	404	23 AAO14136	Protein of a compl
19	851	71.6	366	23 AAO14132	Protein of hTACI (
20	599	65.9	247	21 AAY93998	Human BR43x2, an i
21	490.5	54.0	334	23 AAO14133	Protein of hTACI (
22	419.5	46.1	249	21 AAY94006	A murine ztnf4, a
23	342	37.6	59	23 AAE15500	Human TACI cystein
24	279.5	30.7	57	23 AAU10953	Human AGP-3 recept
25	224	24.6	38	23 AAU10952	Human AGP-3 recept
26	218	24.0	37	23 AAU10951	Human TACI cystein
27	204	22.4	34	23 AAE15496	Human TACI cystein
28	201	22.1	33	23 AAE15495	Human AGP-3 recept
29	168	18.5	32	23 AAU10950	Human TANGO 140-2.
30	95	10.5	197	21 AAB01421	Human polypeptide
31	93	10.2	1589	22 AAM42025	Human protein sequ
32	93	10.2	1727	22 AAB95554	Human polypeptide
33	93	10.2	1878	22 AAM40239	Human polypeptide
34	92	10.1	266	22 AAM39716	Human polypeptide
35	89	9.8	1878	19 AAW81170	Human BAZ2-alpha p
36	88.5	9.7	665	22 ABB68244	Drosophila melanog
37	88	9.7	795	22 ABG07025	Novel human diagno
38	87.5	9.6	463	20 AAV13392	Amino acid sequenc
39	87.5	9.6	463	21 AAB01373	Neuron-associated
40	87.5	9.6	463	21 AAY95343	Human PRO328 antit
41	87.5	9.6	463	22 AAU12351	Human PRO328 polyp
42	87.5	9.6	463	22 AAB88408	Human membrane or
43	87.5	9.6	463	22 AAB80260	Human PRO328 prote
44	87.5	9.6	463	22 AAB53088	Human angiogenesis
45	87	9.6	251	22 AAE13153	Human mature stem

ALIGNMENTS

RESULT 1

AAW75785

ID AAW75785 standard; Protein; 166 AA.

AC AAW75785;

DT 18-JAN-1999 (first entry)

DE Human lymphocyte surface receptor extracellular domain.

KW TACI; transmembrane activator and CAML-interactor;

KW calcium signal-modulating cyclophilin ligand; human;

KW lymphocyte surface receptor; human; B-cell; B lymphocyte;

KW infection; cancer; rheumatoid arthritis; autoimmune disease;

KW glomerulonephritis; immunosuppressive; graft versus host disease;

KW transplant rejection; therapy; signal transduction.

OS Homo sapiens.

PN WO9839361-A1.

PD 11-SEP-1998.

PF 03-MAR-1998; 98WO-US04270.

PR 03-MAR-1997; 97US-0810572.

PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.

PI Bram RJ, Von Bulow G;

DR WPI, 1998-506346/43.

DR N-PSDB, AAV57330.

XX New isolated transmembrane activator protein - used to develop
PT products for treating e.g. infections, cancers, autoimmune and
PT inflammatory conditions, transplant rejection or graft-versus-host
PT disease
PS
XX Claim 8; Page 73; 89pp; English.
XX
XX This is the amino acid sequence of the N-terminal, i.e. the
CC extracellular, domain of novel human transmembrane activator and
CC CAML-interactor (TACI) protein (see AAW/5783). TACI is a lymphocyte
CC receptor protein that is involved in the calcium activation pathway.
CC It is normally present in B-lymphocytes, and to a much lesser extent
CC in immature T-lymphocytes, and can therefore be targeted to
CC specifically regulate B cell responses without affecting T cell
CC activity. The extracellular domain of TACI functions as a binding
CC site for a ligand that stimulates the activation of the cell by
CC inducing the binding of the C-terminal portion (see AAW/5784) of
CC TACI to the N-terminal domain of CAML. A recombinant form of the
CC extracellular portion of TACI acts as a dominant-negative or
CC blocking agent and acts to suppress the immune system. It can be
CC used to treat or prevent autoimmune disease, graft rejection or
CC graft versus host disease. The extracellular region is also used
CC in a claimed method for identifying a ligand for TACI, in which
CC binding of a candidate molecule is determined by detecting cellular
CC activation of the AP-1, CAMP or NF-KB pathway, of NF-AT
CC transcription factor, or of NF-AT dependent transcription.
XX
SQ Sequence 166 AA;
Query Match 100.0%; Score 909; DB 19; Length 166;
Best Local Similarity 100.0%; Pred. No. 2, 8e-83;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSGLGSRGRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLGTGMSCKTICNHQSOR 60
DB 1 MSGLGSRGRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLGTGMSCKTICNHQSOR 60
QY 61 TCAAFCRSLSCRKQKGFYDHLRLDCISGASICGHPKQCAVFCENKLRSPVNLPEELRR 120
DB 61 TCAAFCRSLSCRKQKGFYDHLRLDCISGASICGHPKQCAVFCENKLRSPVNLPEELRR 120
QY 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGKLSADQVALVYST 166
DB 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGKLSADQVALVYST 166
RESULT 2
ID AAE15494 standard; Protein; 166 AA.
XX
XX AAE15494;
XX
XX 12-MAR-2002 (first entry)
XX
XX Human TACI extracellular domain.
XX
XX Human, transmembrane activator and intracellular CAML interactor; TACI;
KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.
XX
XX Homo sapiens.
XX
XX WO200187979-A2.
XX
XX 22-NOV-2001.
XX
XX 14-MAY-2001; 2001WO-US15567.

XX
XX 12-MAY-2000; 2000US-204039P.
XX
XX 27-JUN-2000; 2000US-214591P.
XX
XX 14-MAY-2001; 2001US-0214591.
XX
XX (AMGE-) AMGEN INC.
XX
XX The111 LE, Yu G;
XX
XX WPI; 2002-066686/09.
XX
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor
PT family ligand
XX
XX
XX Claim 1; Fig 12a; 94pp; English.
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering
CC a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
CC family ligand), having the consensus sequence of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung
CC gastrointestinal, pancreatic or prostate tumour, APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human TACI protein extracellular domain.
XX
SQ Sequence 166 AA;
Query Match 100.0%; Score 909; DB 23; Length 166;
Best Local Similarity 100.0%; Pred. No. 2, 8e-83;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSGLGSRGRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLGTGMSCKTICNHQSOR 60
DB 1 MSGLGSRGRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLGTGMSCKTICNHQSOR 60
QY 61 TCAAFCRSLSCRKQKGFYDHLRLDCISGASICGHPKQCAVFCENKLRSPVNLPEELRR 120
DB 61 TCAAFCRSLSCRKQKGFYDHLRLDCISGASICGHPKQCAVFCENKLRSPVNLPEELRR 120
QY 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGKLSADQVALVYST 166
DB 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGKLSADQVALVYST 166
RESULT 3
ID AAE09244 standard; Protein; 265 AA.
XX
XX AAE09244;
XX
XX 19-NOV-2001 (first entry)
XX
XX Human TACI splice variant protein.
XX
XX Human, TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
KW TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KW psoriasis.
XX
XX Homo sapiens.
XX
XX OS

CC well as other disorders, such as viral infection, rheumatoid arthritis,
CC graft rejection, and immunoglobulin (Ig) E-mediated allergic reactions
CC and inflammation. The interaction is used to study cellular processes
CC associated with tumour necrosis factor (TNF)-receptors such as immune
CC regulation, cell proliferation, cell death and inflammatory responses.
CC The interaction between the extracellular region of TACI and TACI-L can
CC be used to further develop understanding of which cell types TACI-L
CC acts upon.

CC Sequence 293 AA;

Query Match 100.0%; Score 909; DB 22; Length 293;

Best Local Similarity 100.0%; Pred. No. 5.6e-83;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGIGSRGRRGSRVDOERFPQGLMTGVAMRSCPEBQVWDPDLGTQMSCKTICNHQSOR 60
DB 1 MSGIGSRGRRGSRVDOERFPQGLMTGVAMRSCPEBQVWDPDLGTQMSCKTICNHQSOR 60
QY 61 TCAAFCRSLSCRKEQKGYDHLRDCTSCASICQHPKQCAFCENKLRSPVNLPEELRR 120
DB 61 TCAAFCRSLSCRKEQKGYDHLRDCTSCASICQHPKQCAFCENKLRSPVNLPEELRR 120
QY 121 QRSGEVNNNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166

RESULT 9

AAU99512

ID AAU99512 standard; Protein; 293 AA.

XX AAU99512;

DT 07-OCT-2002 (first entry)

DE Human TACI-IgG Fc fusion protein.

KM Human; tumour necrosis factor; TNF delta; pulmonary system disorder;
KM immunoglobulin production; B-cell proliferation; immune system disorder;
KM autoimmune disease; cancer; lymphoproliferative disorder; pain;
KM microbial infection; parasitic infection; bone disease; atherosclerosis;
KM cardiovascular disorder; neurodegenerative disease; wound healing;
KM graft versus host disease; haematopoietic cell disorder; nephritis;
KM transmembrane activator and CAML-interactor; TACI; TNF epsilon; IgG;
KM immunoglobulin G; Fc portion.

XX Homo sapiens.

OS US2002064829-A1.

PN 30-MAY-2002.

PD 14-JUN-2001; 2001US-0879919.

PF 14-MAR-1996; 96US-016812P.
PR 15-JUN-2000; 2000US-211537P.
PR 23-OCT-2000; 2000US-241952P.
PR 13-DEC-2000; 2000US-254875P.
PR 16-MAR-2001; 2001US-276248P.
PR 23-MAR-2001; 2001US-277978P.
PR 25-MAY-2001; 2001US-293499P.
PR 12-MAR-1997; 97US-0815783.

XX (HUMA-) HUMAN GENOME SCI INC.

PA Yu G, Ni J, Gentz RL, Dillon PJ;

XX WPI; 2002-556722/59.

XX Novel human multimeric tumour necrosis factor delta or epsilon protein
PT useful for treating disease or disorder of immune system such as
PT autoimmune disease, immunodeficiency, or cancer of immune system

XX Example 29; Page 125; 143pp; English.

XX The present invention relates to the isolation of human tumour necrosis
XX factor (TNF) delta and TNF epsilon proteins, and the polynucleotide
XX sequences encoding them. The proteins are useful for modulating
XX immunoglobulin production or for modulating proliferation of B-cells.
XX The sequences of the invention are useful for treating diseases or
XX disorders of the immune system. Such disorders include autoimmune
XX diseases (e.g. systemic lupus erythematosus (SLE), acquired
XX immunodeficiency syndrome (AIDS)), cancers of the immune system
XX (e.g. chronic lymphocytic leukaemia (CLL), multiple myeloma,
XX non-Hodgkin's lymphoma or Hodgkin's disease), lymphoproliferative
XX disorders, microbial infections (e.g. viral, bacterial), parasitic
XX infections, nephritis, bone disease (e.g. osteoporosis), atherosclerosis,
XX pain, cardiovascular diseases (e.g. myocardial infarction, stroke),
XX neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's
XX disease), graft versus host disease, wound healing, haematopoietic cell
XX disorders (e.g. anaemia), inflammatory disorders (e.g. asthma),
XX diseases or disorders associated with various mucous membranes of the
XX body (e.g. mucositis), and disorders of the pulmonary system. The
XX proteins are also useful as a vaccine adjuvant that enhances immune
XX responsiveness to specific antigens. The present sequence for human
XX transmembrane activator and CAML-interactor (TACI)-immunoglobulin G
XX (IgG) Fc fusion protein is used in the examples of the present
XX invention.

Sequence 293 AA;

Query Match 100.0%; Score 909; DB 23; Length 293;

Best Local Similarity 100.0%; Pred. No. 5.6e-83; Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGIGSRGRRGSRVDOERFPQGLMTGVAMRSCPEBQVWDPDLGTQMSCKTICNHQSOR 60
DB 1 MSGIGSRGRRGSRVDOERFPQGLMTGVAMRSCPEBQVWDPDLGTQMSCKTICNHQSOR 60
QY 61 TCAAFCRSLSCRKEQKGYDHLRDCTSCASICQHPKQCAFCENKLRSPVNLPEELRR 120
DB 61 TCAAFCRSLSCRKEQKGYDHLRDCTSCASICQHPKQCAFCENKLRSPVNLPEELRR 120
QY 121 QRSGEVNNNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166

RESULT 10

ABB81488

ID ABB81488 standard; Protein; 293 AA.

XX ABB81488;

DT 02-SEP-2002 (first entry)

DE Human TACI receptor related protein SEQ ID NO:8.

KM Human; Ztnfr12; tumour necrosis factor receptor; cytosolic;
KM immunosuppressive; dermatological; anti-inflammatory; antidiabetic;
KM neuroprotective; antirheumatic; antiarthritic; antidiabetic;
KM nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
KM autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
KM multiple sclerosis; insulin dependent diabetes mellitus; asthma;
KM rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
KM glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
KM myelonephritis; renal neoplasia; multiple myeloma; amyloidosis;
KM light chain neuropathy; hypertension; large vessel disease;
KM graft-versus host disease; graft rejection; Crohn's disease.

XX Homo sapiens.

OS WO200238766-A2.

PN 16-MAY-2002.

PD

XX 05-NOV-2001; 2001WO-US47018.
 XX 07-NOV-2000; 2000US-246449P.
 PR 20-DEC-2000; 2000US-257131P.
 PR 28-JUN-2001; 2001US-301715P.
 PR 29-AUG-2001; 2001US-315565P.
 XX (ZYMO) ZYMOGENETICS INC.
 PA Gross JA, Xu W, Henne RM, Grant FJ;
 PI WPI; 2002-508212/54.
 DR Novel isolated human tumor necrosis factor receptor polypeptide, termed
 PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end
 PT stage renal failure or renal disease and lymphoma -
 XX Disclosure; Page 136-137; 154pp; English.
 XX The present invention describes a human tumor necrosis factor receptor
 CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,
 CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
 CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
 CC activities, and can be used in gene therapy. (I) can be used for
 CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
 CC (e.g. ZTNF4), for treating disorders and diseases associated with B
 CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
 CC inhibiting the proliferation of tumour cells. (I) is useful for treating
 CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
 CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure,
 CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
 CC leukaemia, nephritis, and pyelonephritis, and for treating renal
 CC neoplasms, multiple myeloma, lymphomas, light chain neuropathy, or
 CC amyloidosis, hypertension, large vessel diseases, (II) is useful for
 CC disease, graft rejection and Crohn's disease. (II) is useful for
 CC modulating the immune system, for regulating B cell responses and
 CC development, for modulating development of other cells, antibody
 CC production and cytokine production, and for modulating T and B cell
 CC communication. The present sequence represents a protein which is
 CC given in the exemplification of the present invention.
 XX Sequence 293 AA;
 SQ Query Match 100.0%; Score 909; DB 23; Length 293;
 Best Local Similarity 100.0%; Pred. No. 5.6e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSGLGRRRGRSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLGTCMCKTICNHQSQR 60
 Db 1 MSGLGRRRGRSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLGTCMCKTICNHQSQR 60
 QY 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCSICGQHPKQCFNCENKLRSPVNLPELRR 120
 Db 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCSICGQHPKQCFNCENKLRSPVNLPELRR 120
 QY 121 QRSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVYST 166
 Db 121 QRSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVYST 166
 RESULT 11
 AA014130
 ID AA014130 standard; Protein; 293 AA.
 XX AA014130;
 AC AA014130;
 XX 02-MAY-2002 (first entry)
 DT Human transmembrane activator CAML
 DE Human transmembrane activator CAML
 KW Human transmembrane activator CAML

KW cell proliferation; tumour; vulnery; renal cell cancer; mastocytoma;
 KW Kaposi's sarcoma; breast; ovarian carcinoma; rectal; throat; melanoma;
 KW colon; bladder; mammary adenocarcinoma; gastrointestinal; hyperplasia;
 KW pharyngeal squamous cell; stomach; cellular hyperproliferation; pannus;
 KW scleroderma; rheumatoid arthritis; scarring; liver; lung fibrosis;
 XX uterine.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Domain 1..114
 FT /label= Extracellular_domain
 XX WO200181417-A2.
 XX 01-NOV-2001.
 PD 27-APR-2001; 2001WO-US40626.
 PF 27-APR-2000; 2000US-199946P.
 PR (BIOJ) BIOGEN INC.
 PA (APOT-) APOTECH R & D SA.
 XX Ambrose C, Thompson J, Schneider P, Rennert P;
 WPI; 2002-062027/08.
 DR N-PSDB; AAK98726.
 XX Treating mammal for condition associated with undesired cell
 PT proliferation e.g., solid tumour or reducing solid tumour size located in
 PT mammal comprises administering transmembrane activator CAML interactor
 PT protein reagent -
 XX Claim 8; Fig 1; 42pp; English.
 XX This sequence represents the human transmembrane activator CAML
 CC interactor protein (TACI). The invention relates to treating a mammal for
 CC a condition associated with undesired cell proliferation (e.g. a solid
 CC tumour, or reducing the size of a solid tumour located on or in a mammal)
 CC comprising administering a transmembrane activator CAML interactor
 CC protein (TACI) reagent. The TACI reagent has cytostatic and vulnery
 CC activity. Treating a mammal (e.g. human, cow, horse, dog, mouse, rat or
 CC cat) for a condition associated with undesired cell proliferation (e.g.
 CC cancer such as renal cell cancer, Kaposi's sarcoma, breast cancer,
 CC sarcoma, ovarian carcinoma, rectal cancer, throat cancer, melanoma, colon
 CC cancer, bladder cancer, mastocytoma, lung cancer, mammary adenocarcinoma,
 CC pharyngeal squamous cell carcinoma, gastrointestinal cancer or stomach
 CC cancer). The method is also useful for treating cellular
 CC hyperproliferation (hyperplasia) such as scleroderma, pannus formation in
 CC rheumatoid arthritis, post-surgical scarring and lung, liver and uterine
 CC fibrosis. The TACI reagent of the invention can extend mean survival time
 CC of a mammal by 25% as compared to the mean survival time of a mammal in
 CC the absence of administering the TACI reagent. The TACI reagent also
 CC reduces the size of the tumour by 25% or more.
 XX Sequence 293 AA;
 SQ Query Match 100.0%; Score 909; DB 23; Length 293;
 Best Local Similarity 100.0%; Pred. No. 5.6e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSGLGRRRGRSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLGTCMCKTICNHQSQR 60
 Db 1 MSGLGRRRGRSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLGTCMCKTICNHQSQR 60
 QY 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCSICGQHPKQCFNCENKLRSPVNLPELRR 120
 Db 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCSICGQHPKQCFNCENKLRSPVNLPELRR 120
 QY 121 QRSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVYST 166
 Db 121 QRSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVYST 166

RESULT 12
AAU75408
ID AAU75408 standard; Protein; 293 AA.
XX
AC AAU75408;
XX
DT 09-APR-2002 (first entry)
XX
DE Tumour necrosis factor (TNF) receptor TACI-Fc fusion.
XX
KW Tumour necrosis factor; TNF; cytostatic; aretiostclerosis;
KW analgesic; cerebroprotective; neurotropic; neuroprotective; hepatotropic;
KW immunoglobulin production; B cell proliferation; immunosuppressive;
KW HIV; human immunodeficiency virus; autoimmune disease; immunodeficiency;
KW Sjogren's syndrome; systemic lupus erythematosus; Hodgkin's disease;
KW common variable immunodeficiency; CVID; non-Hodgkin's lymphoma; AIDS;
KW acylated immunodeficiency virus; cancer; multiple myeloma; CLL;
KW chronic lymphocytic leukaemia; lymphoproliferative disorder;
KW bacterial infection; viral infection; osteoporosis; atherosclerosis;
KW pain; cardiovascular disease; stroke; allergy; Alzheimer's disease;
KW neurodegenerative disease; inflammation; liver disease; cirrhosis;
KW cardiomyopathy; diabetes; psoriasis; glomerulonephritis;
KW ulcerative colitis; angiogenesis; septic shock; wound healing;
KW tumour necrosis factor receptor; TACI; immunoglobulin; IgG.
XX
OS Homo sapiens.
OS Synthetic.
PN WO200196528-A2.
XX
PD 20-DEC-2001.
XX
PF 14-JUN-2001; 2001WO-US19026.
XX
PR 15-JUN-2000; 2000US-211537P.
PR 23-OCT-2000; 2000US-241952P.
PR 13-DEC-2000; 2000US-254875P.
PR 16-MAR-2001; 2001US-276248P.
PR 23-MAR-2001; 2001US-277978P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Yu G, Ni J, Gentz RL, Dillon PJ, Hilbert D;
XX
DR WPI: 2002-130727/17.
DR N-PSDB; ABR13415.
XX
XX
XX Novel multicentric human tumour necrosis factor delta or epsilon protein
PT useful for treating cancer, immune system disorders, infection,
PT cardiovascular disorders, liver disease, cardiomyopathy, diabetes and
PT psoriasis -
XX
PS Example 29; Page 341-342; 344pp; English.
XX
XX The invention describes a multicentric human tumour necrosis factor (TNF)
CC delta or epsilon protein (I). (I) or a composition containing them (II)
CC are useful for modulating immunoglobulin production or proliferation of B
CC cells. (II) or (I) is useful for treating a disease or disorder of the
CC immune system, preferably an autoimmune disease (e.g. Sjogren's syndrome,
CC systemic lupus erythematosus or common variable immunodeficiency (CVID));
CC an immunodeficiency e.g. acquired immunodeficiency syndrome (AIDS);
CC cancer of the immune system (e.g. Hodgkin's disease, non-Hodgkin's
CC lymphoma, multiple myeloma and chronic lymphocytic leukaemia (CLL)); in
CC the diagnosis and treatment or prevention of cancer, lymphoproliferative
CC disorder, bacterial and viral infections, osteoporosis, atherosclerosis,
CC pain, cardiovascular disorders (e.g. stroke), allergy, inflammation,
CC neurodegenerative disease (e.g. Alzheimer's disease), liver disease (e.g.
CC cirrhosis), cardiomyopathy, diabetes, psoriasis, septic shock,
CC glomerulonephritis, ulcerative colitis, arteriosclerosis, for promoting
CC angiogenesis and wound healing, as a diagnostic research reagent, as an

CC agent to target and kill cells expressing a TNFdelta and/or TNFepsilon
CC receptor; in apoptosis of transformed cell lines; mediation of cell
CC activation and proliferation; and as an immunogen to produce (II). (II)
CC is useful to purify, detect and target (I), for measuring levels of (I)
CC in biological samples, for immunophenotyping samples, and to treat,
CC inhibit or prevent diseases and disorders associated with aberrant
CC expression and/or activity of (I). This is the amino acid sequence of a
CC fusion protein of tumour necrosis factor receptor TACI and immunoglobulin
CC G (19g) crystallisation fragment, described in the method of the
CC invention.
XX
SQ Sequence 293 AA;
XX
Query Match 100.0%; Score 909; DB 23; Length 293;
Best Local Similarity 100.0%; Pred. No. 5, 6e-83;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSGIGRSRRGRSPYDSEEPFGILMTGVAMRSCPEBOYMDPLGTGMSCKTICNHSOR 60
DB 1 MSGILRSRRGRSRVYDSEEPFGILMTGVAMRSCPEBOYMDPLGTGMSCKTICNHSOR 60
QY 61 TCAATCRSLSCRKQGGKTYDHLRDCISCASICGHPKQCAIFCENKLRSPVNLPEELRR 120
DB 61 TCAATCRSLSCRKQGGKTYDHLRDCISCASICGHPKQCAIFCENKLRSPVNLPEELRR 120
QY 121 ORSGEVNNSDNGSRVYDGLHRRGSEASPALPQLKLSADQVALVYST 166
DB 121 ORSGEVNNSDNGSRVYDGLHRRGSEASPALPQLKLSADQVALVYST 166
XX
RESULT 13
AAE15493
ID AAE15493 standard; Protein; 293 AA.
XX
AC AAE15493;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human transmembrane activator and intracellular CAML interactor protein.
XX
KW Human; transmembrane activator and intracellular CAML interactor; TACI;
KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.
XX
OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
FH Region 34..66 /note= "Cysteine-rich consensus region"
FT Region 71..104
FT Domain /note= "Cysteine-rich consensus region"
FT 167..186 /label= Transmembrane_domain
XX
XX WO200187979-A2.
XX
XX 22-NOV-2001.
XX
XX 14-MAY-2001; 2001WO-US15567.
XX
XX 12-MAY-2000; 2000US-204039P.
XX 27-JUN-2000; 2000US-214591P.
XX 14-MAY-2001; 2001US-0214591.
XX
XX (AMGE-) AMGEN INC.
XX
XX Theill LE, Yu G;

DR WPI; 2002-066686/09.
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor
PT family ligand
XX
PS Disclosure; Fig 12A; 94pp; English.
XX
CC The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering
CC a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
XX is human TACI protein.
XX
SQ Sequence 293 AA;
Query Match 100.0%; Score 909; DB 23; Length 293;
Best Local Similarity 100.0%; Pred. No. 5.6e-83;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSGLGRSGRRGSRVDOERFPQGLWTGVAMRSCPEQYWDPLLTGTCMSCKTICNHQSQR 60
DB 1 MSGLGRSGRRGSRVDOERFPQGLWTGVAMRSCPEQYWDPLLTGTCMSCKTICNHQSQR 60
QY 61 TCAAFCSLSCKRQKGFYDHLRDCISCAISCGQHPKQCAFCENKLRSPVNLPELRR 120
DB 61 TCAAFCSLSCKRQKGFYDHLRDCISCAISCGQHPKQCAFCENKLRSPVNLPELRR 120
QY 121 QRSGEVNNDSNGRYQGLEHGRGSEASPALGLKLSADQVALVYST 166
DB 121 QRSGEVNNDSNGRYQGLEHGRGSEASPALGLKLSADQVALVYST 166
RESULT 14
AAU09900
XX AAU09900 standard; Protein; 293 AA.
AC AAU09900;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human AGP-3 related protein receptor.
XX
KW Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;
KW dermatological; neuroprotective; nootropic; immunomodulator; metabolic;
KW antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever;
KW antiparkinsonian; antiparalytic; vasotropic; antibacterial; asthma;
KW AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor;
KW mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder;
KW rheumatoid arthritis; graft-versus-host disease; Crohn's disease;
KW pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease;
KW diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia;
KW multiple sclerosis; Parkinson's disease; transgenic animal.
XX
OS Homo sapiens.
XX
PN WO200185782-A2.
XX

PD 15-NOV-2001.
XX
XX 12-FEB-2001; 2001WO-US04568.
XX
XX 11-FEB-2000; 2000US-181800P.
XX
XX (AMGE-) AMGEN INC.
XX
XX Boyle WJ, Hsu H;
XX
XX WPI; 2002-049441/06.
XX
XX N-PSDB; AAS18558.
XX
XX Composition, useful for identifying modulator of receptor for treating
XX asthma and glomerulonephritis, comprises AGP-3 (tumour necrosis factor
XX ligand family member) receptor and encoding nucleic acids -
XX
XX Disclosure; Page 117-119; 124pp; English.
XX
XX The invention relates to a composition (I) comprising AGP-3 receptor
XX (tumour necrosis factor ligand family member) related protein (II)
XX attached to a vehicle protein. (I) is useful for modulating AGP-3-related
XX activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in
XX assays to identify cells and tissues that express AGP-3R or proteins
XX related to AGP-3R-related protein and for identifying compounds
XX (agonists or antagonists) that interact with AGP-3R proteins. (II) is
XX also useful for identifying intracellular proteins that interact with
XX the respective cytoplasmic domains by yeast two-hybrid screening
XX process. (II) is involved in B cell growth, survival and activation
XX particularly in lymph node, spleen, and Peyer's patches. AGP-3R
XX agonists and antagonists identified using (II) are used for modulating
XX B cell response and are used to treat diseases characterised by
XX inflammatory processes or deregulated immune response such as
XX rheumatoid arthritis, graft-versus-host disease, Crohn's disease,
XX lupus, etc. (II) is also useful in the production of hybridoma cells
XX which are derived from B cells which involve treating the hybridoma
XX cells with (II). (II) is useful in the treatment of inflammatory
XX conditions of joints, e.g., rheumatoid arthritis, osteoarthritis, etc.
XX (II), its agonists or antagonists are useful for treating acute
XX pancreatitis, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,
XX asthma, atherosclerosis, cachexia/anorexia, diabetes, fever,
XX glomerulonephritis, inflammatory bowel disease, ischaemic injury
XX including cerebral ischaemia, multiple myeloma, multiple sclerosis,
XX osteoporosis, Parkinson's disease, pain, reperfusion injury, septic
XX shock, etc. The nucleic acids are also useful for developing transgenic
XX animals expressing (II), which are useful for producing the polypeptides
XX and for the study of in vivo biological activity. The present sequence
XX represents the amino acid sequence of human AGP-3 related protein
XX receptor.
XX
SQ Sequence 293 AA;
Query Match 100.0%; Score 909; DB 23; Length 293;
Best Local Similarity 100.0%; Pred. No. 5.6e-83;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSGLGRSGRRGSRVDOERFPQGLWTGVAMRSCPEQYWDPLLTGTCMSCKTICNHQSQR 60
DB 1 MSGLGRSGRRGSRVDOERFPQGLWTGVAMRSCPEQYWDPLLTGTCMSCKTICNHQSQR 60
QY 61 TCAAFCSLSCKRQKGFYDHLRDCISCAISCGQHPKQCAFCENKLRSPVNLPELRR 120
DB 61 TCAAFCSLSCKRQKGFYDHLRDCISCAISCGQHPKQCAFCENKLRSPVNLPELRR 120
QY 121 QRSGEVNNDSNGRYQGLEHGRGSEASPALGLKLSADQVALVYST 166
DB 121 QRSGEVNNDSNGRYQGLEHGRGSEASPALGLKLSADQVALVYST 166
RESULT 15
AAO14135
XX AAO14135 standard; Protein; 312 AA.
XX

AC AA014135;
XX 02-MAY-2002 (first entry)
DE Protein of N-terminus FLAG-tagged human full length TACI from pJST552.
XX
XX Human transmembrane activator CAML interactor protein, TACI, cytosolic;
KW cell proliferation; tumour; vulvectomy; renal cell cancer; mastocytoma;
KW Kaposi's sarcoma; breast; ovarian carcinoma; rectal; throat; melanoma;
KW colon; bladder; mammary adenocarcinoma; gastrointestinal; hyperplasia;
KW pharyngeal squamous cell; stomach; cellular hyperproliferation; pannus;
KW scleroderma; rheumatoid arthritis; scarring; mean survival time; liver;
KW lung fibrosis; uterine; a proliferation inducing ligand; N-terminus;
pJST552; APRIL-R2.
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 302 /label= Xaa
FT /note= "Xaa is encoded by 'TAA'"
FT
XX
XX MO200181417-AZ.
XX
XX 01-NOV-2001.
XX
XX 27-APR-2001; 2001WO-US40626.
XX
XX 27-APR-2000; 2000US-199946P.
XX
XX (BIOJ) BIOGEN INC.
XX (APOT-) APOTEC R & D SA.
XX
XX Ambrose C, Thompson J, Schneider P, Rennert P;
XX
XX WPI; 2002-062027/08.
DR N-PSDB; AAK98731.
XX
XX
XX Treating mammal for condition associated with undesired cell
PT proliferation e.g., solid tumour or reducing solid tumour size located in
PT mammal comprises administering transmembrane activator CAML interactor
PT protein reagent -
XX
XX Example 1; Fig 2; 42pp; English.
PS
XX This sequence represents the protein of an N-terminus FLAG-tagged human
XX full length TACI from pJST552 (FLAG-tagged human APRIL-R2 (a
XX proliferation inducing ligand)). The invention relates to treating a
XX mammal for a condition associated with undesired cell proliferation (e.g.
XX a solid tumour, or reducing the size of a solid tumour located on or in a
XX mammal) comprising administering a transmembrane activator CAML
XX interactor protein (TACI) reagent. The TACI reagent has cytostatic and
XX vulvectomy activity. Treating a mammal (e.g. human, cow, horse, dog,
XX mouse, rat or cat) for a condition associated with undesired cell
XX proliferation (e.g. cancer such as renal cell cancer, Kaposi's sarcoma,
XX breast cancer, sarcoma, ovarian carcinoma, rectal cancer, throat cancer,
XX melanoma, colon cancer, bladder cancer, mastocytoma, lung cancer, mammary
XX adenocarcinoma, pharyngeal squamous cell carcinoma, gastrointestinal
XX cancer or stomach cancer). The method is also useful for treating
XX cellular hyperproliferation (hyperplasia) such as scleroderma, pannus
XX formation in rheumatoid arthritis, post-surgical scarring and lung, liver
XX and uterine fibrosis. The TACI reagent of the invention can extend mean
XX survival time of a mammal by 25% as compared to the mean survival time of
XX a mammal in the absence of administering the TACI reagent. The TACI
XX reagent also reduces the size of the tumour by 25% or more.
SO Sequence 312 AA;

Query March 99.4%; Score 904; DB 23; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.9e-82;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2. SGLGRSRGRGSRVDOERFPQGLMTGVAMRSCPEOXYWDPILGCMCKTICNHQSORT 61
DB 10 SGLGRSRGRGSRVDOERFPQGLMTGVAMRSCPEOXYWDPILGCMCKTICNHQSORT 69
QY 62 CAAFGRSLSCREKQGFYDHLIRDCISCASTICGHPKQCAIFCENKLRSPVNLPEELRQ 121
DB 70 CAAFGRSLSCREKQGFYDHLIRDCISCASTICGHPKQCAIFCENKLRSPVNLPEELRQ 129
QY 122 RSGEVENNSDNGRYQGLEHRSSEASPALPGIKLSADQVALVYST 166
DB 130 RSGEVENNSDNGRYQGLEHRSSEASPALPGIKLSADQVALVYST 174

Search completed: January 7, 2003, 09:37:28
Job time : 61.4937 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:35:04 ; Search time 23,7143 Seconds
(without alignments)
672.941 Million cell updates/sec

Title: US-09-855-158-15

Perfect score: 909

Sequence: 1 MSGLGRSRGRSRVDQER.....SPALPGLKLSADQVALVYST 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73.*

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	97.5	10.7	1548	2 S34583	serine proteinase
2	86.5	9.5	353	2 T06466	cathepsin B-like c
3	86	9.5	1299	2 T43251	furin (EC 3.4.21.7
4	84.5	9.3	355	2 AD0299	conserved hypothet
5	83	9.1	13288	2 T03099	mucin, submaxillar
6	82.5	9.1	899	2 G02428	subtilisin-like pr
7	82.5	9.1	915	2 J06148	subtilisin-like pr
8	82	9.0	932	2 I52527	PACE4A - mouse lfr
9	82	9.0	1650	2 S34577	dominant autoantig
10	82	9.0	4660	2 T42737	gp330 protein prec
11	81	8.9	773	1 JH0609	protein-tyrosine-p
12	81	8.9	1124	1 I5388	gene PACE4 protein
13	80.5	8.9	937	2 I5388	hypothetical prote
14	80	8.8	108	2 H9834	hypothetical prote
15	80	8.8	330	2 T5169	hypothetical prote
16	80	8.8	996	2 J02037	apolipoprotein E r
17	79.5	8.7	1984	2 T13171	probable vitelloge
18	79	8.7	269	2 C69312	molybdopterin oxid
19	78.5	8.6	630	2 A49656	estrogen-responsiv
20	78.5	8.6	1170	2 A53612	laminin B1k chain
21	78	8.6	596	2 A45664	variant-specific s
22	77.5	8.5	230	2 T19364	hypothetical prote
23	77.5	8.5	2195	2 T34264	hypothetical prote
24	77.5	8.5	2871	2 A5624	fibritin-1 precur
25	77	8.5	620	2 AF0273	probable iron-sulf
26	77	8.5	751	2 T15230	hypothetical prote
27	77	8.5	1184	2 T09484	cartilage intermed
28	76.5	8.4	1680	2 A43434	furin (EC 3.4.21.7
29	76.5	8.4	1872	2 JC4976	plexin 3 precursor

30 76 8.4 367 2 T45812
31 76 8.4 574 2 B88465
32 76 8.4 915 2 B48225
33 76 8.4 1748 2 S42136
34 75.5 8.3 427 2 S38032
35 75.5 8.3 1620 2 T27283
36 75 8.3 969 2 JC5571
37 75 8.3 989 1 A39490
38 75 8.3 975 2 TC5970
39 75 8.3 2664 2 T28626
40 75 8.3 3002 2 A47221
41 75 8.3 4544 1 S02392
42 75 8.3 4545 1 S25111
43 74.5 8.2 382 1 S48748
44 74.5 8.2 501 2 I61512
45 74.5 8.2 773 2 I46059

ALIGNMENTS

RESULT 1
S34583
serine proteinase (EC 3.4.21.-) PC6B - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S34583
R:Nakagawa, T.; Murakami, K.; Nakayama, K.
FEBS Lett. 327, 165-171, 1993
A:Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a
A:Reference number: S34583; MUID:93327934; PMID:8335106
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1548 <NAK>
A:Cross-references: GB:DL7583; NID:G407344; PIDN:BAA04507.1; PID:d1005033; PID:G440374
C:Keywords: hydrolase; serine proteinase

Query Match 10.7%; Score 97.5; DB 2; Length 1548;
Best Local Similarity 30.2%; Pred. No. 1;
Matches 29; Conservative 12; Mismatches 32; Indels 23; Gaps 7;

QY 14 RVDQ--ERRFPQGLWTGVAMRSCPEEQYWDPLLG--TCMSCKTICN-----HQSORTCAAF 65
DB 627 RADKHGQERF---LYHGBCLNCPVGHY--PAKGHTCLPCPDNCELVCYNPHICRCMSGY 681
QY 66 -----CRSLSCRKQKQKPYDHLRLDCISCASIC 93
DB 682 VIIPNHTCQKLECR--QGEFQDSEYEECMPCERGC 715

RESULT 2
T06466
cathepsin B-like cysteine proteinase (EC 3.4.22.-) (clone A116) - wheat (fragment)
C:Species: Triticum aestivum (common wheat)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C:Accession: T06466
R:Cejudo, F. J.; Murphy, G.; Chinoy, C.; Baulcombe, D. C.
Plant J. 2, 937-948, 1992
A:Title: A gibberellin-regulated gene from wheat with sequence homology to cathepsin B
A:Reference number: Z15659; MUID:93258430; PMID:1302642
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-353 <CEJ>
A:Cross-references: EMBL:X66013; NID:G21698; PIDN:CAA46811.1; PID:G21699
A:Experimental source: cv. Chinese Spring, etiolated shoots
C:Genetics:
A:Note: Intronic positions not resolved (incomplete sequence)
C:Superfamily: papain
C:Keywords: cysteine proteinase; glycoprotein; hydrolase

Query Match 9.5%; Score 86.5; DB 2; Length 353;

30 76 8.4 367 2 T45812
31 76 8.4 574 2 B88465
32 76 8.4 915 2 B48225
33 76 8.4 1748 2 S42136
34 75.5 8.3 427 2 S38032
35 75.5 8.3 1620 2 T27283
36 75 8.3 969 2 JC5571
37 75 8.3 989 1 A39490
38 75 8.3 975 2 TC5970
39 75 8.3 2664 2 T28626
40 75 8.3 3002 2 A47221
41 75 8.3 4544 1 S02392
42 75 8.3 4545 1 S25111
43 74.5 8.2 382 1 S48748
44 74.5 8.2 501 2 I61512
45 74.5 8.2 773 2 I46059

[illegible]

RESULT 3
T43251
Furin (EC 3.4.21.75) - fall armyworm
N:Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serine
C:Species: Spodoptera frugiperda (fall armyworm)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
R:Accession: T43251
R:Cieplik, M., Klenk, H.
S:Submitted to the EMBL Data Library, January 1996
A:Description: Cloning and functional characterization of FURIN from Spodoptera frugiperda
A:Reference number: Z2358
A:Accession: T43251
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1299 <CIE>
A:Cross-references: EMBL.Z68888; NID.G16785; PID.e219690; PIDN.CAA93116.1
A:Experimental source: clone Sturin 6; ovary
A:Function:
A:Description: responsible for the endoproteolytic processing of proproteins with specific
:Keywords: hydrolase; serine proteinase

Query	March	Similarity	25.0%	Score	86	DB	2	Length	1299
Best	Local	Similarity	25.0%	Pred.	No.	9.2			
Matches	39	Conservative	16	Mismatches	51	Indels	50	Gaps	9

QY	22	PGGLTGVAMNSCPBEQYWDPLLTGTCMSCKTICNHSORTCAFCRSLSCREGGKFX---	78
DB	1104	PRFMIDGGLCMCEGLCSQYYDARSCTCRSDASC-----RTCG-----PGFQFECT	1148
QY	79	-----YDHLRLRDISCSICG-----QHPKOCAYFCENKLRSPVNLPELRLRQSGSVE	127
DB	1149	TCSRPLRLIDRLANNOCPPCCSERGVNTSNPTPTDCH-CN-----PE-----NGECI	1192
QY	128	NNSDNSGRYQGLHRGSEASPALPGKLUSADQVALY	163
DB	1193	NSS-VAGKKRIAEWGAALHTAPSAD---AAPSVAIV	1223

RESULT 4
AD0299
Conserved hypotheical protein YPO2451 [imported] - Yersinia pestis (strain CO92)
C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C/Accession: AD0299
R/Parikhilli, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarrada, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Hall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
Nature 413 523-527, 2001
A>Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001, MUID:21470413, PMID:1156360
A/Accession: AD0299
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-355 <KUR>
A/Cross-references: GB:ALU590842; PIDN:CAC91256.1, PID:GL5960445; GSPDB:GN00175
C/Genetics:
C/Gene: YPO2451

C:\Superfamily: Escherichia coli ycea protein

```
Query Match          9.3%; Score 84.5; DB 2; Length 355;  
Best Local Similarity 24.4%; Pred.No.4;  
Matches 30; Conservative 20; Mismatches 48; Indels 25; Gaps 5;
```

QY 37 EGYMPILGTGTCAGCAKTIENHQSOFRCACFAFRSLSPKEQGEKYDHLIRDCISCAATCGQH 96
 ||::||::||::||::||::||::||::||::||::||::||::||::||
DB 257 ERISDDVIAHGCHQCCTPCDAHTN-----CKNDGC-----HLL--FIQCPVCAKF 299

QY 97 PQGVAFCEFNKRISRVRVNPPELLRQRSGEVENNSDNGSRVOGLEHRSASPALGLKLKS 156
 ::::~::~:~::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 300 EECGGCQLIQEELK----LPQEGRSRRBRAGRENGINIFPKSKL-----LQATHNIIPSEKS 351

QY 157 ADO 159
 ||:
DB 352 ADE 354

RESULT 5
 T03099
 mucin, submaxillary - pig
 N:Alternate names: apomucin
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 24-Mar-1999 #sequence revision 24-Mar-1999 #text_change 02-Jun-2000
 C:Accession: T03099; A40009; A28528; B29789
 R:Reichardt, A.E.; Timpte, C.S.; Abernethy, J.L.; Zhao, Y.; Hill, R.L.
 J: Biol. Chem. 272, 33204-33210, 1997
 A:Title: The complete cDNA sequence and structural polymorphism of the polypeptide chain
 A:Reference number: Z14839; MUID:98070526; PMID:9407109
 A:Accession: T03099
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-13288 <EC3>
 A:Cross-references: EMBL:AF005273; NID:g2581863; PIRN:AAC62527.1; PID:g2581864
 R:Reichardt, A.E.; Timpte, C.S.; Abernethy, J.L.; Zhao, Y.; Hill, R.L.
 J: Biol. Chem. 266, 9678-9688, 1991
 A:Title: Porcine submaxillary mucin contains a cysteine-rich, carboxyl-terminal domain I
 A:Reference number: A40009; MUID:91236743; PMID:2035060
 A:Accession: A40009
 A:Molecule type: mRNA
 A:Residues: 12139-12167, 'T', 12169-13288 <EC3>
 A:Cross-references: GB:M61883; NID:g454837; PIRN:AAA30998.1; PID:g164374
 R:Timpte, C.S.; Reichardt, A.E.; Abernethy, J.L.; Hill, R.L.
 J: Biol. Chem. 263, 1081-1088, 1988
 A:Title: Porcine submaxillary gland apomucin contains tandemly repeated, identical sequ
 A:Reference number: A28528; MUID:88087170; PMID:2826455
 A:Accession: A28528
 A:Molecule type: mRNA
 A:Residues: 12139-12167, 'T', 12169-12641 <TIM>
 A:Cross-references: GB:M21174; GB:J03512; NID:g464321; PIRN:AAA30990.1; PID:g552360
 A:Experimental source: submaxillary gland
 R:Reichardt, A.E.; Timpte, C.S.; Abernethy, J.L.; Toumadje, A.; Johnson Jr., W.C.; Hill, R.
 J: Biol. Chem. 262, 11339-11344, 1987
 A:Title: Structural properties of porcine submaxillary gland apomucin.
 A:Reference number: A92066; MUID:87280230; PMID:3611111
 A:Accession: B29789
 A:Molecule type: protein
 A:Residues: 1572-1607 <EC2>
 C:Superfamily: pig submaxillary mucin
 C:Keywords: tandem repeat

 Query Match 9.1%; Score 83; DB 2; length 13288;
 Best Local Similarity 23.5%; Pred. No. 1.3e02;
 Matches 32; Conservative 18; Mismatches 44; Indels 42; Gaps 8;

 QY 18 EERPGGLTGVAMR-SCSEEQYMD-----PLTGWCSCKTICNHSQRTCAFGRSLS 70
 DB 13075 EKSPEQVITACHKCTGREATVDCRKEKCSPTKCGELIRKADTCC--CEIGH 13131
 QY 71 CRK-----EGRKTYDHLRDCI--SCASI-----CGQH-----PKO 99
 DB 13132 CEKRTCTFNNITVEYGVSSDDPNNPCVTYSCCQNTGTAVVQNCCKPQWCAEIRVYDSKD 13191

QY 100 CAYFCENKLR-SPVNL 114
Db 13192 CCYCKSSCKSPSPV 13207

RESULT 6

G02428
subtilisin-like proprotein convertase (EC 3.4.21.-) 5 precursor - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Mar-2000
C:Accession: G02428
R:Reudelhuber, T.L. LBL Data Library, February 1996
submitted to the EMBL Data Library, February 1996
A:Reference number: H01242
A:Accession: G02428
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-899 <REU>
A:Cross-references: EMBL:U49114; NID:g1218057; PIDN:AAA91807.1; PID:g1218058
C:Genetics:
A:Gene: PCS
C:Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C:Keywords: hydrolase; serine proteinase
F:148-386/Domain: subtilisin homology <SBT>

Query Match 9.1%; Score 82.5; DB 2; Length 899;
Best Local Similarity 26.0%; Pred. No. 14;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;
QY 27 TGVAMRSCPEQYWDPLLTGCMSCKTICNHQSORTCAAF-----CR-----SLSC 71
Db 703 TNSCVTHCPDGSYQDTKNLCKKSENC-----KTCTEFHNCTECRDGLSLQGRCSVSC 757
QY 72 RKEQGFYDHLRLDCISCASC-----GOHPKQC-----AYFCEN 106
Db 758 --EDGRYFNG--QDCQPCHRFCATCAGAGDGCINCTEGYFME 797

RESULT 7

JC6148
subtilisin-like proprotein convertase (EC 3.4.21.-) homolog - human
N:Alternate names: pCaA protease
C:Species: Homo sapiens (man)
C>Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999
C:Accession: JC6148
R:Miranda, L.; Wolf, J.; Pichuanes, S.; Duke, R.; Franzusoff, A.
Proc. Natl. Acad. Sci. U.S.A. 93, 7695-7700, 1996
A:Title: Isolation of the human pCa gene encoding the putative host protease for HIV-1
A:Reference number: JC6148; MUID:96353880; PMID:8755538
A:Contents: CEM T-cell
A:Accession: JC6148
A:Molecule type: mRNA
A:Residues: 1-915 <MR>
A:Cross-references: GB:U56387; NID:g1498312; PIDN:AA50643.1; PID:g1498313
C:Comment: This protein functions as a soluble enzyme within the secretory pathway. It
C:Genetics:
A:Gene: pCaA
C:Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C:Keywords: glycoprotein; hydrolase; serine proteinase
F:164-402/Domain: subtilisin homology <SBT>

Query Match 9.1%; Score 82.5; DB 2; Length 915;
Best Local Similarity 26.0%; Pred. No. 14;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;
QY 27 TGVAMRSCPEQYWDPLLTGCMSCKTICNHQSORTCAAF-----CR-----SLSC 71
Db 719 TNSCVTHCPDGSYQDTKNLCKKSENC-----KTCTEFHNCTECRDGLSLQGRCSVSC 773
QY 72 RKEQGFYDHLRLDCISCASC-----GOHPKQC-----AYFCEN 106
Db 774 --EDGRYFNG--QDCQPCHRFCATCAGAGDGCINCTEGYFME 813

RESULT 8

I52527
FACE4A - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
C:Accession: I52527
R:Hosaka, M.; Murakami, K.; Nakayama, K.
Biomed. Res. 15, 383-390, 1994
A:Title: PACE4A is a ubiquitous endoprotease that has similar but not identical substrate
A:Reference number: I52527
A:Accession: I52527
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-932 <RES>
A:Cross-references: GB:D50060; NID:g769700; PIDN:BA08777.1; PID:g769701
C:Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
F:172-410/Domain: subtilisin homology <SBT>

Query Match 9.0%; Score 82; DB 2; Length 932;
Best Local Similarity 25.0%; Pred. No. 16;
Matches 28; Conservative 16; Mismatches 44; Indels 24; Gaps 5;
QY 16 DOERFPQGLWTGVAMRSCPEEQYWDPLLTGCMSCK--TICNHQSORTCAAFCSLSCKR 73
Db 650 DEEB-----YGVCHPECGDKGCGDNADQCLNCVHFSLGNSKTNKCVSEC-----696
QY 74 EQGFYDHLRLDCISCASC-----GOHPKQC-----AYFCENKLRSPVNLPP 116
Db 697 PLGVFGDAARRCRCHKGCETCTGRSPAQCCLSCRCRGFYHHQETNTCVTLCP 748

RESULT 9

S53457
dominant autoantigen gp 330 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 18-Aug-2000
C:Accession: S53457
R:Jokhadze, G.G.; Oleinikov, A.V.; Kanalas, J.J.; Makker, S.P.
Biochem. J. 305, 711-713, 1995
A:Title: Different molecular forms of rat kidney gp330, the dominant autoantigen of acti
A:Reference number: S53457; MUID:95151000; PMID:7848267
A:Accession: S53457
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1650 <JOK>
C:Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
F:29-65/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:72-106/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:111-147/Domain: EGF homology <EG1>
F:153-188/Domain: EGF homology <EG2>
F:196-235/Domain: LDL receptor WYTD-containing repeat homology <YW01>
F:236-278/Domain: LDL receptor WYTD-containing repeat homology <YW02>
F:279-329/Domain: LDL receptor WYTD-containing repeat homology <YW03>
F:330-373/Domain: LDL receptor WYTD-containing repeat homology <YW04>
F:374-414/Domain: LDL receptor WYTD-containing repeat homology <YW05>
F:415-457/Domain: LDL receptor WYTD-containing repeat homology <YW06>
F:466-505/Domain: EGF homology <EG3>
F:509-545/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:550-586/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F:595-631/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F:636-672/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F:679-715/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F:720-755/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F:760-794/Domain: LDL receptor ligand-binding repeat homology <LDL8>
F:799-833/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F:843-879/Domain: LDL receptor ligand-binding repeat homology <LDL10>
F:884-921/Domain: LDL receptor ligand-binding repeat homology <LDL11>
F:929-963/Domain: LDL receptor ligand-binding repeat homology <LDL12>
F:971-1006/Domain: EGF homology <EG4>
F:1012-1048/Domain: EGF homology <EG5>
F:1055-1099/Domain: LDL receptor WYTD-containing repeat homology <YW07>

F:1100-1154/Domain: LDL receptor WTD-containing repeat homology #status atypical <YW08>
 F:1155-1188/Domain: LDL receptor WTD-containing repeat homology #status atypical <YW08>
 F:1189-1233/Domain: LDL receptor WTD-containing repeat homology <YW10>
 F:1234-1273/Domain: LDL receptor WTD-containing repeat homology <YW11>
 F:1274-1316/Domain: LDL receptor WTD-containing repeat homology <YW12>
 F:1326-1359/Domain: EGF homology <EG6>

Query Match 9.0%; Score 82; DB 2; Length 1650;
 Best Local Similarity 25.8%; Pred. No. 26;
 Matches 40; Conservative 15; Mismatches 64; Indels 36; Gaps 8;

33 SCPEBOY-WDPULGTGCMCKTICNHQ---SQRTCAAFGRSLSCRKEGKFYDH----- 81
 Db 71 TCFPHQFPCDN--GHCIEMGRVCHNHVDDCSNDSEKGGIGNECDSSISRCDHCTDTIT 128
 QY 82 -----LNRDCTICGASI--CGQHPKOCATPCENKLRSPV-NLPPELRQRSGEVE 127
 Db 129 SFYSCGLPGYKLMDSKRCVPIDECKESPOLCSQKCEVNVGSYICKCAPGYIREPDGKSC 188
 QY 128 NNSDN-----SGRY--QGLEHNGSEASPALPGL 153
 Db 189 RQNSNIPEYLIFFSNRYIRNLTTDGSYSYLIOGL 223

RESULT 10
 gp330 protein precursor - rat
 T42737
 A:Accession: T42737
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
 A:Accession: T42737
 R:Salto, A.; Pietromono, S.; Loo, A.K.C.; Faruqi, M.G.
 Proc. Natl. Acad. Sci. U.S.A. 91: 9725-9729, 1994
 A:Title: Complete cloning and sequencing of rat gp330/megalin, a distinctive member of the LDL receptor family.
 A:Reference number: A58173; MUID:95024033; PMID:7937880
 A:Accession: T42737
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-4660 <SAI>
 A:Cross-references: EMBL:L34049; NID:9561852; PID:9561853; PIDN:AAA51369.1
 A:Experimental source: strain Sprague-Dawley; kidney
 A:Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-4660/Product: gp330 protein #status predicted <MAT>

Query Match 9.0%; Score 82; DB 2; Length 4660;
 Best Local Similarity 25.8%; Pred. No. 63;
 Matches 40; Conservative 15; Mismatches 64; Indels 36; Gaps 8;

33 SCPEBOY-WDPULGTGCMCKTICNHQ---SQRTCAAFGRSLSCRKEGKFYDH----- 81
 Db 3076 TCFPHQFPCDN--GHCIEMGRVCHNHVDDCSNDSEKGGIGNECDSSISRCDHCTDTIT 313
 QY 82 -----LNRDCTICGASI--CGQHPKOCATPCENKLRSPV-NLPPELRQRSGEVE 127
 Db 3134 SFYSCGLPGYKLMDSKRCVPIDECKESPOLCSQKCEVNVGSYICKCAPGYIREPDGKSC 3133
 QY 128 NNSDN-----SGRY--QGLEHNGSEASPALPGL 153
 Db 3194 RQNSNIPEYLIFFSNRYIRNLTTDGSYSYLIOGL 3228

RESULT 11
 JH0609
 protein-tyrosine-phosphatase (EC 3.1.3.48) p19 - mouse
 N:Alternate names: protein-tyrosine-phosphatase PTPY43
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 A:Accession: JH0609; PS0365; PS0366; G61180
 R:den Hertog, J.; Pals, C.E.G.M.; Jonk, L.J.C.; Kruijer, W.
 Biochem. Biophys. Res. Commun. 184: 1241-1249, 1992
 A:Title: Differential expression of a novel murine non-receptor protein tyrosine phosphatase
 A:Reference number: JH0609; MUID:92272714; PMID:1590786

A:Accession: JH0609
 A:Molecule type: mRNA
 A:Residues: 1-773 <DEN>
 A:Cross-references: GB:K63440; GB:S36169; NID:9416181; PIDN:CAA45037.1; PID:9416182
 A:Experimental source: embryonic carcinoma cell, p19 cell
 A:Accession: PS0365
 A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA
 A:Residues: 88-91, 'G', '93-110', 'G', '112-118', 'S', '120', 'T', '122' <DE2>
 A:Experimental source: embryonic carcinoma cell, p19 cell, clone PTP33
 A:Accession: PS0369
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 88-91, 'G', '93-109', 'IG', '112-120', 'T', '122' <DE3>
 A:Experimental source: embryonic carcinoma cell, p19 cell, clone PTP59
 A:Accession: PS0366
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 88-91, 'KV', '94-109', 'LA', '112-118', 'S', '120-122' <DE4>
 A:Experimental source: embryonic carcinoma cell, p19 cell, clone PTP42
 R:Yi, T.; Cleveland, J.L.; Ihle, J.N.
 Blood 78: 2222-2228, 1991
 A:Title: Identification of novel protein tyrosine phosphatases of hematopoietic cells
 A:Reference number: A61180; MUID:92032882; PMID:1932742
 A:Accession: G61180
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 124-127, 'I', '129-229' <YIA>
 C:Comment: This protein is located in the cytoplasm.
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 12; protein-tyrosine-phosphatase
 F:55-299/Domain: phosphoric monoester hydrolase; tyrosine-specific phosphatase
 F:58-282/Domain: protein-tyrosine-phosphatase homology <PPP>
 F:337/Active site: Cys (phosphotyrosine intermediate) #status predicted
 F:337/Binding site: substrate phosphate (Arg) #status predicted

Query Match 8.9%; Score 81; DB 1; Length 773;
 Best Local Similarity 25.4%; Pred. No. 16;
 Matches 45; Conservative 18; Mismatches 48; Indels 66; Gaps 11;

37 EOYWDPLG---TCMCKTICNHQSORTCAAFGRS--LSCRKEGKFY-----DH- 81
 Db 144 ERYW-PLYGEDPTPAFKIKSCNEQAR-DYFIRTLLEFONESRRRLYQPHYVWMPDHD 201
 QY 82 -----LNRDCTICGASI--CGQHPKOCATPCENKLRSPV-NLPPELRQRSGEVE 127
 Db 202 VPESFSDILDMISLMRKQEHEDVPICHISAGCGRTAICADYTNLTKGKIPBEFN 261
 QY 111 PVNLPPELRQRSGEVE-----NNSDNGRYQGLEHNGSEASPALP 151
 Db 262 VFPLIEQMTQKSHSAVQTKQYELVHRAIQAQLFESYNOMKR--MEHRSVVMVMTLP 316

RESULT 12
 I58386
 protein-tyrosine kinase (EC 2.7.1.112), receptor type tek precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
 A:Accession: I58386
 R:Ziegler, S.F.; Bird, T.A.; Schneringer, J.A.; Schooley, K.A.; Baum, P.R.
 Oncogene 8: 663-670, 1993
 A:Title: Molecular cloning and characterization of a novel receptor protein tyrosine kinase
 A:Reference number: I58386; MUID:93173509; PMID:8382358
 A:Accession: I58386
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1124 <RS8>
 A:Cross-references: GB:L06139; NID:9292823; PIDN:AAA61139.1; PID:9292824
 C:Genetic: GDB:TEK
 A:Gene: GDB:TEK
 A:Cross-references: GDB:344185; OMIM:600221
 A:Map position: 9p21-9p21
 C:Function:

Qy 81 HLRDCTS-CASICGQH--PKQCYFCENKLRSPVNLPPELRRQSRGE-----VENNSD-- 131

Db 118 SCLPEENRCMQOCTQOOTAQOQOPIQOQC-----QQECGSTGNMYNNQDPY 166

Tue Jan 7 10:36:50 2003

us-09-855-158-15.rpr

Page 6

QY 132 NSGRYQGLEHRSSE 145
| : | : | :
Db 167 NQWQYGGYNQGSNQ 180

Search completed: January 7, 2003, 09:41:18
Job time : 31.7143 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:31:59 ; Search time 12.4812 Seconds
(without alignments)
551.635 Million cell updates/sec

Title: US-09-855-158-15

Perfect score: 909

Sequence: 1 MSGLGRSRGGRSRVDQER.....SPALPGLKLSADQVALVYST 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	909	100.0	293	T13X_HUMAN	O14836 homo sapien
2	419.5	46.1	249	T13X_MOUSE	Q98t35 mus musculus
3	97.5	16.7	1877	PK5_MOUSE	Q04592 mus musculus
4	89	9.8	867	YMA2_CAEEL	P34447 caenorhabdi
5	86	9.5	297	XEDA_HUMAN	Q9hav5 homo sapien
6	83	9.1	971	RECK_MOUSE	P12021 mus musculus
7	83	9.1	1150	APMU_FIG	P12021 sus scrofa
8	82.5	9.0	913	PK5_HUMAN	Q92824 homo sapien
9	82	9.0	4660	LRP2_RAT	P98158 rattus norv
10	81	8.9	971	RECK_HUMAN	Q95980 homo sapien
11	81	8.9	1124	TIE2_HUMAN	Q02763 homo sapien
12	80.5	8.9	937	PAC4_RAT	Q63415 rattus norv
13	79.5	8.7	1172	LMB3_HUMAN	Q13751 homo sapien
14	79.5	8.7	1984	YL_DROME	P98163 drosophila
15	78.5	8.6	630	Z147_HUMAN	Q14258 homo sapien
16	77.5	8.5	2871	FBN1_MOUSE	Q61554 mus musculus
17	76.5	8.4	1680	FUR2_DROME	P30432 drosophila
18	76	8.4	603	CPA1_MOUSE	Q61129 mus musculus
19	76	8.4	1877	PK5_RAT	P41413 rattus norv
20	75.5	8.3	427	YKT5_YEAST	P36046 saccharomyc
21	75	8.3	400	LM6_HIRME	Q25092 hirudo medi
22	75	8.3	446	FA7_MOUSE	P70375 mus musculus
23	75	8.3	448	EDAR_HUMAN	Q9une0 homo sapien
24	75	8.3	969	PAC4_HUMAN	P29122 homo sapien
25	75	8.3	2871	LRN1_HUMAN	P35555 homo sapien
26	75	8.3	4544	LRN1_MOUSE	Q07954 homo sapien
27	74.5	8.2	501	TRAI_MOUSE	P39429 mus musculus
28	74.5	8.2	773	TIE2_BOVIN	P53712 bos taurus
29	74	8.1	1125	TIE2_BOVIN	Q06807 bos taurus
30	74	8.1	1426	EGFR_DROME	Q04412 drosophila
31	74	8.1	2569	LM3A_MOUSE	Q61789 mus musculus
32	73.5	8.1	775	PTNC_MOUSE	P35831 mus musculus
33	73.5	8.1	798	ITB1_MOUSE	P09055 mus musculus

34	73.5	8.1	1693	1	RIP2_MOUSE
35	73	8.0	61	1	MTID_FIG
36	73	8.0	4393	1	PGEM_HUMAN
37	72.5	8.0	450	1	NH14_CAEEL
38	72.5	8.0	634	1	2147_MOUSE
39	72.5	8.0	780	1	PTNC_HUMAN
40	72.5	8.0	788	1	ITB6_HUMAN
41	72.5	8.0	1696	1	PK5_BRACL
42	72	7.9	220	1	HXD8_HUMAN
43	72	7.9	308	1	ACPI_ENTHI
44	72	7.9	354	1	VEGD_HUMAN
45	72	7.9	448	1	EDAR_MOUSE

ALIGNMENTS

RESULT 1
T13X_HUMAN
ID T13X_HUMAN STANDARD; PRT; 293 AA.
AC O14836;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane activator and CAML interactor).
GN TNFRSF13B OR TACI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN RNM
RS SEQUENCE FROM N.A.
RC TISSUE=B-Cell;
RX MEDLINE=97458245; PubMed=9311921;
RA von Buelow G.-U., Bram R.J.;
RT "NF-AT activation induced by a CAML-interacting member of the tumor necrosis factor receptor superfamily.";
RL Science 278:138-141(1997).
[2]
RN RNM
RS SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
[3]
RN RNM
RS FUNCTION
MEDLINE=20519647; PubMed=10956646;
RA Wu Y., Bressette D., Carrell J.A., Kaufman T., Peng P., Taylor K., Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dimke D., Lafleur D., Migone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J., Olsen H.S., Kanakaraj P., Moore P.A., Baker K.P.;
RT "Tumor necrosis factor (TNF) receptor superfamily member TACI is a high affinity receptor for TNF family members APRIL and BLys.";
RL J. Biol. Chem. 275:35478-35485(2000).
[4]
RN RNM
RS FUNCTION
MEDLINE=21170294; PubMed=10973284;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M., McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M., Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating humoral immunity.";
RL Nat. Immunol. 1:252-256(2000).
CC -!
CC -! FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS that binds both ligands with similar high affinity. Mediates cell factor-dependent activation of NF-AT, as well as activation of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-cell function and the regulation of humoral immunity.
CC -!
CC -! SUBUNIT: Binds TRAF2, TRAF3 and TRAF6. Binds the NH2-terminal domain of CAMLg with its C-terminus.
CC -!
CC -! SUBCELLULAR LOCATION: Type III membrane protein.
CC -!
CC -! TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small intestine and peripheral blood leukocytes. Expressed in resting B-

P97433	mus musculus
P79377	sus scrofa
P98160	homo sapien
Q02151	caenorhabdi
Q61510	mus musculus
Q05209	homo sapien
P18564	homo sapien
Q9nj15	branchiosto
P13378	homo sapien
P36184	entamoeba h
O43915	homo sapien
Q9r187	mus musculus

cells and activated T-cells, but not in resting T-cells.

CC - SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.

CC - CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.

CC -----

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CC -----

DR EMBL; AF023614; AAC51790.1; -

DR EMBL; BC028072; AAH28072.1; -

DR Genev; HGNC:18153; TNFRSF13B.

DR MIM; 604907; -

DR InterPro; IPR001368; TNFR_C6.

DR PROSITE; PS00652; TNFR_NGFR_1; 1.

DR PROSITE; PS50050; TNFR_NGFR_2; FALSE NEG.

KW Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;

KW Repeat.

FT DOMAIN 1 165 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 166 186 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)

FT REPEAT 187 293 (POTENTIAL).

FT REPEAT 33 67 CYTOPLASMIC (POTENTIAL).

FT REPEAT 70 104 TNFR-CYS 1.

FT DISULFID 34 47 TNFR-CYS 2.

FT DISULFID 50 62 BY SIMILARITY.

FT DISULFID 54 66 BY SIMILARITY.

FT DISULFID 71 86 BY SIMILARITY.

FT DISULFID 89 100 BY SIMILARITY.

FT DISULFID 93 104 BY SIMILARITY.

FT CARBOHD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHD 251 251 P -> L (IN REF. 2).

FT SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;

Query Match 100.0%; Score 909; DB 1; Length 293;

Best Local Similarity 100.0%; Pred. No. 4.3e-79;

Matches 166; Conservative 100; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRSGRGRSRVDOERPFQGLMTGVAMRSCEPEQYMDLGLTGMSCCKTICNHQSOR 60

DB 1 MSGLSRSGRGRSRVDOERPFQGLMTGVAMRSCEPEQYMDLGLTGMSCCKTICNHQSOR 60

QY 61 TCAACFCSLSCKEKGKFPYDHLRLDPCISCAISICGHPKQCAFCENKLRSPVNLPEELRR 120

DB 61 TCAACFCSLSCKEKGKFPYDHLRLDPCISCAISICGHPKQCAFCENKLRSPVNLPEELRR 120

QY 121 QRSGEVNNSDNSGRYQGLEHRSSEASPLPGLKLSADQVALVYST 166

DB 121 QRSGEVNNSDNSGRYQGLEHRSSEASPLPGLKLSADQVALVYST 166

RESULT 2

113X_MOUSE STANDARD; PRT; 249 AA.

AC Q9ET35; Q9DBZ3; -

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DE 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane

DE activator and CAML interactor).

GN TNFRSF13B OR TACI.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_Taxid=10090;

RX NCBI_Taxid=10090;

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RX MEDLINE=21177254; PubMed=10881172;

Yan M., Maisters S.A., Grewal I.S., Wang H., Ashkenazi A.,

RA Dixit V.M.;

RT "Identification of a receptor for Blys demonstrates a crucial role in

RT humoral immunity.";

RL Nat. Immunol. 1:37-41(2000).

RL [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Lung;

RK MEDLINE=21085660; PubMed=11217851;

RA Kawai T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aikawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batelov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Schirli L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RL [3]

RP FUNCTION

RK MEDLINE=20341628; PubMed=10880535;

RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,

RA Theill L.E., Colombero A., Solovayev I., Lee F., McCabe S., Elliott R.,

RA Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,

RA Weng S.-Y., Boyle W.J., Han H.;

RT "TRAC1 is a TRAF-interacting receptor for TALL-1, a tumor necrosis

RT factor family member involved in B cell regulation.";

RL J. Exp. Med. 192:137-143(2000).

RL [4]

RP FUNCTION

RK MEDLINE=21322748; PubMed=11429548;

RA Wang H., Maisters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,

RA Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.;

RT "TRAC1-ligand interactions are required for T cell activation and

RT collagen-induced arthritis in mice.";

RL Nat. Immunol. 2:632-637(2001).

CC - FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/BAFF/Blys

CC that binds both ligands with similar high affinity. Mediates

CC calcineurin-dependent activation of NF-AT, as well as activation

CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-

CC cell function and the regulation of humoral immunity (by

CC similarity).

CC - SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal

CC domain of CAML with its C-terminus (by similarity).

CC - SUBCELLULAR LOCATION: Type III membrane protein (Probable).

CC - SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.

CC -----

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CC -----

DR EMBL; AF57673; AAC00081.1; -

DR EMBL; AK004668; BAB23457.1; -

DR MGD; MGI:188941; Tnfrsf13b.

DR PROSITE; PS00652; TNFR_NGFR_1; 1.

DR PROSITE; PS50050; TNFR_NGFR_2; 2.

KW Receptor; Immune response; Signal-anchor; Transmembrane; Repeat.

FT DOMAIN 1 128 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 129 149 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)

```
FT DOMAIN 150 249 (POTENTIAL).
FT REPEAT 5 38 CYTOPLASMIC (POTENTIAL).
FT REPEAT 42 76 TNFR-CYS 1.
FT REPEAT 6 19 TNFR-CYS 2.
FT DISULFID 22 34 BY SIMILARITY.
FT DISULFID 26 38 BY SIMILARITY.
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 61 72 BY SIMILARITY.
FT DISULFID 65 76 BY SIMILARITY.
FT CONFLICT 137 137 I -> F (IN REF. 2). CRC64;
SQ SEQUENCE 249 AA; 26947 MW; CB2F2D61C2931D81 CRC64;

Query Match 46.1%; Score 419.5; DB 1; Length 249;
Best Local Similarity 55.1%; Pred. No. 8.6e-33;
Matches 76; Conservative 22; Mismatches 31; Indels 9; Gaps 2;

QY 29 VAMRSCPEQYWDPLGLTGMCKTTCNHOQSTCAAFCSLSCREKQKGYDHLRLDCIS 88
Db 1 MAMAFPCPKDQYWDSSRKSCVSCALTCQSRSORTCTDFCKFINCRKEQGRYYDHLHGACVS 60
QY 89 CASICQHPKQCAFCENKLRSPVNLPELRQRSGEVNNSDNGRYQGLEHGRGSEASP 148
Db 61 CDSCTCTHPQCAHFCRPRSQANLPGLRPOAGEVEVRSDNSGRHOGSEHG----- 114
QY 149 ALPGLKLSADQVALVYST 166
Db 115 --PGLRLSSDQLTL-YCT 129

RESULT 3
PKCS_MOUSE STANDARD; PRT; 1877 AA.
AC Q04592; Q62040;
DT 01-FEB-1995 (Rel. 31, Created)
DT 16-FEB-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Proteolysin convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
DE (Proteolysin convertase PC5) (Subtilisin/kexin-like protease PC5)
DE (Convertase PC5) (PC6) (Subtilisin-like proprotein convertase 6)
DE (SPC6).
GN PCSK5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 330-1877 FROM N.A. (ISOFORM PC5B).
RC STRAIN=ICR; TISSUE=Intestine;
RX MEDLINE=93327934; PubMed=8335106;
RA Nakagawa T., Murakami K., Nakayama K.;
RT "Identification of an isoform with an extremely large Cys-rich region
of PC6, a Kex2-like processing endoprotease.";
RL FEBS Lett. 327:165-171(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM PC5A).
RC TISSUE=Brain, and Intestine;
RX MEDLINE=93224489; PubMed=8468318;
RA Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.;
RA Nakayama K.;
RT "Identification and functional expression of a new member of the
mammalian Kex2-like processing endoprotease family: its striking
structural similarity to PACE4.";
RJ J. Biochem. 113:132-135(1993).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM PC5A).
RC TISSUE=Adrenal cortex;
RX MEDLINE=93342056; PubMed=8341687;
RA Lusson J., Vieau D., Hamelin J., Day R., Chretien M., Seidah N.G.;
RT "cDNA structure of the mouse and rat subtilisin/kexin-like PC5: a
candidate proprotein convertase expressed in endocrine and
nonendocrine cells.";
RT Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
```

```
RN PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.
RX MEDLINE=97103178; PubMed=8947550;
RA De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,
RA Bendayan M., Seidah N.G.;
RT "The isoforms of proprotein convertase PC5 are sorted to different
subcellular compartments";
RJ Cell Biol. 135:1261-1275(1996).
RN [5]
RP DEVELOPMENTAL EXPRESSION.
RX MEDLINE=96293359; PubMed=8698813;
RA Constam D.B., Galfon M., Robertson E.J.;
RT morphogenetic proteins at distinct sites during embryogenesis.";
RJ J. Cell Biol. 134:181-191(1996).
RN [6]
RP DEVELOPMENTAL EXPRESSION.
RX MEDLINE=97436919; PubMed=9291583;
RA Rancourt S.L., Rancourt D.E.;
RT "Murine subtilisin-like proteinase SPC6 is expressed during embryonic
implantation, somitogenesis, and skeletal formation.";
RJ Dev. Genet. 21:75-81(1997).
CC -!- FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPEPTIDASE ACTIVITY
WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE
OF CLEAVAGE AT THE RX(K/R) CONSENSUS MOTIF. MAY BE RESPONSIBLE
FOR THE MATURATION OF GASTROINTESTINAL PEPTIDES. MAY BE INVOLVED
IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA THE ACTIVATION
OF GROWTH FACTORS.
CC -!- CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
PROTEINS BY CLEAVAGE OF ARG-XAA-YAA-ARG-|-ZAA BONDS, WHERE XAA
CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
CC -!- SUBCELLULAR LOCATION: PCSA IS SECRETED THROUGH THE REGULATED
SECRETORY PATHWAY. PCSB IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO
A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH
EARLY ENDOSOMES.
CC -!- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; PCSB/LONG (SHOWN HERE)
AND PCSA/SHORT; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: PCSA IS EXPRESSED IN MOST TISSUES BUT IS MOST
ABUNDANT IN THE INTESTINE AND ADRENALS. PCSB IS EXPRESSED IN THE
INTESTINE, ADRENALS AND LUNG BUT NOT IN THE BRAIN.
CC -!- DEVELOPMENTAL STAGE: WEAKLY EXPRESSED THROUGHOUT THE EMBRYO,
EXCEPT IN THE DEVELOPING NERVOUS SYSTEM, THE RIBS AND THE LIVER,
BUT MARKEDLY UPREGULATED AT DISCRETE SITES DURING DEVELOPMENT. AT
E6.5, PROMINENT EXPRESSION OBSERVED IN DIFFERENTIATED DECIDUA. AT
E7.5, INTENSE EXPRESSION IN EXTRAEMBRYONIC ENDODERM, AMNION AND
NASCENT MESODERM. AT 8.5, ABUNDANT EXPRESSION IN SOMITES AND YOLK
SAC FOLLOWED BY A CONFINATION TO DERMATOTOME COMPARTMENT. BETWEEN
E9.5 AND E11.5, ABUNDANT EXPRESSION IN AER (THICKENED ECTODERMAL
CELLS OF LIMB BUDS). AT E12.5, EXPRESSION IN THE LIMBS IS CONFINED
TO THE CONDENSING MESENCHYM SURROUNDING THE CARTILAGE. AT THIS
STAGE, STRONG EXPRESSION ALSO DETECTED IN VERTEBRAL AND FACIAL
CARTILAGE PRIMORDIA AND IN THE MUSCLE OF THE TONGUE. AT E16.5,
ABUNDANT EXPRESSION IN EPITHELIAL CELLS OF THE INTESTINAL VILLI.
CC -!- ISOFORM A IS MOST ABUNDANT AT ALL STAGES BUT SIGNIFICANT LEVELS OF
ISOFORM B OCCUR AT E12.5
CC -!- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
ASSISTING THE FOLDING OF THE ZIMOGEN WITHIN THE ENDOPLASMIC
RETICULUM.
CC -!- DOMAIN: AC 1 AND AC 2 (CLUSTERS OF ACIDIC AMINO ACIDS) CONTAIN
SORTING INFORMATION. AC 1 DIRECTS TGN LOCALIZATION AND INTERACTS
WITH THE TGN SORTING PROTEIN PACS-1.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 8.
CC -!- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
-----
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CC EMBL; D17583; BAA04507.1; -.
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RESULT 5
XEDA HUMAN
AC Q9HAV5: STANDARD; PRT; 297 AA.
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member XEDAR (X-linked
DE ecdysyplasin-A2 receptor) (EDA-A2 receptor).
GN XEDAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF GLU-256.
RC TISSUE=Fetal kidney;
RX MEDLINE=20495245; PubMed=11039935;
RA Yan M., Wang L.-C., Hymowitz S.G., Schilbach S., Lee J., Goddard A.,
RA de Vos A.M., Gao W.-Q., Dixit V.M.;
RT "Two-amino acid molecular switch in an epithelial morphogen that
RT regulates binding to two distinct receptors.";
RL Science 290:523-527(2000).
CC -!- FUNCTION: Receptor for EDA isoform A2, but not for EDA isoform
CC A1. Mediates the activation of NF-kappa-B. Activation seems to
CC be mediated by binding to TRAF6.
CC -!- SUBUNIT: Associates with TRAF1, TRAF3 and TRAF6.
CC -!- CELLULAR LOCATION: Type III membrane protein.
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC
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CC
CC EMBL; AF298812; AAG28761.1; -.
CC MIM; 300276; -.
CC InterPro; IPR001368; TNFR_c6.
CC Pfam; PF00020; TNFR_c6; 2.
CC SMART; SM00208; TNFR; 2.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS00505; TNFR_NGFR_2; 2.
CC Receptor; Developmental protein; Differentiation; Transmembrane;
CC Glycoprotein; Repeat.
CC DOMAIN 1 138 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 139 159 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
CC
CC DOMAIN 160 297 CYTOPLASMIC (POTENTIAL).
CC REPEAT 2 41 TNFR-CYS 1.
CC REPEAT 43 83 TNFR-CYS 2.
CC REPEAT 85 118 TNFR-CYS 3.
CC DISULFID 3 15 BY SIMILARITY.
CC DISULFID 18 31 BY SIMILARITY.
CC DISULFID 21 41 BY SIMILARITY.
CC DISULFID 44 58 BY SIMILARITY.
CC DISULFID 61 75 BY SIMILARITY.
CC DISULFID 84 83 BY SIMILARITY.
CC DISULFID 86 104 BY SIMILARITY.
CC DISULFID 107 118 BY SIMILARITY.
CC DISULFID 174 74 N-LINKED (GLCNAC... ) (POTENTIAL).
CC CARBOHYD 74 74 E->R: ABOLISHES TRAF6 ASSOCIATION.
CC MUTAGEN 256 256
CC SEQUENCE 297 AA; 32728 MW; 0E71127C648240C CRC64;
SQ
Query Match 9.5%; Score 86; DB 1; Length 297;
Best Local Similarity 22.0%; Pred. No. 0.4;
Matches 26; Conservative 19; Mismatches 31; Indels 42; Gaps 7;
34 CPSEQYWDPLLLGTCMSCKTIC--NHQSORTCA-----AFCRSLSCRKEQGFYDHLIRD 85
3 COENEYWDQ-WGRCVTCQR-CGPGQELSDCGVGEGGDAYCTACPPRYKSSWGHRCQS 60
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QY 86 CISCA-----SICGHPKQCAFCENKLRSPVNLPPELRRORSCEVEN 128
DB 61 CITCAVINRVQKNCVNTATSNVCGD-----C-----LPRFYRKRTRIGLQD 101
RESULT 6
RECK_MOUSE
ID RECK_MOUSE STANDARD; PRT; 971 AA.
AC Q9Z0J1; 2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Reversion-inducing cysteine-rich protein with Kazal motifs precursor
DE (mRECK).
DE
DE
GN RECK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99007295; PubMed=9789069;
RA Takahashi C., Sheng Z., Horan T.P., Kitayama H., Maki M., Hitomi K.,
RA Kitaura Y., Takai S., Saeghara R.M., Horimoto A., Ikawa Y.,
RA Ratzkin B.J., Arakawa T., Noda M.;
RT "Regulation of matrix metalloproteinase-9 and inhibition of tumor
RT invasion by the membrane-anchored glycoprotein RECK.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:13221-13226(1998).
CC -!- FUNCTION: Negatively regulates matrix metalloproteinase-9 (MMP-9)
CC by suppressing MMP-9 secretion, and by direct inhibition of its
CC enzymatic activity. RECK down-regulation by oncogenic signals may
CC facilitate tumor invasion and metastasis. Appears to also
CC regulate MMP-2 and Mti-MMP, which are involved in cancer
CC progression (By similarity).
CC -!- SUBUNIT: Interacts with MMP-9.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- DEVELOPMENTAL STAGE: In E10.5 embryos the RECK protein is widely
CC expressed in mesenchymal tissues and is relatively abundant in the
CC marginal zone of the neural tube and large blood vessels such as
CC the aorta.
CC -!- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.
CC
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CC
CC EMBL; AB006960; BAA34061.1; -.
CC MCD; MG1.1855698; Reck.
CC InterPro; IPR002350; Kazal.
CC Pfam; PF00050; kazal; 2.
CC SMART; SM00280; KAZAL; 2.
CC PROSITE; PS00282; KAZAL; 1.
CC Signal; Glycoprotein; GPI-anchor; Serine protease inhibitor;
CC Membrane; Anti-oncogene; Repeat.
CC SIGNAL 1 22 POTENTIAL.
CC CHAIN 23 942 REVERSION-INDUCING CYSTEINE-RICH PROTEIN
CC WITH KAZAL MOTIFS.
CC PROPEP 943 971 REMOVED IN MATURE FORM (POTENTIAL).
CC LIPID 942 942 GPI-ANCHOR (POTENTIAL).
CC DOMAIN 633 677 KAZAL-LIKE 1.
CC DOMAIN 704 750 KAZAL-LIKE 2 (DEGENERATE).
CC DOMAIN 751 787 KAZAL-LIKE 3 (DEGENERATE).
CC DOMAIN 37 338 5 X KNOT REPEATS.
CC REPEAT 37 84 KNOT 1.
CC REPEAT 104 141 KNOT 2.
CC REPEAT 151 197 KNOT 3.
CC REPEAT 216 263 KNOT 4.
CC REPEAT 292 338 KNOT 5.
```

FT	DISULFID	635	654	BY SIMILARITY.
FT <td>DISULFID</td> <td>633</td> <td>658</td> <td>BY SIMILARITY.</td>	DISULFID	633	658	BY SIMILARITY.
FT	DISULFID	643	677	BY SIMILARITY.
FT	CARBOHYD	39	39	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	86	86	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	200	200	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	297	297	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	352	352	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	971 AA;	106134 MM;	2PC8BEB38A20F86d CRC64;

Query Match	Best Local Similarity	9.1%	Score 83;	DB 1;	Length 971;
Matches 33;	Conservative 16;	Mismatches 42;	Indels 56;	Gaps	

QY	34	CPEE--QWMDL-----	IGTC-----	MSCKITCNHQSORTCAFCRSLS	70
DB	74	CPEIWEIWSGNSNLSIPGVFKSDGKVGIGCCELAIIGLCRQACRQAKASIKNDI----	SKY	129	
QY	71	CRKEGCKFYDHLRLDCIS-----	CASICGQHPKQCAIFCENKLRSPVNLPELRORS	123	
DB	130	CRKE-----YENLFFSCISINEMSGVCCSYAGHH-TNCRFCQAIKFT-----	171		
QY	124	GEVENNSDNGRGYGLERHRSBASPAL	150		
DB	172	----DSSPEGSGIKAVENYCAISIPOL	194		

APMU PIG	STANDARD;	PRT;	1150 AA.
AC	PI2021;		
DT	01-OCT-1989 (Rel. 12, Created)		
DT	01-DEC-1992 (Rel. 24, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Apomucin (Mucin core protein) (Fragment).		
OC	Sus scrofa (pig)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
OX	NCBI_TaxID=98823;		
PN	SEQUENCE FROM N.A.		
RP	TISSUE=Submaxillary gland;		
RC	MEDLINE=91236743; PubMed=2033060;		
RC	Eckhardt A.E., Timpe C.S., Abernethy J.L., Zhao Y., Hill R.L.;		
RA	"Porcine submaxillary mucin contains a cysteine-rich,		
RT	carboxyl-terminal domain in addition to a highly repetitive,		
RT	glycosylated domain."		
RL	J. Biol. Chem. 266:9678-9686 (1991).		
RL	(2)		
RP	SEQUENCE OF 1-503 FROM N.A.		
RP	TISSUE=Submaxillary gland;		
RC	MEDLINE=88087170; PubMed=2826455;		
RC	Timpe C.S., Eckhardt A.E., Abernethy J.L., Hill R.L.;		
RA	"Porcine submaxillary gland apomucin contains tandemly		
RT	identical sequences of 81 residues."		
RL	J. Biol. Chem. 263:1081-1088 (1988).		
RL	(3)		
RP	SEQUENCE OF 45-80.		
RC	TISSUE=Submaxillary gland;		
RC	MEDLINE=87280230; PubMed=3611111;		
RA	Eckhardt A.E., Timpe C.S., Abernethy J.L., Tounadje A.,		
RA	Johnson W.C. Jr., Hill R.L.;		
RT	"Structural properties of porcine submaxillary gland apomucin."		
RL	J. Biol. Chem. 262:11339-11344 (1987).		
RL	(4)		
RP	CARBOHYDRATE-LINKAGE SITES, AND SEQUENCE OF 45-125.		
RC	TISSUE=Submaxillary gland;		
RC	MEDLINE=97248516; PubMed=9092502;		
RA	Geeken T.A., Owen C.L., Pasanaraty M.;		
RA	Determination of the site-specific O-glycosylation pattern of the		
RT	porcine submaxillary mucin tandem repeat glycopeptide. Model proposed		
RT	for the polypeptide-galnac transferase peptide binding site."		
RL	J. Biol. Chem. 272:9709-9719 (1997)		

[illegible]

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FT CARBOHYD 96 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 98 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 101 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 103 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 104 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 106 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 107 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 108 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 110 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 111 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 112 O-LINKED (GALNAC. . .) (MUCIN TYPE)
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FT CARBOHYD 117 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 123 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 124 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 148 O-LINKED (GALNAC. . .) (MUCIN TYPE)
FT CARBOHYD 547 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 547 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 917 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 985 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 1002 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 1068 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 1150 AA; 109615 MW; 3CB68B5D29DD7F5A CRC64;

Query Match 9.1%; Score 83; DB 1; Length 1150;
Best Local Similarity 23.5%; Pred. No. 3;
Matches 32; Conservative 18; Mismatches 44; Indels 42; Gaps 8;

QY 18 ERFPGGLTGVAMR-SCPEQVWD-----PLLGTCMCKTICNHOSORTCAAFCSLS 70
DB 937 EKSQGDVMTANCHKCTCTEAKTVCKPCPSPPICKTGERLKFKANDTC--CEIGH 993
QY 71 CRK-----EKGKFDHLLRDCI--SCASI-----CGOH-----PKQ 99
DB 994 CEKRTCLFNNTDYEVSFDDPNPCVTYSCQNTGTAVVQNCPRKTCWCAEDRVDSKQ 1053
QY 100 CAYFCENKLR-SPVNL 114
DB 1054 CYYTCKSSCKPSFVNV 1069

RESULT 8
PKCS HUMAN
ID PKCS HUMAN STANDARD; PRT; 913 AA.
AC Q92824; Q13527;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protease convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
DE (Protein convertase PCS) (Subtilisin/kexin-like protease PCS)
DE (Convertase PCS) (PCS) (hPC6).
GN PKCS5 OR PCS OR PC6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini, Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=csl;
RX MEDLINE=9635380; PubMed=875538;
RA Miranda L., Wolf J., Pichuanes S., Duke R., Franzosoff A.;
RT "Isolation of the human PC6 gene encoding the putative host protease
for HIV-1 gp160 processing in CD4+ T lymphocytes.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:7695-7700(1996).
RN [2]
RP REVISIONS.
RA Franzosoff A., Miranda L., Wolf J., Pichuanes S., Lu Y., Duke R.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 15-913 FROM N.A.
RA Reudelhuber T.L.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPEPTIDASE ACTIVITY
CC WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE
CC OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF.
CC -!- CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR

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CC PROTEINS BY CLEAVAGE OF ARG-XAA-YAA-ARG-|-ZAA BONDS, WHERE XAA
CC CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS SEEMS TO BE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN T-LYMPHOCYTES.
CC -!- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
CC ASSISTING THE FOLDING OF THE ZMOGEN WITHIN THE ENDOPLASMIC
CC RETICULUM. BELONGS TO PEPTIDASE FAMILY S8.
CC -!- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U56387; AAC50643.2; -
CC EMBL; U49114; AAA91807.1; -
CC HSP; Q99405; IMPT.
CC MEROPS; S08.076; -
CC Genew; HGNC:8747; PCSK5.
CC MW; 600488; -
CC InterPro; IPR002174; Furin-like.
CC InterPro; IPR002884; P domain.
CC InterPro; IPR002029; Peptidase S8.
CC Pfam; PF00082; Peptidase S8; 1.
CC Pfam; PF01483; P; PARTIAL.
CC PRINTS; PR00723; SUBTILISIN.
CC PRODOM; PD000717; F domain; 1.
CC SMART; SM00281; FU; 5.
CC PROSITE; PS00136; SUBTILASE ASP; 1.
CC PROSITE; PS00137; SUBTILASE HIS; 1.
CC PROSITE; PS00138; SUBTILASE SER; 1.
CC Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;
CC Cleavage on pair of basic residues; Repeat.
CC SIGNAL 1 32
CC FT PROPEP 33 114 BY SIMILARITY.
CC FT CHAIN 115 913 PROPEPTIDE CONVERTASE SUBTILISIN/KEXIN
CC TYPE 5.
CC FT DOMAIN 115 454 CATALYTIC.
CC FT DOMAIN 462 600 HOMO B.
CC FT DOMAIN 636 913 CYS-RICH MOTIF (CRM) REGION.
CC SITE 114 115 CLEAVAGE (AUTO-) (BY SIMILARITY).
CC SITE 519 521 CELL ATTACHMENT SITE (POTENTIAL).
CC ACT_SITE 171 171 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC ACT_SITE 212 212 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC CARBOHYD 225 225 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC CARBOHYD 381 381 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 665 665 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 752 752 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 802 802 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 852 852 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CONFLICT 118 121 S -> F (IN REF. 3).
CC CONFLICT 121 121 V -> A (IN REF. 3).
CC CONFLICT 511 511 R -> A (IN REF. 3).
CC CONFLICT 601 601 R -> Q (IN REF. 3).
SQ SEQUENCE 913 AA; 101775 MW; 21389264CAD7546C CRC64;

Query Match 9.1%; Score 82.5; DB 1; Length 913;
Best Local Similarity 26.0%; Pred. No. 2.7;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;

QY 27 TGVAMRSCPEQYWDPLLGTCMCKTICNHOSORTCAAF-----CR-----SLSC 71
DB 717 TNSCVTHCPDGSQYDTKKNLCRKCSENC-----KTCTEFHNCTCRDGLSLQSGRCVSC 771
QY 72 RKEGKFDHLLRDCISASCISIC-----GOHPKQC-----AYECEN 106

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DR 772 -- EDGRYFNG--QDCPCRFCAACAGADGCGCTGEGYFMD 811

RESULT 9

LRP2_RAT STANDARD; PRT; 4660 AA.

AC P98158; 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE low-density lipoprotein receptor-related protein 2 precursor (Megalin) (Glycoprotein 330).

DE LRP2.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1] SEQUENCE FROM N.A.

RP STRAIN=Sprague-Dawley; TISSUE=Kidney;

RC MEDLINE=95024033; PubMed=7937880;

RA Saito A., Pietermonaco S., Loo A.K.C., Fargnhar M.G.;

RT "Complete cloning and sequencing of rat gp330/'megalin,' a

RT distinctive member of the low density lipoprotein receptor gene

RT family";

RL Proc. Natl. Acad. Sci. U.S.A. 91:9725-9729 (1994).

RN [2]

RP FUNCTION.

RA MEDLINE=95386696; PubMed=7544804;

RA Moestrup S.K., Cui S., Vorum H., Bregengaard C., Bjorn S.E.,

RA Norris K., Gilemann J., Christensen E.I.;

RT "Evidence that epithelial glycoprotein 330/megalin mediates uptake of

RT polybasic drugs";

RL J. Clin. Invest. 96:1404-1413 (1995).

RN [3]

RP TISSUE SPECIFICITY.

RA MEDLINE=94172242; PubMed=7510321;

RA Zheng G., Bachinsky D.R., Stamenkovic I., Strickland D.K., Brown D.,

RA Andres G., McCluskey R.T.;

RT "Organ distribution in rats of two members of the low-density

RT lipoprotein receptor gene family, gp330 and LRP/alpha 2MR, and the

RT receptor-associated protein (RAP).";

RL J. Histochem. Cytochem. 42:531-542 (1994).

CC - FUNCTION: BINDS PLASMINOGEN, EXTRACELLULAR MATRIX COMPONENTS,

CC PLASMINOGEN ACTIVATOR-PLASMINOGEN ACTIVATOR INHIBITOR TYPE I

CC COMPLEX, APOLIPOPROTEIN E-ENRICHED BETA-VLDL, LIPOPROTEIN LIPASE,

CC LACOPERRIN, CLUSTERIN AND CALCITON.

CC - FUNCTION: RECEPTOR-MEDIATED UPTAKE OF POLYBASIC DRUGS SUCH AS

CC - SUBUNIT FORMS A MULTIMERIC COMPLEX TOGETHER WITH A RECEPTOR-

CC ASSOCIATED PROTEIN (RAP).

CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXPRESSED IN

CC CLATHRIN-COATED PITS; A SOLUBLE FORM IS POSSIBLY DERIVED BY

CC CLEAVAGE AT THE CELL SURFACE.

CC - TISSUE SPECIFICITY: EPITHELIAL CELLS OF KIDNEY GLOMERULUS AND

CC PROXIMAL TUBULE, LUNG, EPIDIDYMS, YOLK SAC, AMONG OTHERS.

CC - SIMILARITY: CONTAINS 36 LDL-RECEPTOR CLASS A DOMAINS.

CC - SIMILARITY: CONTAINS 37 LDL-RECEPTOR CLASS B DOMAINS.

CC - SIMILARITY: CONTAINS 17 EGF-LIKE DOMAINS.

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CC -----

DR EMBL: U3049; AA51369.1; -

DR HSSP: 007954; 1CR8

DR GlycoSuiteDB: P98158; -

DR InterPro: IPR000152; Asx_hydroxyl.

DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR001881; EGF CA.

DR InterPro: IPR002172; LDL_recept A.

DR InterPro: IPR000033; LDL_receptor_rep.

DR Pfam: PF00057; 1d1_recept_a; 36.

DR Pfam: PF00058; 1d1_recept_b; 33.

DR PRINTS: PR00261; LDL_recept.

DR SMART: SM00179; EGF_CA; 3.

DR SMART: SM00001; EGF_Like; 15.

DR SMART: SM00192; LDLA; 36.

DR SMART: SM00135; LY; 35.

DR PROSITE: PS00010; ASX_HYDROXYL; 4.

DR PROSITE: PS00022; EGF_1; 1.

DR PROSITE: PS01186; EGF_2; 8.

DR PROSITE: PS01187; EGF_CA; 3.

DR PROSITE: PS01209; LDLRA_1; 31.

DR PROSITE: PS50068; LDLRA_2; 36.

DR GlycoSuite: Repeat; Endocytosis; Coated pits; Transmembrane;

KW Receptor; EGF-like domain; SH3-binding; Signal.

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FT SIGNAL 1 25

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FT FT 26 1791

FT FT 26 1832

FT FT 26 1882

FT FT 26 1930

FT FT 26 1972

FT FT 26 2013

FT FT 26 2060

FT FT 26 2108

FT FT 26 2156

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FT FT 26 4425

FT FT 26 4426

FT FT 26 4446

FT FT 26 4447

FT FT 26 4660

FT FT 26 64

FT FT 26 105

FT FT 26 144

FT FT 26 145

FT FT 26 181

FT FT 26 219

FT FT 26 258

FT FT 26 307

FT FT 26 346

FT FT 26 385

FT FT 26 476

FT FT 26 519

FT FT 26 566

FT FT 26 611

FT FT 26 652

FT FT 26 704

FT FT 26 793

FT FT 26 835

FT FT 26 879

FT FT 26 923

FT FT 26 1013

FT FT 26 1063

FT FT 26 1064

FT FT 26 1103

FT FT 26 1146

FT FT 26 1186

FT FT 26 1225

FT FT 26 1269

FT FT 26 1308

FT FT 26 1351

FT FT 26 1390

FT FT 26 1430

FT FT 26 1479

FT FT 26 1520

FT FT 26 1563

FT FT 26 1609

FT FT 26 1654

FT FT 26 1696

FT FT 26 1742

FT FT 26 1791

FT FT 26 1832

FT FT 26 1882

FT FT 26 1930

FT FT 26 1972

FT FT 26 2013

FT FT 26 2060

FT FT 26 2108

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FT FT 26 144

FT FT 26 145

FT FT 26 181

FT FT 26 219

FT FT 26 258

FT FT 26 307

FT FT 26 346

FT FT 26 385

FT FT 26 476

FT FT 26 519

FT FT 26 566

FT FT 26 611

FT FT 26 652

FT FT 26 704

FT FT 26 793

FT FT 26 835

FT FT 26 879

FT FT 26 923

FT FT 26 1013

FT FT 26 1063

FT FT 26 1064

FT FT 26 1103

FT FT 26 1146

FT FT 26 1186

FT FT 26 1225

FT FT 26 1269

FT FT 26 1308

FT FT 26 1351

FT FT 26 1390

FT FT 26 1430

FT FT 26 1479

FT FT 26 1520

FT FT 26 1563

FT FT 26 1609

FT FT 26 1654

FT FT 26 1696

FT FT 26 1742

FT FT 26 1791

FT FT 2

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FT DOMAIN 2479 2518 LDL-RECEPTOR CLASS B 26.
FT DOMAIN 2520 2562 LDL-RECEPTOR CLASS B 27.
FT DOMAIN 2564 2604 LDL-RECEPTOR CLASS B 28.
FT DOMAIN 2605 2647 LDL-RECEPTOR CLASS B 29.
FT DOMAIN 2652 2694 EGF-LIKE 10.
FT DOMAIN 2699 2739 LDL-RECEPTOR CLASS A 16.
FT DOMAIN 2740 2778 LDL-RECEPTOR CLASS A 17.
FT DOMAIN 2779 2820 LDL-RECEPTOR CLASS A 18.
FT DOMAIN 2821 2862 LDL-RECEPTOR CLASS A 19.
FT DOMAIN 2863 2903 LDL-RECEPTOR CLASS A 20.
FT DOMAIN 2906 2947 LDL-RECEPTOR CLASS A 21.
FT DOMAIN 2948 2992 LDL-RECEPTOR CLASS A 22.
FT DOMAIN 2993 3031 LDL-RECEPTOR CLASS A 23.
FT DOMAIN 3032 3072 LDL-RECEPTOR CLASS A 24.
FT DOMAIN 3075 3112 LDL-RECEPTOR CLASS A 25.
FT DOMAIN 3113 3153 EGF-LIKE 11.
FT DOMAIN 3154 3194 LDL-RECEPTOR CLASS B 30.
FT DOMAIN 3241 3282 LDL-RECEPTOR CLASS B 31.
FT DOMAIN 3284 3323 LDL-RECEPTOR CLASS B 32.
FT DOMAIN 3335 3377 LDL-RECEPTOR CLASS B 33.
FT DOMAIN 3379 3420 LDL-RECEPTOR CLASS B 34.
FT DOMAIN 3421 3461 EGF-LIKE 13.
FT DOMAIN 3467 3511 LDL-RECEPTOR CLASS A 26.
FT DOMAIN 3512 3552 LDL-RECEPTOR CLASS A 27.
FT DOMAIN 3553 3593 LDL-RECEPTOR CLASS A 28.
FT DOMAIN 3594 3634 LDL-RECEPTOR CLASS A 29.
FT DOMAIN 3635 3675 LDL-RECEPTOR CLASS A 30.
FT DOMAIN 3678 3718 LDL-RECEPTOR CLASS A 31.
FT DOMAIN 3719 3758 LDL-RECEPTOR CLASS A 32.
FT DOMAIN 3759 3797 LDL-RECEPTOR CLASS A 33.
FT DOMAIN 3798 3836 LDL-RECEPTOR CLASS A 34.
FT DOMAIN 3842 3882 LDL-RECEPTOR CLASS A 35.
FT DOMAIN 3883 3924 LDL-RECEPTOR CLASS A 36.
FT DOMAIN 3928 3966 EGF-LIKE 14.
FT DOMAIN 3968 4008 EGF-LIKE 15.
FT DOMAIN 4009 4050 CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 4156 4197 LDL-RECEPTOR CLASS B 35.
FT DOMAIN 4244 4284 LDL-RECEPTOR CLASS B 36.
FT DOMAIN 4332 4370 LDL-RECEPTOR CLASS B 37.
FT DOMAIN 4379 4413 EGF-LIKE 16.
FT DOMAIN 4454 4460 SH3-BINDING (POTENTIAL).
FT SITE 4457 4463 SH3-BINDING (POTENTIAL).
FT SITE 4606 4609 SH2-BINDING (POTENTIAL).
FT SITE 4619 4625 SH3-BINDING (POTENTIAL).
FT SITE 4624 4630 SH3-BINDING (POTENTIAL).
FT SITE 1743 1745 CELL ATTACHMENT SITE (POTENTIAL).
FT SITE 4522 4527 ENDOCYTOSIS SIGNAL (POTENTIAL).
FT SITE 4601 4606 ENDOCYTOSIS SIGNAL (POTENTIAL).
FT DISULFID 28 40 BY SIMILARITY.
FT DISULFID 35 53 BY SIMILARITY.
FT DISULFID 47 62 BY SIMILARITY.
FT DISULFID 67 80 BY SIMILARITY.
FT DISULFID 74 93 BY SIMILARITY.
FT DISULFID 87 103 BY SIMILARITY.
FT DISULFID 108 120 BY SIMILARITY.
FT DISULFID 115 132 BY SIMILARITY.
FT DISULFID 127 142 BY SIMILARITY.
FT DISULFID 147 157 BY SIMILARITY.

Query Match 9.0%; Score 82; DB 1; Length 4660;
Best Local Similarity 25.8%; Pred. No. 15;
Matches 40; Conservative 15; Mismatches 64; Indels 36; Gaps 8;

QY 33 SCPEQY-WDPLGLGCMCKTICNHQ---SORTCAAFRCRLSCRKEQGFYDH----- 81
DB 3076 TGPLHQFRCDN--GHCIEGRVNCVHVDGSDNSDEKGCINECLDSSISRCNDHCTDIT 3133
QY 82 -----LLRDCISCAI--CGQHPKQCAFCENKLRSPV-NLPPELRRQSRGVE 127
DB 3134 SFVCSCLPGYKLMDSKSCVDIDECKESPOLCSQKCNVGVSVICKCAPGYREPDKSC 3193
QY 128 NNSDN-----SGRY-QGLEHRGSEASPALPGL 153

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Db 3194 RQNSNIEPYLFISNRYIRNLTDTGSSYSLLIQL 3228
RESULT 10
RECK_HUMAN
ID RECK_HUMAN STANDARD; PRT; 971 AA.
AC O95980; OSWK37;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Reversion-inducing cysteine-rich protein with Kazal motifs precursor
DE (hRECK) (suppressor of tumorigenicity 15) (STI15).
GN RECK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A., AND N-GLYCOSYLATION.
RC TISSUE=Fibroblast;
RX MEDLINE=99007295; PubMed=9789069;
RA Takahashi C., Sheng Z., Horan T.P., Kitayama H., Maki M., Hitomi K.,
RA Kitaura Y., Takai S., Saehara R.M., Horimoto A., Ikawa Y.,
RA Ratzkin B.J., Arakawa T., Noda M.;
RT Regulation of matrix metalloproteinase-9 and inhibition of tumor
RT invasion by the membrane-anchored glycoprotein RECK.;
RL Proc. Natl. Acad. Sci. U.S.A. 95:13221-13226(1998).
[2]
SEQUENCE OF 363-971 FROM N.A.
RA Kimberley A.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Negatively regulates matrix metalloproteinase-9 (MMP-9)
CC by suppressing MMP-9 secretion and by direct inhibition of its
CC enzymatic activity. RECK down-regulation by oncogenic signals may
CC facilitate tumor invasion and metastasis. Appears to also
CC regulate MMP-2 and MT1-MMP, which are involved in cancer
CC progression.
CC -!- SUBUNIT: Interacts with MMP-9.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- TISSUE SPECIFICITY: Expressed in various tissues and untransformed
CC cells. It is undetectable in tumor-derived cell lines and
CC oncogenically transformed cells.
CC -!- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D50406; BAA34060.1;
CC EMBL; AL158850; CADI3384.1;
CC Genew; HGNC:11345; RECK.
CC MIM; 605227;
CC HSP; P80424; IAN1.
CC InterPro; IPR002350; Kazal.
CC SMART; SM00280; KAZAL; 3.
CC PROSITE; PS00282; KAZAL; 1.
CC Signal; Glycoprotein; GPI-anchor; Serine protease inhibitor;
CC Membrane; Anti-oncogene; Repeat.
CC SIGNAL 1 22
CC CHAIN 23 942
CC PROPEP 943 971
CC LIPID 942 942
CC DOMAIN 632 677
CC FT DOMAIN 708 750
CC FT DOMAIN 753 787
CC FT DOMAIN 37 338
CC FT

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FT REPEAT 37 84 KNOT 1.
FT REPEAT 104 141 KNOT 2.
FT REPEAT 151 197 KNOT 3.
FT REPEAT 216 263 KNOT 4.
FT REPEAT 292 338 KNOT 5.
FT DISULFID 635 654 BY SIMILARITY.
FT DISULFID 633 658 BY SIMILARITY.
FT DISULFID 633 677 BY SIMILARITY.
FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 971 AA; 106456 MW; 173D47D6AE6F834 CRC64;

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Query Match 8.9%; Score 81; DB 1; Length 971;
Best Local Similarity 21.8%; Pred. No. 3.9;
Matches 32; Conservative 18; Mismatches 41; Indels 56; Gaps 8;

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QY 34 CPEE--QYVDPV-----LGTG-----MSCKTICNHQSGRTCAAFCRSL 70
DB 74 CETWWEIWMNMSLPGVFKKSDGHWGLGCELTALATRCROKQASAKNDI---SKV 129
QY 71 CRKGGKFDHLRDCIS-----CASICGPHKQCAFCCEKRLSPVNLPELRORS 123
DB 130 CRKE---YENLFSCISNENMGVCSSYAGHH-TWCRGYCAIFRT----- 171
QY 124 GEVENNSDNGRYGGLHEHGSASPAL 150
DB 172 ---DSSPSPQIKAVENCAISIFOL 194

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RESULT 11
TIE2_HUMAN STANDARD; PRT; 1124 AA.
ID TIE2_HUMAN
AC 002763;
DT 01-FEB-1994 (Rel. 28, Created)
DT 15-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiopoietin 1 receptor precursor (EC 2.7.1.112) (Tyrosine-protein
DE kinase receptor TIE-2) (Tyrosine-protein kinase receptor TEK) (P140
DE TEK) (Hnuka interna endothelial cell kinase) (CD202b antigen).
GN TEK OR TIE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=93173509; PubMed=8382358;
RA Ziegler S.F., Bird T.A., Scherlinger J.A., Schooley K.A., Baum P.R.;
RT "Molecular cloning and characterization of a novel receptor protein
RT tyrosine kinase from human placenta."
RL Cytogene 8:663-670(1993).
RN 12
RP VARIANT VMCN1 TRP-849.
RX MEDLINE=97134663; PubMed=8980225;
RA Virkula M., Boon L.M., Cartaway K.L. III, Calvert J.T., Diamond A.J.,
RA Gummertov B., Paayk K.A., Marchuk D.A., Waman M.L., Cantley L.C.,
RA Mulliken J.B., Olse B.R.;
RT "Vascular dysmorphogenesis caused by an activating mutation in the
RT receptor tyrosine kinase TIE2."
RL Cell 87:1181-1190(1996).
RN 13
RP VARIANTS VMCN1 TRP-849 AND SER-897.
RX MEDLINE=9929243; PubMed=10369874;
RA Calvert J.T., Riney T.J., Kontos C.D., Cha E.H., Prieto V.G.,
RA Shea C.R., Berg J.N., Nevin N.C., Simpson S.A., Paayk K.A.,
RA Speer M.C., Peters K.G., Marchuk D.A.;
RT "Allelic and locus heterogeneity in inherited venous malformations."
RL Hum. Mol. Genet. 8:1279-1289(1999).
CC -!- FUNCTION: THIS PROTEIN IS A PROTEIN TYROSINE-KINASE TRANSMEMBRANE

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CC RECEPTOR FOR ANGIOPOIETIN 1. IT MAY CONSTITUTE THE EARLIEST
CC MAMMALIAN ENDOTHELIAL CELL LINEAGE MARKER. PROBABLY REGULATES
CC ENDOTHELIAL CELL PROLIFERATION, DIFFERENTIATION AND GUIDES THE
CC PROPER PATTERNING OF ENDOTHELIAL CELLS DURING BLOOD VESSEL
CC FORMATION.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN ENDOTHELIAL CELLS
CC AND THEIR PROGENITORS, THE ANGIOBLASTS. HAS BEEN DIRECTLY FOUND
CC IN PLACENTA AND LUNG, WITH A LOWER LEVEL IN UMBILICAL VEIN
CC ENDOTHELIAL CELLS, BRAIN AND KIDNEY.
CC -!- DISEASE: DEFECTS IN TEK ARE A CAUSE OF DOMINANTLY INHERITED VENOUS
CC MALFORMATIONS (VMCN1), AN ERROR OF VASCULAR MORPHOGENESIS
CC CHARACTERIZED BY DILATED, SERPIGINOUS CHANNELS.
CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. TIE
CC SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
CC -!- DATABASE: NAME=PROV; NOTE=PROV 3.12-14(2002);
CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/1715848914.g.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.ebi.ac.uk/annouce/
CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; L06139; AAA61139.1; --
DR HSSP; F11362; 1FGK.
DR Genew; HSNK; 11724; TEK.
DR MIM; 600221; --
DR MIM; 600195; --
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR001245; TYR_pkinase.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Euk_pkinase; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00001; EGF-like; 1.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00022; EGF_1; 3.
DR PROSITE; PS01186; EGF_2; 3.
DR Receptor_Tyrosine-protein_kinase; Transferase; Signal; ATP-binding;
DR Repeat_EGF-like_domain; Transmembrane; Immunoglobulin domain;
DR Glycoprotein; Phosphorylation; Multigene family; Disease mutation.
FT SIGNAL 1 18
FT CHAIN 19 1124
FT DOMAIN 19 745
FT TRANSMEM 746 770
FT DOMAIN 771 1124
FT DOMAIN 44 102
FT DOMAIN 210 252
FT DOMAIN 254 299
FT DOMAIN 301 341
FT DOMAIN 370 424
FT DOMAIN 444 536
FT DOMAIN 541 634
FT DOMAIN 638 732
FT DOMAIN 824 1096
FT NP BIND 830 838
FT BINDING 855 855

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RA Pulikniren L., Gerecke D.R., Christiano A.M., Magman D.W.,
RA Burgeson R.E., Uitto J.,
RT "Cloning of the beta 3 chain gene (LAMB3) of human laminin 5, a
RT candidate gene in junctional epidermolysis bullosa.",
RL Genomics 25:192-198 (1995).
RN [21]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 172-190.
RX MEDLINE=94209274; PubMed=7512558;
RA Gerecke D.R., Magman D.W., Champilaud M.F., Burgeson R.E.;
RT "The complete primary structure for a novel laminin chain, the
RT laminin Bk chain".
RL J Biol. Chem. 269:11073-11080 (1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21221101; PubMed=11296269;
RA Robbins P.B., Lin O., Goodnough U.B., Tian H., Chen X., Khavari P.A.;
RT "In vivo restoration of laminin 5 beta 3 expression and function in
RT junctional epidermolysis bullosa".
RL Proc. Natl. Acad. Sci. U.S.A. 98:5193-5198 (2001).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=Epidermis;
RX MEDLINE=96015057; PubMed=8530036;
RA Morishima Y., Aiyama T., Yamashiki K., Abe T., Ueda E., Yasuno H.,
RA Inazawa J.,
RT "Chromosomal loci of 50 human keratinocyte cDNAs assigned by
RT fluorescence in situ hybridization.";
RL Genomics 28:273-279 (1995).
RN [5]
RP SEQUENCE FROM N.A.
RA Grafham D.,
RL Submitted (APR-1999) to the EMBL/Genbank/DBJ databases.
RN [6]
RP VARIANT JEB LEU-679.
RX MEDLINE=96055522; PubMed=7550237;
RA Pulikniren L., McGrath J.A., Christiano A.M., Uitto J.;
RT "Detection of sequence variants in the gene encoding the beta 3 chain
RT of laminin 5 (LAMB3)".
RL Hum. Mutat. 6:77-84 (1995).
RN [7]
RP VARIANT GABEB LYS-210.
RX MEDLINE=9308987; PubMed=9767255;
RA Welletto J.B., Eady R.A., Atherton D.J., Lake B.D., McGrath J.A.;
RT "E210K mutation in the gene encoding the beta3 chain of laminin-5
RT (LAMB3) is predictive of a phenotype of generalized atrophic benign
RT epidermolysis bullosa".
RL Br. J. Dermatol. 139:325-331 (1998).
CC -I- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration, and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -I- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end.
CC THE BETA-3 CHAIN IS A SUBUNIT OF LAMININ-5 (EPILGRIN/KALININ/
CC NICEIN).
CC -I- SUBCELLULAR LOCATION: Extracellular.
CC -I- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
CC COMPONENT).
CC -I- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -I- DOMAIN: DOMAIN VI IS GLOULAR.
CC -I- DISEASE: DEFECTS IN LAMB3 ARE A CAUSE OF JUNCTIONAL EPIDERMOLYSIS
CC BULLOSA (JEB) GRAVIS, ALSO KNOWN AS HERLITZ TYPE JEB. IT IS A
CC BUBBLING DISORDER IN SKIN THAT IS CHARACTERIZED BY A SEPARATION
CC OF BASAL CELLS FROM THE BASEMENT MEMBRANE DUE TO A DECREASED
CC NUMBER OF HEMIDESMOSOMES. LAMININ-5 IS MISSING FROM THE BASEMENT
CC MEMBRANE OF PATIENTS WITH THE GRAVIS FORM OF EPIDERMOLYSIS
CC BULLOSA.
CC -I- DISEASE: DEFECTS IN LAMB3 ARE A CAUSE OF GENERALIZED ATROPHIC
CC BENIGN EPIDERMOLYSIS BULLOSA (GABEB). THIS NONLETHAL FORM OF


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FT DISULFID 293 313 BY SIMILARITY.
FT DISULFID 316 325 BY SIMILARITY.
FT DISULFID 318 343 BY SIMILARITY.
FT DISULFID 346 355 BY SIMILARITY.
FT DISULFID 358 372 BY SIMILARITY.
FT DISULFID 379 392 BY SIMILARITY.
FT DISULFID 381 399 BY SIMILARITY.
FT DISULFID 401 410 BY SIMILARITY.
FT DISULFID 413 428 BY SIMILARITY.
FT DISULFID 431 444 BY SIMILARITY.
FT DISULFID 433 451 BY SIMILARITY.
FT DISULFID 453 462 BY SIMILARITY.
FT DISULFID 465 478 BY SIMILARITY.
FT DISULFID 481 493 BY SIMILARITY.
FT DISULFID 483 500 BY SIMILARITY.
FT DISULFID 502 511 BY SIMILARITY.
FT DISULFID 519 531 BY SIMILARITY.
FT DISULFID 534 546 BY SIMILARITY.
FT DISULFID 536 553 BY SIMILARITY.
FT DISULFID 555 564 BY SIMILARITY.
FT DISULFID 567 578 BY SIMILARITY.
FT DISULFID 581 581 INTERCHAIN (PROBABLE).
FT DISULFID 584 584 INTERCHAIN (PROBABLE).
FT DISULFID 1171 1171 INTERCHAIN (PROBABLE).
FT CARBOHYD 220 220 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 604 604 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 810 810 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 210 210 E -> K (IN CABEE).
FT VARIANT 679 679 /FTID=VAR 004170.
FT CONFLICT 124 124 P -> L (IN JEB).
FT CONFLICT 269 269 Q -> R (IN REF. 2).
FT CONFLICT 368 368 MISSING (IN REF. 2).
FT CONFLICT 426 427 P -> A (IN REF. 2).
FT CONFLICT 440 441 QG -> RR (IN REF. 2).
FT CONFLICT 489 500 RD -> E (IN REF. 2).
FT CONFLICT 489 500 LSPQCNQFTGQC -> PQPTQVPHRAV (IN REF. 4).
FT CONFLICT 603 603 R -> P (IN REF. 2).
FT CONFLICT 815 815 G -> A (IN REF. 2).

Query Match 8.7%; Score 79.5; DB 1; Length 1172;
Best Local Similarity 25.3%; Pred. No. 6.6;
Matches 41; Conservative 16; Mismatches 66; Indels 39; Gaps 8;

QY 19 ERPPQGLWTGVAMRSCPEEQYWDPLLTGTCMSKTCICNHQSQRTCAAFCSRSLSC--RKEQG 76
DB 504 EGFGLMCSAAAIQCPRDRTYGDVATG-----CRACDCDFRGTEG 543
QY 77 KFYDHLRLDCISCASICGQHPKOCAY-FCENKLRSPV-----NLPPELRQ--RSG 124
DB 544 PGCDKASGRCLCRPGLTGPDCDQCGYCN--RYPCVACHPCFQTYDADLREQALRFG 600
QY 125 EVENNDSNGRYOGLHRCSEASPALPGKLKSADQVALVYST 166
DB 601 RURNATASLWSGFLDRGL-ASRLIDA-KSKIEQTRAVLSS 640

RESULT 14
YL_DROME STANDARD; PRT; 1984 AA.
AC P98163;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Putative vitellogenin receptor precursor (YL).
GN YL OR VOLKLESS.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=Ovary;
RX MEDLINE=951813490; PubMed=7878005;
RA Schonbaum C.P., Lee S., Mahowald A.P.;
RT "The Drosophila yolkless gene encodes a vitellogenin receptor
RT belonging to the low density lipoprotein receptor superfamily.";
RI Proc Natl Acad Sci U S A 92:1485-1489(1995).
CC - FUNCTION INVOLVED IN UPTAKE OF VITELLOGENIN BY ENDOCYTOSIS.
CC - TISSUE SPECIFICITY: OVARY.
CC - SIMILARITY: CONTAINS 13 LDL-RECEPTOR CLASS A DOMAINS.
CC - SIMILARITY: CONTAINS 7 EGF-LIKE DOMAINS.
CC -----
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CC -----
CC EMBL; U13637; AAB60217.1; -.
CC HSSP; P01130; 1AJJ.
CC FLYBase; FBgn004649; Yl.
CC InterPro; IPR000152; Asx_hydroxyl.
CC InterPro; IPR000561; EGF-like.
CC InterPro; IPR001881; EGF Ca.
CC InterPro; IPR002172; LDL_recept A.
CC InterPro; IPR000033; Ldl_receptor_rep.
CC Pfam; PF00008; EGF_5.
CC Pfam; PF00057; ldl_recept_a; 13.
CC Pfam; PF00056; ldl_recept_b; 6.
CC PRINTS; PR00261; LDLRECEPTOR.
CC SMART; SM00179; EGF_CA; 2.
CC SMART; SM00001; EGF_Like; 4.
CC SMART; SM00192; LDLA; 13.
CC SMART; SM00135; LY; 8.
CC PROSITE; PS00010; ASX_HYDROXYL; 2.
CC PROSITE; PS01186; EGF_2; 3.
CC PROSITE; PS01187; EGF_CA; 2.
CC PROSITE; PS01209; LDLRA_1; 11.
CC PROSITE; PS00068; LDLRA_2; 13.
CC Glycoprotein; Signal; Transmembrane; EGF-like domain; Receptor;
KW Repeat; Endocytosis.
FT SIGNAL 1 ?
FT CHAIN ? 1984 PUTATIVE VITELLOGENIN RECEPTOR.
FT DOMAIN ? 1800 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1801 1821 POTENTIAL.
FT DOMAIN 1822 1984 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 88 126 LDL-RECEPTOR CLASS A 1.
FT DOMAIN 127 167 LDL-RECEPTOR CLASS A 2.
FT DOMAIN 182 222 LDL-RECEPTOR CLASS A 3.
FT DOMAIN 225 264 LDL-RECEPTOR CLASS A 4.
FT DOMAIN 264 306 LDL-RECEPTOR CLASS A 5.
FT DOMAIN 306 347 EGF-LIKE 1.
FT DOMAIN 348 388 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 660 701 EGF-LIKE 3.
FT DOMAIN 984 1026 EGF-LIKE 4.
FT DOMAIN 1029 1064 LDL-RECEPTOR CLASS A 6.
FT DOMAIN 1072 1111 LDL-RECEPTOR CLASS A 7.
FT DOMAIN 1116 1154 LDL-RECEPTOR CLASS A 8.
FT DOMAIN 1156 1195 LDL-RECEPTOR CLASS A 9.
FT DOMAIN 1196 1234 LDL-RECEPTOR CLASS A 10.
FT DOMAIN 1241 1281 LDL-RECEPTOR CLASS A 11.
FT DOMAIN 1281 1320 LDL-RECEPTOR CLASS A 12.
FT DOMAIN 1338 1377 LDL-RECEPTOR CLASS A 13.
FT DOMAIN 1375 1417 EGF-LIKE 5.
FT DOMAIN 1418 1457 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1734 1770 EGF-LIKE 7.
FT SITE 1837 1878 CRITICAL FOR ENDOCYTOSIS (POTENTIAL).
FT SITE 1878 1878 CRITICAL FOR ENDOCYTOSIS (POTENTIAL).
FT SITE 1892 1892 CRITICAL FOR ENDOCYTOSIS (POTENTIAL).
FT DISULFID 90 102 BY SIMILARITY.
FT DISULFID 97 115 BY SIMILARITY.
FT DISULFID 109 124 BY SIMILARITY.

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Query Match      8.6%; Score 78.5; DB 1; Length 630;
Best Local Similarity 23.0%; Pred. No. 4.4;
Matches 38; Conservative 20; Mismatches 54; Indels 53; Gaps 9;

QY 22 POGIWTGVAMRSCPEEQYWDPLLGTCMSCKTICNH-----QSQRTG-----AARCRS-LSCR 72
Db 86 PADVWTFPPARASAPSP-----NAQVADHCLKEAAVKICLVCMASPCQEHLP 134
QY 73 KEQKFDHLL-----RDCISCASICGHPKQCAIFC-----ENKURSPVNL 115
Db 135 FDSFADFQHPQPPVRDLL--RRKCSQHNRLREFFCFEHSCEICICLVVEHKTCSASL- 191
QY 116 PELRRQRSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQV 160
Db 192 -----SQASADLEAT-----LRHKLTVMYSQINGASRALDDV 223
```

Search completed: January 7, 2003, 09:38:11
Job time : 16.4812 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 7, 2003, 09:34:29 ; Search time 47.0125 Seconds
(without alignments)
727.547 Million cell updates/sec

Title: US-09-855-158-15
Sequence: 1 MSGLSRRGRSRVDQEEER.....SPALPGLKLSADQVALVYST 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	140	15.4	156	Q9N146	Q9N146 macaca mula
2	93	10.2	840	Q96H26	Q96H26 homo sapien
3	93	10.2	1240	Q15030	Q15030 homo sapien
4	91	10.0	1704	Q94446	Q94446 chironomus
5	89	9.8	839	Q10652	Q10652 caenorhabdi
6	89	9.8	1878	Q9UIF9	Q9UIF9 homo sapien
7	88.5	9.7	665	Q9W241	Q9W241 drosophila
8	88.5	9.7	676	Q8SWW8	Q8SWW8 drosophila
9	87.5	9.6	415	Q8TCB8	Q8TCB8 homo sapien
10	87	9.6	272	Q9BXY4	Q9BXY4 homo sapien
11	87	9.6	292	Q96K87	Q96K87 homo sapien
12	86.5	9.5	310	Q03108	Q03108 triticum ae
13	86.5	9.5	353	Q03107	Q03107 triticum ae
14	86	9.5	1299	Q26489	Q26489 spodoptera
15	85	9.4	267	Q919M0	Q919M0 neoceratodu
16	85	9.4	1137	Q9H8C1	Q9H8C1 homo sapien

17	85	9.4	1918	4	Q9BOM7	Q9BOM7 homo sapien
18	85	9.4	1925	4	Q9P2E3	Q9P2E3 homo sapien
19	84.5	9.3	358	16	Q82DV4	Q82DV4 versinia pe
20	84.5	9.3	588	11	Q8H151	Q8H151 mus musculu
21	84.5	9.3	702	5	Q9VH96	Q9VH96 drosophila
22	83	9.1	820	10	Q9FFK8	Q9FFK8 arabidopsis
23	83	9.1	13288	6	O18758	O18758 sus scrofa
24	82.5	9.1	913	4	Q96EP4	Q96EP4 homo sapien
25	82.5	9.1	1382	13	Q9EVZ4	Q9EVZ4 xenopus lae
26	82	9.0	2239	13	Q9OZL0	Q9OZL0 fugu rubrip
27	82	9.0	868	5	Q9YIV3	Q9YIV3 polyandroca
28	82	9.0	932	11	Q62030	Q62030 mus musculu
29	82	9.0	1650	11	Q9QVT6	Q9QVT6 rattus sp.
30	81.5	9.0	316	11	Q922H9	Q922H9 mus musculu
31	81	8.9	567	4	Q8WUL3	Q8WUL3 homo sapien
32	81	8.9	704	3	O74567	O74567 trichoderma
33	81	8.9	1140	4	Q96KG7	Q96KG7 homo sapien
34	80	8.8	108	16	O07571	O07571 bacillus su
35	80	8.8	330	5	O18118	O18118 caenorhabdi
36	80	8.8	996	11	Q924X6	Q924X6 mus musculu
37	80	8.8	1664	5	Q9TVQ2	Q9TVQ2 caenorhabdi
38	80	8.8	1792	13	O57484	O57484 gallus gall
39	79.5	8.7	98	5	O16939	O16939 ancylostoma
40	79.5	8.7	593	10	Q9SEW4	Q9SEW4 juglans reg
41	79.5	8.7	1963	5	Q9VY56	Q9VY56 drosophila
42	79.5	8.7	2189	5	Q9B105	Q9B105 eimaria ten
43	79	8.7	217	11	Q9CSB2	Q9CSB2 mus musculu
44	79	8.7	269	17	O29751	O29751 archaeoglob
45	79	8.7	317	11	O70524	O70524 cricetus

ALIGNMENTS

RESULT 1
Q9N146 Q9N146 PRELIMINARY; PRT; 156 AA.
ID Q9N146
AC Q9N146;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE Transmembrane activator (Fragment).
GN NF-AT.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Arredondo J.
RT "Cytokine Signal Transduction Genes from Rhesus Macaques."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF227558; AAF73400.1; -;
FT NON_CODING
SQ SEQUENCE 156 AA; 16170 MW; 8AD74E4D17D511D0 CRC64;
Query Match 15.4%; Score 140; DB 6; Length 156;
Best Local Similarity 96.6%; Pred. No. 6.1e-08;
Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 138 GLEHGRSEASPALPGLKLSADQVALVYST 166

Db 1 GLEHGRSEASPALPGLKLSADQVALVYST 29

RESULT 2

Q96H26 Q96H26 PRELIMINARY; PRT; 840 AA.
ID Q96H26
AC Q96H26;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

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DE Similar to bromodomain adjacent to zinc finger domain, 2A
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH.
RA Strussberg R.
RL Submitted(MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC008965; AAH08965.1; -.
DR InterPro; IPR001967; AT_hook.
DR InterPro; IPR001965; Znf_PHD.
DR Pfam; PF02178; AT_hook; 2.
DR Pfam; PF00628; PHD; 1.
DR PROSITE; PS50014; BROMODOMAIN_2; 1.
FT NON-TER
SQ
SEQUENCE 840 AA; 94884 MW; 3F8147D9B7034B45 CRC64;

Query Match 10.2%; Score 93; DB 4; Length 840;
Best Local Similarity 25.8%; Pred. No. 0.086;
Matches 40; Conservative 17; Mismatches 68; Indels 30; Gaps 7;

OY 22 PGGLMTGVAMRSCEPQWYDPLGTGMSCKTI--CNHQSORTCA-----AFCSLSGR 72
DB 561 PEGTTTISYEITPRIRVROTLECRSAQVCLTGLQLERSIAMEKSVNKVTC--LVCR 618
OY 73 KEQGFYHLRLDCISCAISCG---QHPKQCA-----YFC-----ENKLRSPVNLPP 116
DB 619 KQDN---DEFLLLCDGCDRGCHHYCHRPKMEAVPEGDWFCVYCLAQVGEFQKGFPK 675
OY 117 ELRRQSGEVENNSDNGRYOGLERHSGEASPAAP 151
DB 676 RGQKRKSGYSINFSEGDGRRRVLLRGRESPPAAGP 710

RESULT 3
O15030 PRELIMINARY; PRT; 1240 AA.
AC 015030;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE KIAA0314 protein (Fragment).
GN KIAA0314.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RA MEDLINE=97349984; PubMed=9205841;
RA Nagase T., Ishikawa K., Nakajima D., Ohira M., Seki N., Miyajima N.,
RA Tanaka A., Kozani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. VII.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Ref. 4114; 150(1997).
DR EMBL; AB003312; BAA20773.1; -.
DR HSP; Q92831; I891.
DR InterPro; IPR000637; AT_hook.
DR InterPro; IPR001487; Bromodomain.
DR InterPro; IPR004022; DDT_dom.
DR InterPro; IPR001965; Znf_PHD.
DR Pfam; PF02178; AT_hook; 3.
DR Pfam; PF00439; bromodomain; 1.
DR Pfam; PF02791; DDT; 1.
DR Pfam; PF00628; PHD; 1.
DR PRINTS; PR00929; ATHOOK.

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DR PRINTS; PR00503; BROMODOMAIN.
DR SMART; SM00384; AT_hook; 3.
DR SMART; SM00297; BROMO; 1.
DR SMART; SM00249; PHD; 1.
DR PROSITE; PS50014; BROMODOMAIN_2; 1.
FT NON-TER
SQ
SEQUENCE 1240 AA; 140417 MW; 20BDBF1AA6BGSAL CRC64;

Query Match 10.2%; Score 93; DB 4; Length 1240;
Best Local Similarity 25.8%; Pred. No. 0.13;
Matches 40; Conservative 17; Mismatches 68; Indels 30; Gaps 7;

OY 22 PGGLMTGVAMRSCEPQWYDPLGTGMSCKTI--CNHQSORTCA-----AFCSLSGR 72
DB 961 PEGTTTISYEITPRIRVROTLECRSAQVCLTGLQLERSIAMEKSVNKVTC--LVCR 1018
OY 73 KEQGFYHLRLDCISCAISCG---QHPKQCA-----YFC-----ENKLRSPVNLPP 116
DB 1019 KQDN---DEFLLLCDGCDRGCHHYCHRPKMEAVPEGDWFCVYCLAQVGEFQKGFPK 1075
OY 117 ELRRQSGEVENNSDNGRYOGLERHSGEASPAAP 151
DB 1076 RGQKRKSGYSINFSEGDGRRRVLLRGRESPPAAGP 1110

RESULT 4
O94446 PRELIMINARY; PRT; 1704 AA.
AC O94446;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE 220 kDa silk protein.
GN SP220.
OS Chironomus thummi (midge).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
OC Chironomidae; Chironomidae; Chironominae; Chironomus.
OC NCBI_TaxID=7154;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SALIVARY GLAND;
RA Case S.T., Cox C., Bell W.C., Hoffman R.T., Martin J., Hamilton R.;
RT "Extraordinary conservation of cysteines among homologous Chironomus
RT silk proteins sp185 and sp220."
RT submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U54641; AAA9804.1; -.
DR InterPro; IPR004153; CXCXC_repeat.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000853; McIlhion_nemat.
DR Pfam; PF03128; CXCXC; 69.
DR PRINTS; PR00876; MTNEMATODE.
DR PROSITE; PS00022; EGF_1; UNKNOWN_2.
DR PROSITE; PS0186; EGF_2; UNKNOWN_1.
DR SEQUENCE 1704 AA; 185746 MW; 3A3F20247C8F1E28 CRC64;

Query Match 10.0%; Score 91; DB 5; Length 1704;
Best Local Similarity 21.4%; Pred. No. 0.33;
Matches 31; Conservative 22; Mismatches 44; Indels 48; Gaps 7;

OY 32 RSCPEQWYD-----PLGTC-----MCKTCHNQ-----SQTCAFC 66
DB 1357 QCPNAGQWDSYTCGCSFPAKCTGAQFMCAGKQKCYCPQENCKSPKVDQTSCTSCQC 1416
OY 67 -RSLSCRKEQ--GKFIYH-----LRLDCISCAISCGQHPKQC---AYF 103
DB 1417 PKNWQPPPGECTAGRTWDATCTEKATVNCESPMVFDATCGCKGCKNKKPKLPADRW 1476
OY 104 CENKLRSPVNLPPELRRQSGEVEN 128
DB 1477 CDKCAVCSLPPITQCPYSGQTVN 1501

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RESULT 5
Q10652
ID Q10652 PRELIMINARY; PRT; 839 AA.
AC Q10652;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 20, Last annotation update)
DE Zinc finger protein CEZF.
GN CEZF.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoides;
OC Rhabditidae; Euthertia; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BRISTOL N2;
RX MEDLINE=96003854; PubMed=7568208;
RA Saha V., Chaplin T., Gregorini A., Ayton P., Young B.D.;
RT "The leukemia-associated-protein (LAP) domain, a cysteine-rich motif,
RT is present in a wide range of proteins, including MLL, AF10, and MLLT6
RT proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 92:9737-9741(1995).
CC -1- SIMILARITY: CONTAINS A CYS-RICH (PHD-FINGER) DOMAIN SIMILAR TO
CC THOSE FROM HAT3.1, MAIZE HOXA AND PARSLEY PRH.
CR EMBL; U20555; AAC46918.1; -
DR InterPro; IPR001965; Znf_PHD.
DR Pfam; PF00628; PHD; 1.
DR SMART; SM00249; PHD; 2.
KW DNA-binding; Zinc-finger; Metal-binding.
FT DOMAIN 8 54 CYS-RICH (PHD-FINGER).
FT DOMAIN 619 655 LEUCINE ZIPPER.
FT ZN_FING 127 151 POTENTIAL.
FT SEQUENCE 839 AA; 89439 MW; AFBFF99D1D3584B8 CRC64;
SQ
Query Match 9.8%; Score 89; DB 5; Length 839;
Best Local Similarity 32.5%; Pred. No. 0.24;
Matches 27; Conservative 8; Mismatches 28; Indels 20; Gaps 5;

QY 34 CPBEOYQWDPFLGTCMSC-KTICNHQSQTCAAFRCSLSCRKEQKGFYDHLRLDCISCAI 92
Db 130 CNBERENDAKGACMCKNSKTSRSHVTCQAQ-RKGLLC-BEGAI----- 172
QY 93 CGOHPKQCAFYCNKLRSPNLP 115
Db 173 -SRNVKCYG-CENHLKKAINDP 193

RESULT 6
Q9W241
ID Q9W241 PRELIMINARY; PRT; 1878 AA.
AC Q9W241;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Bromodomain adjacent to zinc finger domain 2A.
GN BAZ2A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthertia; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20130112; PubMed=10662543;
RA Jones M.H., Hamana N., Nezu J., Shimane M.;
RT "A novel family of bromodomain genes."
RL Genomics 63:40-45(2000).
DR EMBL; AB032254; BAA89211.1; -
DR HSSP; O92831; 1B91.
DR InterPro; IPR000637; AT_hook.
DR InterPro; IPR001487; Bromodomain.
DR InterPro; IPR004022; DDT_dom.
DR InterPro; IPR001739; Methyl_CpG_bind.
DR InterPro; IPR001965; Znf_PHD.

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DR Pfam; PF02178; AT_hook; 4.
DR Pfam; PF00439; Bromodomain; 1.
DR Pfam; PF02791; DDT; 1.
DR Pfam; PF01439; MBD; 1.
DR Pfam; PF00632; PHD; 1.
DR PRINTS; PR00503; BROMODOMAIN.
DR SMART; SM00384; AT_hook; 3.
DR SMART; SM00297; BROMO; 1.
DR SMART; SM00391; MBD; 1.
DR SMART; SM00249; PHD; 1.
DR PROSITE; PS00014; BROMODOMAIN 2; 1.
SQ SEQUENCE 1878 AA; 208639 MW; 12683AFE636A93A6 CRC64;

Query Match 9.8%; Score 89; DB 4; Length 1878;
Best Local Similarity 23.3%; Pred. No. 0.61;
Matches 37; Conservative 18; Mismatches 66; Indels 38; Gaps 6;

QY 22 PQGLWTGVAMRSCPEEQYWDPLGLTCTMCKTIC-----NHQSQTCAAFRCRS 68
Db 1599 PEGTTEISYEITPRIRIWRQTLQRCSAAHVCLGLHLERSIAWKSVMKVC----- 1652
QY 69 LSCRKEQKGFYDHLRLDCISCAICG---QHPKQCA-----YFC-----ENKLRSPV 112
Db 1653 LVCRKGDN---DEFLLLCDGCDRGCHVCHRPKMEAVPEGDFCTVCLAQQVGEFTQKP 1709
QY 113 NLPPELPRQRSGEVNNSDNGRYOGLHGRGSEASPALP 151
Db 1710 GFPRGQKRKSGYSINFSEGDGRRRRVLLKGRSPAGP 1748

RESULT 7
Q9W241
ID Q9W241 PRELIMINARY; PRT; 665 AA.
AC Q9W241;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE CG12489 protein.
GN CG12489.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.Y.,
RA Brandon R.C., Rogers Y.-H.C., Blazei G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.P., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fogle A., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lin X., Mattai B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milchunas N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

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RX MEDLINE=93258430; PubMed=1302642;
 RA Celudo F.J., Murphy G., Chinyo C., Baulcombe D.C.;
 RT "A gibberellin-regulated gene from wheat with sequence homology to
 RT carboxypeptin B of mammalian cells.";
 RL Plant J. 2:937-948 (1992).
 DR EMBL: X66013; CAA46811.1; -
 DR HSSP: P07688; 1000.
 DR MEROPS: C01.949.
 DR InterPro: IPR001668; Peptidase_C1.
 DR InterPro: IPR001691; SHPOC_acid.
 DR Pfam: PF00112; Peptidase_C1; 1.
 DR PRINTS: PR00705; PAFAIN.
 DR ProDom: PD000158; Peptidase_C1; 1.
 DR PROSITE: PS00139; THIOL_PROTEASE_CYS; 1.
 DR PROSITE: PS00639; THIOL_PROTEASE_HIS; 1.
 KW Hydrolase; Thiol protease.
 FT NON_TER
 SQ SEQUENCE 353 AA; 38355 MW; A10E7C84ED46E44 CRC64;

Query Match 9.5%; Score 86.5; DB 10; Length 353;
 Best Local Similarity 24.7%; Pred. No. 0.18;
 Matches 36; Conservative 12; Mismatches 63; Indels 35; Gaps 5;
 OY 22 PGLMTGVAMRSCEP-----EQYWPDLTGTCMSCKTICNHQSQRCAAFCRSLSCR 72
 DB 80 PGLLAGVPIKIHPEMDLPKEFAPRTQWS-----SCSTIGNILDQHGCAWPAVAV 132
 OY 73 KGGKRYDHL-----LRDCTSCASICGHPKQCAVFCENKLRSPVNLPELRRQSGE 125
 DB 133 ALQDRFCIHLNMSVSLSVNDLAC-----CGFLCGSGNGGYPISAMRYPRRSQV 182
 OY 126 VENNNSNGRYOGLERHSGEASPALP 151
 DB 183 VTRECDPYPDQTCQHPGCE--PAYP 206

RESULT 14
 ID Q26489 PRELIMINARY; PRT; 1299 AA.
 AC Q26489;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Endoprotease furin.
 GN Spodoptera frugiperda (Fall armyworm).
 OS Spodoptera frugiperda (Fall armyworm).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Noctuidae; Noctuidae; Amphipylinae; Spodoptera.
 OX NCBI_TaxID=7108;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SF9;
 RA Ciaplik M., Klenk H.;
 RT "Cloning and functional characterization of FURIN from Spodoptera
 RT frugiperda (SF9) cells.";
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Z68888; CAA3116.1; -
 DR HSSP: Q99405; 1MPT.
 DR InterPro: IPR002174; Furin-like.
 DR InterPro: IPR000209; Peptidase_S8.
 DR Pfam: PF001483; P; 1.
 DR Pfam: PF00082; Peptidase_S8; 1.
 DR PRINTS: PR00723; SUBTILISIN.
 DR ProDom: PD000717; P_domain; 1.
 DR SMART: SM00261; FU; 10.
 DR PROSITE: PS00136; SUBTILASE_ASP; 1.
 DR PROSITE: PS00137; SUBTILASE_HIS; 1.
 DR PROSITE: PS00138; SUBTILASE_SER; 1.
 KW Protease.
 SQ SEQUENCE 1299 AA; 142020 MW; 4C3799C7B8C572AB CRC64;

Query Match 9.5%; Score 86; DB 5; Length 1299;
 Best Local Similarity 25.0%; Pred. No. 0.87;
 Matches 39; Conservative 16; Mismatches 51; Indels 50; Gaps 9;
 OY 22 PGLMTGVAMRSCEPQYWPDLTGTCMSCKTICNHQSQRCAAFCRSLSCRKEGKF--- 78
 DB 1104 PRFMDGGLCMEGLGQYVDATSGTCRSDASC-----RTCSG-----EQFSCT 1148
 OY 79 -----YDHLRDISCASICG---QHPRQCAVFCENKLRSPVNLPELRRQSGEVE 127
 DB 1149 TCSRPLRIDRLANQVPCPSRGVNTSPYDCCG-CN-----PE-----NGECT 1192
 OY 128 NNSDNGRYOGLERHSGEASPALPGLKLSADQVALY 163
 DB 1193 NSS-VAGKRRIAEWGALHTAPSD---AAPSVAIV 1223

RESULT 15
 ID Q919M0 PRELIMINARY; PRT; 267 AA.
 AC Q919M0;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Proenkephalin.
 OS Neoceratodus forsteri (Australian lungfish).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Dipnoi; Ceratodontiformes; Ceratodontidae; Neoceratodus.
 OX NCBI_TaxID=7892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRNIN.
 RA MEDLINE=20417836; PubMed=10960597;
 RA Sollars C., Danielson P., Joss U.M.P., Dore R.M.;
 RT "Deciphering the origin of Met-enkephalin and Leu-enkephalin in Lobe-
 RT fished fish: cloning of Australian lungfish proenkephalin.";
 RL Brain Res. 874:131-136 (2000).
 DR EMBL: AF232671; AAF4658.1; -
 DR InterPro: IPR000094; Opioid_neuropep.
 DR Pfam: PF01160; Opioid_neuropep; 1.
 DR PRINTS: PR01028; OPIOIDPRCSR.
 DR PROSITE: PS01252; OPIOIDS_PRECURSOR; UNKNOWN 1.
 SQ SEQUENCE 267 AA; 30688 MW; 69C92C0F378E0F0 CRC64;

Query Match 9.4%; Score 85; DB 13; Length 267;
 Best Local Similarity 29.4%; Pred. No. 0.19;
 Matches 30; Conservative 7; Mismatches 35; Indels 30; Gaps 5;
 OY 62 CAAFCRSLSCRKEGKFYDHLRDISCASICGQH---PQCAVFCENKLRSPVNSWDMC 110
 DB 15 CA--CLILAVARECK-----DCAHCTYHLGGADINPLSTCLEGCKLPVSRWDMC 65
 OY 111 ----PVNLPELRRQSGEVENNSDN-----SGRYOGLERH 142
 DB 66 KELLYGKPEIMQEGEETASVENDKENDEQRMFAKRYGFMGR 107

Search completed: January 7, 2003, 09:40:10
 Job time : 50.0125 secs

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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:35:14 ; Search time 20.386 seconds
(without alignments)
239.587 Million cell updates/sec

Title: US-09-855-158-15
Perfect score: 909
Sequence: 1 MSGIGRRGRGRSRVDQER.....SPALPGLKLSADQVALVYST 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pap.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pap.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pap.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pap.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	909	100.0	166	2	US-08-810-572A-6
2	909	100.0	166	4	US-09-290-333-6
3	909	100.0	293	2	US-08-810-572A-2
4	909	100.0	293	4	US-09-290-333-2
5	82.5	9.1	799	2	US-08-525-940-23
6	82.5	9.1	799	2	US-08-976-838-23
7	82.5	9.1	881	2	US-08-976-838-21
8	82.5	9.1	881	2	US-08-525-940-18
9	82.5	9.1	915	2	US-08-976-838-18
10	82.5	9.1	915	4	US-08-976-838-2
11	82.5	9.1	915	4	US-09-214-555B-2
12	82.5	9.1	915	4	US-09-214-555B-7
13	81	8.9	704	4	US-09-590-656-2
14	81	8.9	704	4	US-09-590-656-1
15	81	8.9	1124	1	US-08-323-474-2
16	81	8.9	1124	5	PCT-US93-06093-2
17	79.5	8.7	98	2	US-08-465-380-21
18	79.5	8.7	98	2	US-08-480-478-49
19	79.5	8.7	98	2	US-08-486-397-21
20	79.5	8.7	98	2	US-08-461-965-21
21	79.5	8.7	98	2	US-08-461-965-6
22	79.5	8.7	98	2	US-08-326-110A-49
23	79.5	8.7	98	2	US-08-634-641-21
24	79.5	8.7	98	3	US-09-249-471-21
25	79.5	8.7	98	3	US-09-249-471-21
26	79.5	8.7	98	3	US-09-249-451-21
27	79.5	8.7	98	3	US-08-809-455-21

28	79.5	8.7	98	3	US-09-249-461-21	Sequence 21, Appl
29	79.5	8.7	98	3	US-09-249-448-21	Sequence 21, Appl
30	79.5	8.6	518	1	US-08-385-229-4	Sequence 4, Appl
31	77.5	8.5	75	2	US-08-465-380-6	Sequence 6, Appl
32	77.5	8.5	75	2	US-08-465-380-41	Sequence 41, Appl
33	77.5	8.5	75	2	US-08-480-478-35	Sequence 35, Appl
34	77.5	8.5	75	2	US-08-486-397-6	Sequence 6, Appl
35	77.5	8.5	75	2	US-08-486-397-41	Sequence 41, Appl
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37	77.5	8.5	75	2	US-08-486-399-41	Sequence 41, Appl
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39	77.5	8.5	75	2	US-08-461-965-41	Sequence 41, Appl
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41	77.5	8.5	75	2	US-08-634-641-6	Sequence 6, Appl
42	77.5	8.5	75	2	US-08-634-641-41	Sequence 41, Appl
43	77.5	8.5	75	3	US-09-249-471-6	Sequence 6, Appl
44	77.5	8.5	75	3	US-09-249-471-41	Sequence 41, Appl
45	77.5	8.5	75	3	US-09-249-472-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-810-572A-6
; Sequence 6, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/810,572A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-810-572A-6
Query Match 100.0%; Score 909; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-90;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRGGRSRVDOERFPQGLMTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHOSOR 60
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QY 61 TCAAFCRSLSCRKEGKGFYDHLRDCISCAISICGQHPKQCAVFCENKLRSPVNLPEELRR 120
DB 61 TCAAFCRSLSCRKEGKGFYDHLRDCISCAISICGQHPKQCAVFCENKLRSPVNLPEELRR 120

QY 121 ORSGEVNNSDNGRGYQGLEHRSSEASPALPGIKLSADQVALVYST 166
DB 121 ORSGEVNNSDNGRGYQGLEHRSSEASPALPGIKLSADQVALVYST 166

RESULT 2
US-09-290-333-6
Sequence 6, Application US/09290333
Patent No. 6316222
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/290,333
FILING DATE: 12-Apr-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-343-1684
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-290-333-6

Query Match 100.0%; Score 909; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-90;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRGGRSRVDOERFPQGLMTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHOSOR 60
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DB 61 TCAAFCRSLSCRKEGKGFYDHLRDCISCAISICGQHPKQCAVFCENKLRSPVNLPEELRR 120

QY 121 ORSGEVNNSDNGRGYQGLEHRSSEASPALPGIKLSADQVALVYST 166
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RESULT 3
US-08-810-572A-2
Sequence 2, Application US/08810572A
Patent No. 5969102
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,572A
FILING DATE: 28-FEB-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
HYPOTHEICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-810-572A-2

Query Match 100.0%; Score 909; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 4e-90;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRGGRSRVDOERFPQGLMTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHOSOR 60
DB 1 MSGLSRRGGRSRVDOERFPQGLMTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHOSOR 60

QY 61 TCAAFCRSLSCRKEGKGFYDHLRDCISCAISICGQHPKQCAVFCENKLRSPVNLPEELRR 120
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QY 121 ORSGEVNNSDNGRGYQGLEHRSSEASPALPGIKLSADQVALVYST 166
DB 121 ORSGEVNNSDNGRGYQGLEHRSSEASPALPGIKLSADQVALVYST 166

RESULT 4
US-09-290-333-2
; Sequence 2, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/290,333
; FILING DATE: 12-Apr-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION/DOCKET NUMBER: 26,742
; REFERENCE NUMBER: 1340-1-007 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2
Query Match 100.0%; Score 909; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 4e-90;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSGLGRRGGRSRVDQERFFQGLWTGVAMRSCPEEQYWDPLLTGTCMCKTICNHQSOR 60
DB 1 MSGLGRRGGRSRVDQERFFQGLWTGVAMRSCPEEQYWDPLLTGTCMCKTICNHQSOR 60
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DB 61 TCAAFRCRSLSCRKEQKGYDHLRLDRCISCASICGGQHPKQCAFCENKLRSPVNLPELRR 120
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DB 121 QRSGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVYST 166
RESULT 5
US-08-525-940-23
; Sequence 23, Application US/08525940
; Patent No. 5866351
; GENERAL INFORMATION:
; APPLICANT: Franzusoff, Alex
; APPLICANT: Miranda, Luis R.

APPLICANT: Wolf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,852
FILING DATE: 01-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/088,322
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION/DOCKET NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-525-940-23
Query Match 9.1%; Score 82.5; DB 2; Length 799;
Best Local Similarity 26.0%; Pred. No. 1.5;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;
QY 27 TGVAMRSCPEEQYWDPLLTGTCMCKTICNHQSORCAAF-----CR-----SISC 71
DB 603 TNSCVTHCPDGSYQDTKKNLCRKSENC-----KTCTEFHNTCTCRDGLSLQSRCSVSC 657
QY 72 RKEQKGYDHLRLDRCISCASIC-----GQHPKQC-----AYECEN 106
DB 658 --EDGRVFNQ--QDCQCHRPATCAGAGADGCINCTEGYFMD 697
RESULT 6
US-08-976-838-23
; Sequence 23, Application US/08976838
; Patent No. 5981259
; GENERAL INFORMATION:
; APPLICANT: Franzusoff, Alex
; TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
; MOLECULES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/976,838
APPLICATION NUMBER: US/08/976,838
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-976-838-23

Query Match 9.1%; Score 82.5; DB 2; Length 799;
Best Local Similarity 26.0%; Pred. No. 1.5;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;

Qy 27 TGVAMRSCPEEQYMDPLGTGMSCKTICNHOSORTCAAF-----CR-----SLSC 71
Db 603 TNSCVTHCPDGSYDPTKKNLCRKCSENC-----KTCTEFHNCTEGRDGLSLQSRCSVSC 657
Qy 72 RKEQGFYDHLRDCISCSAIC---GQHPKQC---AYFCEN 106
Db 658 --EDGRYFNG--QDCOPCHRFATCAGAGADGCTGTEGYFMD 697

RESULT 7
US-08-525-940-21
Sequence 21, Application US/08525940
Patent No. 5866351
GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
APPLICANT: Miranda, Luis R.
APPLICANT: Wolf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
TITLE OF INVENTION: ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Rose & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,852
FILING DATE: 01-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/088,322
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700

TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 881 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-525-940-21

Query Match 9.1%; Score 82.5; DB 2; Length 881;
Best Local Similarity 26.0%; Pred. No. 1.7;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;

Qy 27 TGVAMRSCPEEQYMDPLGTGMSCKTICNHOSORTCAAF-----CR-----SLSC 71
Db 665 TNSCVTHCPDGSYDPTKKNLCRKCSENC-----KTCTEFHNCTEGRDGLSLQSRCSVSC 739
Qy 72 RKEQGFYDHLRDCISCSAIC---GQHPKQC---AYFCEN 106
Db 740 --EDGRYFNG--QDCOPCHRFATCAGAGADGCTGTEGYFMD 779

RESULT 8
US-08-976-838-21
Sequence 21, Application US/08976838
Patent No. 5981259
GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
APPLICANT: Miranda, Luis R.
APPLICANT: Wolf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Rose P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,838
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 881 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-976-838-21

Query Match 9.1%; Score 82.5; DB 2; Length 881;
Best Local Similarity 26.0%; Pred. No. 1.7;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;

Qy 27 TGVAMRSCPEEQYMDPLGTGMSCKTICNHOSORTCAAF-----CR-----SLSC 71
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Qy 72 RKEQGFYDHLRDCISCSAIC---GQHPKQC---AYFCEN 106
Db 740 --EDGRYFNG--QDCOPCHRFATCAGAGADGCTGTEGYFMD 779

us-09-855-158-15-rai

Tue Jan 7 10:36:49 2003

ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/976,838
APPLICATION NUMBER: US/08/976,838
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 915 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-976-838-18

Query Match 9.1%; Score 82.5; DB 2; Length 915;
Best Local Similarity 26.0%; Pred. No. 1.8;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;

QY 27 TGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSORTCAAF-----CR-----SLSC 71
DB 719 TNSCVTHCPDGSYQDTKKNLCKKSENC-----KCTEFHNCTECDGLSLQGRCSVSC 773
QY 72 RKEQGFYDHLRLDCISCAIC---GQHPKQC-----AYFCEN 106
DB 774 --EDGRYFNG--QDQPCHRFCATCAGAGADGCTGCTEGYFMD 813

RESULT 11
US-09-214-555B-2
; Sequence 2, Application US/09214555B
; Patent No. 6380171
; GENERAL INFORMATION:
; APPLICANT: INSTITUT DE RECHERCHE CLINIQUE DE MONTRAL
; TITLE OF INVENTION: PRO-PROTEIN CONVERTING ENZYME
; FILE REFERENCE: PRO-PROTEIN CONVER ENZ
; CURRENT APPLICATION NUMBER: US/09/214,555B
; PRIOR FILING DATE: 1999-01-04
; PRIOR APPLICATION NUMBER: 60/021,008
; PRIOR FILING DATE: 1996-07-26
; PRIOR APPLICATION NUMBER: 2,203,745
; PRIOR FILING DATE: 1997-04-25
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-555B-2

Query Match 9.1%; Score 82.5; DB 4; Length 915;
Best Local Similarity 26.0%; Pred. No. 1.8;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;

QY 27 TGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSORTCAAF-----CR-----SLSC 71
DB 719 TNSCVTHCPDGSYQDTKKNLCKKSENC-----KCTEFHNCTECDGLSLQGRCSVSC 773

RESULT 9
US-08-525-940-18
; Sequence 18, Application US/08525940
; Patent No. 5981259
; GENERAL INFORMATION:
; APPLICANT: Franzusoff, Alex
; APPLICANT: Miranda, Luis R.
; APPLICANT: Wolf, Joseph R.
; TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
; TITLE OF INVENTION: ENCODING SAID PROTEASES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,852
FILING DATE: 01-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/088,322
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 915 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-525-940-18

Query Match 9.1%; Score 82.5; DB 2; Length 915;
Best Local Similarity 26.0%; Pred. No. 1.8;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;

QY 27 TGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSORTCAAF-----CR-----SLSC 71
DB 719 TNSCVTHCPDGSYQDTKKNLCKKSENC-----KCTEFHNCTECDGLSLQGRCSVSC 773
QY 72 RKEQGFYDHLRLDCISCAIC---GQHPKQC-----AYFCEN 106
DB 774 --EDGRYFNG--QDQPCHRFCATCAGAGADGCTGCTEGYFMD 813

RESULT 10
US-08-976-838-18
; Sequence 18, Application US/08976838
; Patent No. 5981259
; GENERAL INFORMATION:
; APPLICANT: Franzusoff, Alex
; TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:

Query Match 9.1%; Score 82.5; DB 4; Length 915;
Best Local Similarity 26.0%; Pred. No. 1.8;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;

QY 27 TGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSORTCAAF-----CR-----SLSC 71
DB 719 TNSCVTHCPDGSYQDTKKNLCKKSENC-----KCTEFHNCTECDGLSLQGRCSVSC 773

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:40:20 ; Search time 12.4812 Seconds
(without alignments)
252.055 Million cell updates/sec

Title: US-09-855-158-15
Perfect score: 909
Sequence: 1 MSGLSRRGSRVQDER.....SPALFGLKLSADQVALVYST 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaa/FCR_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	909	100.0	166	10	US-09-854-864-15
2	909	100.0	293	9	US-09-779-050A-42
3	909	100.0	293	9	US-10-084-971-2
4	909	100.0	293	10	US-09-879-919-22
5	909	100.0	293	10	US-09-854-864-14
6	909	100.0	293	10	US-09-961-376-2
7	904	99.4	293	10	US-09-854-864-18
8	894.5	98.4	291	9	US-09-779-050A-43
9	393	43.2	67	10	US-09-854-864-16
10	342	37.6	59	10	US-09-854-864-20
11	279.5	30.7	57	9	US-09-779-050A-47
12	224	24.6	38	9	US-09-779-050A-46
13	218	24.0	37	9	US-09-779-050A-45
14	168	18.5	32	9	US-09-779-050A-44
15	93	10.2	81	10	US-09-854-864-13
16	87.5	9.6	463	9	US-09-905-291A-285
17	87.5	9.6	463	9	US-09-902-853-285
18	87.5	9.6	463	9	US-09-824-285
19	87.5	9.6	463	9	US-09-907-841-285

20	87.5	9.6	463	10	US-09-909-320-285	Sequence 285, App
21	87.5	9.6	463	10	US-09-909-088B-285	Sequence 285, App
22	87	9.6	207	9	US-10-077-438-3	Sequence 3, Appli
23	87	9.6	207	9	US-10-077-437-3	Sequence 3, Appli
24	87	9.6	292	10	US-09-745-763-166	Sequence 166, App
25	86	9.5	231	10	US-09-840-795-19	Sequence 19, Appl
26	86	9.5	299	9	US-10-119-466-12	Sequence 12, Appl
27	84	9.2	77	10	US-09-840-795-17	Sequence 17, Appl
28	79.5	8.7	1172	9	US-09-974-298-56	Sequence 56, Appl
29	79.5	8.7	1172	10	US-09-919-172-16	Sequence 16, Appl
30	78.5	8.6	399	10	US-09-907-372-1	Sequence 1, Appli
31	77.5	8.5	220	9	US-10-042-141-54	Sequence 54, Appl
32	77.5	8.5	220	10	US-09-726-643-54	Sequence 54, Appl
33	77.5	8.5	514	10	US-09-800-729-124	Sequence 124, App
34	77.5	8.5	1745	10	US-09-800-729-89	Sequence 89, Appl
35	77.5	8.5	1762	9	US-10-044-807-2	Sequence 2, Appli
36	77.5	8.5	1766	10	US-09-764-853-554	Sequence 554, App
37	77	8.5	1184	9	US-09-992-598-124	Sequence 124, App
38	77	8.5	1184	9	US-09-989-293A-124	Sequence 124, App
39	77	8.5	1184	9	US-09-989-735-124	Sequence 124, App
40	77	8.5	1184	9	US-09-990-444-124	Sequence 124, App
41	77	8.5	1184	9	US-09-989-730-124	Sequence 124, App
42	77	8.5	1184	9	US-09-930-436-124	Sequence 124, App
43	77	8.5	1184	9	US-09-931-181-124	Sequence 124, App
44	77	8.5	1184	9	US-09-931-687-124	Sequence 124, App
45	77	8.5	1184	10	US-09-757-716-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-854-864-15
; Sequence 15, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854.864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-15

Query Match	100.0%	Score	909	DB	10	Length	166
Best Local Similarity	100.0%	Pred. No.	1.6e-75				
Matches	166	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
QY	1	MSGLSRRGSRVQDERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSQR	60				
DB	1	MSGLSRRGSRVQDERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSQR	60				
QY	61	TCAAFCSLSCKRQGFYDHLRDCISCSICQHPKQCAFCECNKLRSPVNLPPELRR	120				
DB	61	TCAAFCSLSCKRQGFYDHLRDCISCSICQHPKQCAFCECNKLRSPVNLPPELRR	120				
QY	121	QRSEVENNSNSRGYQGLEHRSSEASPALFGLKLSADQVALVYST	166				
DB	121	QRSEVENNSNSRGYQGLEHRSSEASPALFGLKLSADQVALVYST	166				

RESULT 2

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US-09-779-050A-42
; Sequence 42, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-5708
; CURRENT APPLICATION NUMBER: US/09/779,050A
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 42
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-42

Query Match          100.0%; Score 909; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.9e-75;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLGRSRGRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLLTGTGCMCKTICNHQSQR 60
DB 1 MSGLGRSRGRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLLTGTGCMCKTICNHQSQR 60
QY 61 TCAAFCRSLSCRKEQKGYDHLRDCISGASICGHPKQCAVFCENKLRSPVNLPEELRR 120
DB 61 TCAAFCRSLSCRKEQKGYDHLRDCISGASICGHPKQCAVFCENKLRSPVNLPEELRR 120
QY 121 QRSGEVNNSDNSGRYQGLGHRGSESPALPGKLKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLGHRGSESPALPGKLKLSADQVALVYST 166

RESULT 3
US-10-084-971-2
; Sequence 2, Application US/10084971
; Patent No. US20020187526A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Neutrokin-alpha Binding Proteins and Methods Based Thereon
; FILE REFERENCE: PF524PCT
; CURRENT APPLICATION NUMBER: US/10/084,971
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/533,822
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/126,599
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/188,208
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-084-971-2

Query Match          100.0%; Score 909; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.9e-75;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSGLGRSRGRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLLTGTGCMCKTICNHQSQR 60
QY 61 TCAAFCRSLSCRKEQKGYDHLRDCISGASICGHPKQCAVFCENKLRSPVNLPEELRR 120
DB 61 TCAAFCRSLSCRKEQKGYDHLRDCISGASICGHPKQCAVFCENKLRSPVNLPEELRR 120
QY 121 QRSGEVNNSDNSGRYQGLGHRGSESPALPGKLKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLGHRGSESPALPGKLKLSADQVALVYST 166
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DB 121 QRSGEVNNSDNSGRYQGLGHRGSESPALPGKLKLSADQVALVYST 166

RESULT 4
US-09-879-919-22
; Sequence 22, Application US/09879919
; Patent No. US20020064829A1
; GENERAL INFORMATION:
; APPLICANT: YU, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253PI
; CURRENT APPLICATION NUMBER: US/09/879,919
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-919-22

Query Match          100.0%; Score 909; DB 10; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.9e-75;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TCAAFCRSLSCRKEQKGYDHLRDCISGASICGHPKQCAVFCENKLRSPVNLPEELRR 120
DB 61 TCAAFCRSLSCRKEQKGYDHLRDCISGASICGHPKQCAVFCENKLRSPVNLPEELRR 120
QY 121 QRSGEVNNSDNSGRYQGLGHRGSESPALPGKLKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLGHRGSESPALPGKLKLSADQVALVYST 166

RESULT 5
US-09-854-864-14
; Sequence 14, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-14

Query Match          100.0%; Score 909; DB 10; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.9e-75;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMCKTICNHQSQR 60
DB 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMCKTICNHQSQR 60

QY 61 TCAAFCSRSLSCRKEQGFYDHLRDCISASICGQHPKQCAFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCSRSLSCRKEQGFYDHLRDCISASICGQHPKQCAFCENKLRSPVNLPPELRR 120

QY 121 QRSGEVNNSDNSGRYQGLEHRRGSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLEHRRGSEASPALPGLKLSADQVALVYST 166

RESULT 6
US-09-961-376-2
; Sequence 2, Application US/09961376
; Patent No. US20020106736A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor Tr17
; FILE REFERENCE: PF524P1
; CURRENT APPLICATION NUMBER: US/09/961.376
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/254,874
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/235,991
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/533,822
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/188,208
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-376-2

Query Match          100.0%; Score 909; DB 10; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.9e-75;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMCKTICNHQSQR 60
DB 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMCKTICNHQSQR 60

QY 61 TCAAFCSRSLSCRKEQGFYDHLRDCISASICGQHPKQCAFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCSRSLSCRKEQGFYDHLRDCISASICGQHPKQCAFCENKLRSPVNLPPELRR 120

QY 121 QRSGEVNNSDNSGRYQGLEHRRGSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLEHRRGSEASPALPGLKLSADQVALVYST 166

RESULT 7
US-09-854-864-18
; Sequence 18, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-86B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-18

Query Match          99.4%; Score 904; DB 10; Length 397;
Best Local Similarity 100.0%; Pred. No. 1.2e-74;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMCKTICNHQSQR 60
DB 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMCKTICNHQSQR 60

QY 61 TCAAFCSRSLSCRKEQGFYDHLRDCISASICGQHPKQCAFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCSRSLSCRKEQGFYDHLRDCISASICGQHPKQCAFCENKLRSPVNLPPELRR 120

QY 121 QRSGEVNNSDNSGRYQGLEHRRGSEASPALPGLKLSADQVALVYS 165
DB 121 QRSGEVNNSDNSGRYQGLEHRRGSEASPALPGLKLSADQVALVYS 165

RESULT 8
US-09-779-050A-43
; Sequence 43, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-43

Query Match          98.4%; Score 894.5; DB 9; Length 291;
Best Local Similarity 99.4%; Pred. No. 6e-74;
Matches 165; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMCKTICNHQSQR 60
DB 1 MSGLGSRGRRGSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMCKTICNHQSQR 60

QY 61 TCAAFCSRSLSCRKEQGFYDHLRDCISASICGQHPKQCAFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCSRSLSCRKEQGFYDHLRDCISASICGQHPKQCAFCENKLRSPVNLPPELRR 120

QY 121 QRSGEVNNSDNSGRYQGLEHRRGSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLEHRRGSEASPALPGLKLSADQVA-VYST 165
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RESULT 9
US-09-854-864-16
; Sequence 16, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/570, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 16
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-16

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Best Local Similarity 43.2%; Score 393; DB 10; Length 67;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 34 CPEQYWDPLGTGCMGCKTICNHOSQRTCAFRSLSCREKQKPYDHLRDCISGASIC 93
Db 1 CPEQYWDPLGTGCMGCKTICNHOSQRTCAFC---CRKQKPYDHLRDCISGASIC 56

Qy 94 GQHPKOCAYFC 104
Db 57 GQHPKOCAYFC 67

RESULT 10
US-09-854-864-20
; Sequence 20, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/570, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 20
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-20

Query Match
Best Local Similarity 37.6%; Score 342; DB 10; Length 59;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 CPEQYWDPLGTGCMGCKTICNHOSQRTCAFRSLSCREKQKPYDHLRDCISGASIC 92
Db 1 CPEQYWDPLGTGCMGCKTICNHOSQRTCAFRSLSCREKQKPYDHLRDCISGASIC 59

RESULT 11
US-09-779-050A-47
; Sequence 47, Application US/09779050A
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; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 47
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-47

Query Match
Best Local Similarity 30.7%; Score 279.5; DB 9; Length 57;
Matches 57; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 108 LRSFVNLPELRORSGEVENNSDNGRYQGLHRSSEASPALPKLSADQVALVYS 165
Db 1 LRSFVNLPELRORSGEVENNSDNGRYQGLHRSSEASPALPKLSADQVA-VYS 57

RESULT 12
US-09-779-050A-46
; Sequence 46, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 46
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-46

Query Match
Best Local Similarity 24.6%; Score 224; DB 9; Length 38;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 SCRKEQKPYDHLRDCISGASICGQHPKOCAYFCNK 107
Db 1 SCRKEQKPYDHLRDCISGASICGQHPKOCAYFCNK 38

RESULT 13
US-09-779-050A-45
; Sequence 45, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 45
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 7, 2003, 09:37:34 ; Search time 278.331 Seconds
(without alignments)
384.527 Million cell updates/sec

Title: US-09-855-158-15

Perfect score: 909

Sequence: 1 MSGLSRRGRSRVDQBER.....SPALPGLKLSADQVALVYST 166

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Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA Main:*

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2:	/cgn2_6/ptodata/1/paa/US07_COMB.pcp.*
3:	/cgn2_6/ptodata/1/paa/US08_COMB.pcp.*
4:	/cgn2_6/ptodata/1/paa/US09_COMB.pcp.*
5:	/cgn2_6/ptodata/1/paa/US081_COMB.pcp.*
6:	/cgn2_6/ptodata/1/paa/US082_COMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	909	100.0	166	12	US-08-810-572-6
2	509	100.0	166	21	US-09-782-857-6
3	509	100.0	166	21	US-09-782-857A-6
4	509	100.0	166	22	US-09-854-864-15
5	509	100.0	166	22	US-09-855-158-15
6	509	100.0	265	21	US-09-724-341-9

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7 909 100.0 293 1 PCT-US00-07966-2 Sequence 2, Appli
8 909 100.0 293 1 PCT-US01-19026-2 Sequence 2, Appli
9 909 100.0 293 1 PCT-US02-16176-6 Sequence 4, Appli
10 909 100.0 293 12 US-08-810-572-2 Sequence 2, Appli
11 909 100.0 293 17 US-09-302-863-2 Sequence 6, Appli
12 909 100.0 293 18 US-09-479-856-6 Sequence 2, Appli
13 909 100.0 293 19 US-09-533-822-2 Sequence 6, Appli
14 909 100.0 293 19 US-09-569-245-6 Sequence 6, Appli
15 909 100.0 293 20 US-09-627-206-6 Sequence 6, Appli
16 909 100.0 293 21 US-09-724-341-2 Sequence 2, Appli
17 909 100.0 293 21 US-09-779-050A-42 Sequence 42, Appli
18 909 100.0 293 21 US-09-782-857-2 Sequence 2, Appli
19 909 100.0 293 21 US-09-782-857A-2 Sequence 2, Appli
20 909 100.0 293 22 US-09-848-295-4 Sequence 4, Appli
21 909 100.0 293 22 US-09-854-864-14 Sequence 14, Appli
22 909 100.0 293 22 US-09-855-158-14 Sequence 14, Appli
23 909 100.0 293 22 US-09-855-564-2 Sequence 2, Appli
24 909 100.0 293 22 US-09-879-919-22 Sequence 2, Appli
25 909 100.0 293 23 US-09-961-376-2 Sequence 2, Appli
26 909 100.0 293 24 US-10-008-063-8 Sequence 8, Appli
27 909 100.0 293 24 US-10-068-725-4 Sequence 4, Appli
28 909 100.0 293 24 US-10-084-971-2 Sequence 2, Appli
29 909 100.0 293 25 US-10-151-892-46 Sequence 46, Appli
30 909 100.0 293 25 US-10-152-363A-2 Sequence 2, Appli
31 904 99.4 397 22 US-09-854-864-18 Sequence 18, Appli
32 904 99.4 397 22 US-09-855-158-18 Sequence 18, Appli
33 894.5 98.4 251 21 US-09-779-050A-43 Sequence 43, Appli
34 890 97.9 245 18 US-09-479-856-9 Sequence 9, Appli
35 890 97.9 245 19 US-09-569-245-9 Sequence 9, Appli
36 890 97.9 245 20 US-09-627-206-9 Sequence 9, Appli
37 700 77.0 392 25 US-10-152-363A-50 Sequence 50, Appli
38 599 65.9 120 18 US-09-479-856-4 Sequence 4, Appli
39 599 65.9 120 19 US-09-569-245-4 Sequence 4, Appli
40 599 65.9 120 20 US-09-627-206-4 Sequence 4, Appli
41 599 65.9 247 18 US-09-479-856-2 Sequence 2, Appli
42 599 65.9 247 19 US-09-569-245-2 Sequence 2, Appli
43 599 65.9 247 20 US-09-627-206-2 Sequence 2, Appli
44 525 57.8 357 25 US-10-152-363A-56 Sequence 56, Appli
45 469 51.6 332 25 US-10-152-363A-62 Sequence 62, Appli

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ALIGNMENTS

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RESULT 1
US-08-810-572-6
; Sequence 6, Application US/08810572
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/810,572
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.

```

REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEITICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-810-572-6

Query Match 100.0%; Score 909; DB 12; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.4e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSGLSRRGGRSRVDOERFPOGLMTGVAMRSCPEEQYMDPLGTGCMCKTICNHQSQR 60
DB 1 MSGLSRRGGRSRVDOERFPOGLMTGVAMRSCPEEQYMDPLGTGCMCKTICNHQSQR 60
OY 61 TCAAFCRSLSCRKQKGFYDHLRDCTSCASICGHPKQCAFCEKRLRSPVNLPEELRR 120
DB 61 TCAAFCRSLSCRKQKGFYDHLRDCTSCASICGHPKQCAFCEKRLRSPVNLPEELRR 120
OY 121 ORSGEVNNSDNGRYOGLERHSGEASPALPGLKLSADQVALVYST 166
DB 121 ORSGEVNNSDNGRYOGLERHSGEASPALPGLKLSADQVALVYST 166

RESULT 2
US-09-782-857-6
Sequence 6, Application US/09782857
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,857
FILING DATE: 14-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/810,572
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEITICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-782-857-6

Query Match 100.0%; Score 909; DB 21; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.4e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSGLSRRGGRSRVDOERFPOGLMTGVAMRSCPEEQYMDPLGTGCMCKTICNHQSQR 60
OY 61 TCAAFCRSLSCRKQKGFYDHLRDCTSCASICGHPKQCAFCEKRLRSPVNLPEELRR 120
DB 61 TCAAFCRSLSCRKQKGFYDHLRDCTSCASICGHPKQCAFCEKRLRSPVNLPEELRR 120
OY 121 ORSGEVNNSDNGRYOGLERHSGEASPALPGLKLSADQVALVYST 166
DB 121 ORSGEVNNSDNGRYOGLERHSGEASPALPGLKLSADQVALVYST 166

RESULT 3
US-09-782-857A-6
Sequence 6, Application US/09782857A
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,857A
FILING DATE: 14-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/810,572
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

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; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-782-857A-6

Query Match      100.0%; Score 909; DB 21; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.4e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSGLGRSRGGRSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60
Db 1 MSGLGRSRGGRSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60

Qy 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCSICGQHPKQCAFCENKLRSPVNLPPELRR 120
Db 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCSICGQHPKQCAFCENKLRSPVNLPPELRR 120

Qy 121 ORSGEVNNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVYST 166
Db 121 ORSGEVNNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVYST 166

RESULT 4
US-09-854-864-15
; Sequence 15, Application US/09854864
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: B1YS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-15

Query Match      100.0%; Score 909; DB 22; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.4e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSGLGRSRGGRSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60
Db 1 MSGLGRSRGGRSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60

Qy 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCSICGQHPKQCAFCENKLRSPVNLPPELRR 120
Db 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCSICGQHPKQCAFCENKLRSPVNLPPELRR 120

Qy 121 ORSGEVNNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVYST 166
Db 121 ORSGEVNNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVYST 166

RESULT 5
US-09-855-158-15
; Sequence 15, Application US/09855158
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: B1YS/AGP-3, AND TACI
```

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; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-15

Query Match      100.0%; Score 909; DB 22; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.4e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSGLGRSRGGRSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60
Db 1 MSGLGRSRGGRSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60

Qy 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCSICGQHPKQCAFCENKLRSPVNLPPELRR 120
Db 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCSICGQHPKQCAFCENKLRSPVNLPPELRR 120

Qy 121 ORSGEVNNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVYST 166
Db 121 ORSGEVNNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVYST 166

RESULT 6
US-09-724-341-9
; Sequence 9, Application US/09724341
; GENERAL INFORMATION:
; APPLICANT: AVI J. ASHKENAZI
; APPLICANT: KELLY H. DODGE
; APPLICANT: IQBAL GREWAL
; APPLICANT: KYUNG JIN KIM
; APPLICANT: SCOT A. MARSTERS
; APPLICANT: ROBERT M. PITTI
; APPLICANT: MINHONG YAN
; TITLE OF INVENTION: USES OF AGONISTS AND ANTAGONISTS TO MODULATE ACTIVITY
; FILE REFERENCE: P1805R1
; CURRENT APPLICATION NUMBER: US/09/724,341
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/182,938
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: US 60/226,986
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 9
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-341-9

Query Match      100.0%; Score 909; DB 21; Length 265;
Best Local Similarity 100.0%; Pred. No. 2.5e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSGLGRSRGGRSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60
Db 1 MSGLGRSRGGRSRVDQERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60

Qy 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCSICGQHPKQCAFCENKLRSPVNLPPELRR 120
Db 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCSICGQHPKQCAFCENKLRSPVNLPPELRR 120

Qy 121 ORSGEVNNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVYST 166
Db 121 ORSGEVNNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVYST 166
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DB 121 QRSGEVNNSDNSGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166

RESULT 7
PCT-US00-07966-2
Sequence 2, Application PC/TUS0007966
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Neutrokin-alpha Binding Proteins and Methods Based Thereon
FILE REFERENCE: PF524PCT
CURRENT FILING DATE: 2000-03-24
EARLIER FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 60/126,599
EARLIER FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 60/188,208
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 293
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US00-07966-2

Query Match
Best Local Similarity 100.0%; Score 909; DB 1; Length 293;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 121 QRSGEVNNSDNSGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166

RESULT 8
PCT-US01-19026-22
Sequence 22, Application PC/TUS0119026
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.; et al.
TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
FILE REFERENCE: PF253PCT
CURRENT FILING DATE: 2001-06-14
CURRENT APPLICATION NUMBER: PCT/US01/19026
PRIOR FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,978
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/254,875
PRIOR FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 60/241,952
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/211,537
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 293
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US01-19026-22

Query Match
Best Local Similarity 100.0%; Score 909; DB 1; Length 293;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRGGRSRVDOERFPQGLMTGVAMRSCPEEQYMDPLGTGCMCKTICNHOSOR 60
DB 1 MSGLSRRGGRSRVDOERFPQGLMTGVAMRSCPEEQYMDPLGTGCMCKTICNHOSOR 60

QY 61 TCAAFCRSLSCRKEQGFYDHLRDCISCAISICGQHPKQCAFCENKLSPVNLPPELR 120
DB 61 TCAAFCRSLSCRKEQGFYDHLRDCISCAISICGQHPKQCAFCENKLSPVNLPPELR 120

QY 121 QRSGEVNNSDNSGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166

RESULT 9
PCT-US02-16106-46
Sequence 46, Application PC/TUS0216106
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
FILE REFERENCE: PF554PCT
CURRENT FILING DATE: 2002-05-22
CURRENT APPLICATION NUMBER: PCT/US02/16106
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn version 3.0
SEQ ID NO 46
LENGTH: 293
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-16106-46

Query Match
Best Local Similarity 100.0%; Score 909; DB 1; Length 293;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRGGRSRVDOERFPQGLMTGVAMRSCPEEQYMDPLGTGCMCKTICNHOSOR 60
DB 1 MSGLSRRGGRSRVDOERFPQGLMTGVAMRSCPEEQYMDPLGTGCMCKTICNHOSOR 60

QY 61 TCAAFCRSLSCRKEQGFYDHLRDCISCAISICGQHPKQCAFCENKLSPVNLPPELR 120
DB 61 TCAAFCRSLSCRKEQGFYDHLRDCISCAISICGQHPKQCAFCENKLSPVNLPPELR 120

QY 121 QRSGEVNNSDNSGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166

RESULT 10
US-08-810-572-2
Sequence 2, Application US/08810572
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CMML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; TOPOLOGY: single
; STRANDEDNESS: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-810-572-2

Query Match          100.0%; Score 909; DB 12; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.8e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLGRRRGRSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60
DB 1 MSGLGRRRGRSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60
QY 61 TCAAFCSLSCKRQKGFYDHLRLDCISASCIGQHPKQCAFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCSLSCKRQKGFYDHLRLDCISASCIGQHPKQCAFCENKLRSPVNLPPELRR 120
QY 121 QRSGEVNNSDNSGRYQGLEHRGSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLEHRGSEASPALPGLKLSADQVALVYST 166

RESULT 11
US-09-302-863-2
; Sequence 2, Application US/09302863
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G
; TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION
; FILE REFERENCE: 2519
; CURRENT APPLICATION NUMBER: US/09/302,863
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Human
US-09-302-863-2

Query Match          100.0%; Score 909; DB 17; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.8e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLGRRRGRSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60
DB 1 MSGLGRRRGRSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60
QY 61 TCAAFCSLSCKRQKGFYDHLRLDCISASCIGQHPKQCAFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCSLSCKRQKGFYDHLRLDCISASCIGQHPKQCAFCENKLRSPVNLPPELRR 120
QY 121 QRSGEVNNSDNSGRYQGLEHRGSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLEHRGSEASPALPGLKLSADQVALVYST 166

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; TOPOLOGY: single
; STRANDEDNESS: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-810-572-2

Query Match          100.0%; Score 909; DB 18; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.8e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLGRRRGRSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60
DB 1 MSGLGRRRGRSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60
QY 61 TCAAFCSLSCKRQKGFYDHLRLDCISASCIGQHPKQCAFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCSLSCKRQKGFYDHLRLDCISASCIGQHPKQCAFCENKLRSPVNLPPELRR 120
QY 121 QRSGEVNNSDNSGRYQGLEHRGSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLEHRGSEASPALPGLKLSADQVALVYST 166

RESULT 12
US-09-479-856-6
; Sequence 6, Application US/09479856
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen
; APPLICANT: Yee, David P.
; TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
; FILE REFERENCE: 98-75
; CURRENT APPLICATION NUMBER: US/09/479,856
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,068
; EARLIER FILING DATE: 1999-01-07
; EARLIER APPLICATION NUMBER: 60/169,890
; EARLIER FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-479-856-6

Query Match          100.0%; Score 909; DB 19; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.8e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLGRRRGRSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60
DB 1 MSGLGRRRGRSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60
QY 61 TCAAFCSLSCKRQKGFYDHLRLDCISASCIGQHPKQCAFCENKLRSPVNLPPELRR 120
DB 61 TCAAFCSLSCKRQKGFYDHLRLDCISASCIGQHPKQCAFCENKLRSPVNLPPELRR 120
QY 121 QRSGEVNNSDNSGRYQGLEHRGSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLEHRGSEASPALPGLKLSADQVALVYST 166

RESULT 13
US-09-533-822-2
; Sequence 2, Application US/09533822
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Neutrokin-alpha Binding Proteins and Methods Based Thereon
; FILE REFERENCE: PF524PCT
; CURRENT APPLICATION NUMBER: US/09/533,822
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,599
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/188,208
; EARLIER FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-533-822-2

Query Match          100.0%; Score 909; DB 19; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.8e-81;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLGRRRGRSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60
DB 1 MSGLGRRRGRSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHQSOR 60
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Tue Jan 7 10:36:49 2003

us-09-855-158-15.rapm

Page 6

Qy	Db	Qy	Db
61	TCAAFCRSLSRCKEGKRYDHLDLDCISCSISICQHQKQCYAFENKILASPVNLPELIR	120	120
61	TCAAFCRSLSRCKEGKRYDHLDLDCISCSISICQHQKQCYAFENKILASPVNLPELIR	120	120
61	TCAAFCRSLSRCKEGKRYDHLDLDCISCSISICQHQKQCYAFENKILASPVNLPELIR	120	120
121	ORSGEVENNSDNGRYQGLERHSGEASPAIPGLKLSADQVALVYST	166	166
121	ORSGEVENNSDNGRYQGLERHSGEASPAIPGLKLSADQVALVYST	166	166
121	ORSGEVENNSDNGRYQGLERHSGEASPAIPGLKLSADQVALVYST	166	166

```

RESULT 14
US-09-569-245-6
: Sequence 6, Application US/09569245
: GENERAL INFORMATION:
: APPLICANT: Gross, Jane A.
: APPLICANT: Xu, Wenfeng
: APPLICANT: Madden, Karen
: APPLICANT: Yee, David P.
: TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
: FILE REFERENCE: 98-75
: CURRENT APPLICATION NUMBER: US/09/569,245
: PRIOR FILING DATE: 2000-05-11
: PRIOR APPLICATION NUMBER: 60/115,068
: PRIOR FILING DATE: 1999-01-07
: PRIOR APPLICATION NUMBER: 60/169,890
: PRIOR FILING DATE: 1999-12-09
: PRIOR APPLICATION NUMBER: 08/479,856
: PRIOR FILING DATE: 2000-01-07
: NUMBER OF SEQ ID NOS: 60
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 6
: LENGTH: 293
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-569-245-6

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	Query Match	Similarity	Score	DB 19:	Length
Best Local	100.0%	100.0%	Pred. No. 2,88-81:		
Matches	166:	Conservative	0:	Mismatches	0: Indels 0: Gaps 0:
QY	1	MSGLSRRRGSGSRVDOERFPQGLMTGYAMASCPEEYOYMDPLTGCNMSCKITCNHNSQR	60		
Db	1	MSGLSRRRGSGSRVDOERFPQGLMTGYAMASCPEEYOYMDPLTGCNMSCKITCNHNSQR	60		
QY	61	TCAACRSLSCKKECKGKFPDHLRLPCTISASISCGGHPKCCATCFCEKSLSPVNLPEELR	120		
Db	61	TCAACRSLSCKKECKGKFPDHLRLPCTISASISCGGHPKCCATCFCEKSLSPVNLPEELR	120		
QY	121	QRSGEVNNSDNGSRVQGLEHRRGSEASPALPGKLSADDAVALVYST	166		
Db	121	QRSGEVNNSDNGSRVQGLEHRRGSEASPALPGKLSADDAVALVYST	166		

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RESULT 15
US-09-627-206-6
: Sequence 6, Application US/09627206
: GENERAL INFORMATION:
: APPLICANT: Gross, Jane A.
: APPLICANT: Xu, Wenfeng
: APPLICANT: Madden, Karen
: APPLICANT: Yee, David P
: TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
: FILE REFERENCE: 98-75C2
: CURRENT APPLICATION NUMBER: US/09/627, 206
: PRIORITY FILING DATE: 2000-07-27
: PRIOR APPLICATION NUMBER: 60/115,068
: PRIOR FILING DATE: 1999-01-07
: PRIOR APPLICATION NUMBER: 60/169,890
: PRIOR FILING DATE: 1999-12-09
: PRIOR APPLICATION NUMBER: 09/479,856
: PRIOR FILING DATE: 2000-01-07
: PRIOR APPLICATION NUMBER: 09/569,245
: PRIOR FILING DATE: 2000-05-11
: NUMBER OF SEQ ID NOS: 60

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 6
;
; LENGTH: 293
;
; TYPE: PR1
;
; ORGANISM: Homo sapiens
US-09-627-206-6

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	Query Match	Similarity	100.0%	Score 909	DB 20	Length 293
	Best Local	Similarity	100.0%	Pred. No. 2.8e-81		
	Matches 166	Conservative	0	Mismatches 0	Indels 0	Gaps 0
Qy	1	MSGLSRSGRGRSRVDSERFPQGLMTGVAMRS	CPEEQYMDPLLATGMSCKTICNHQSOR	60		
Db	1	MSGLSRSGRGRSRVDSERFPQGLMTGVAMRS	CPEEQYMDPLLATGMSCKTICNHQSOR	60		
Qy	61	TCAAFCSRLSCKRKEGKGYDHLRLDCLSCA	ICGHPQCAQFCGCKTKRSPNLPPELR	120		
Db	61	TCAAFCSRLSCKRKEGKGYDHLRLDCLSCA	ICGHPQCAQFCGCKTKRSPNLPPELR	120		
Qy	121	QRSGEVNNSDNGRYGGLERHGSFASPALPGL	KLSADQVALVYST	166		
Db	121	QRSGEVNNSDNGRYGGLERHGSFASPALPGL	KLSADQVALVYST	166		

Search completed: January 7, 2003, 09:53:20
Job time : 279.331 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:38:19 ; Search time 21.6341 Seconds
(without alignments)
543.836 Million cell updates/sec

Title: US-09-855-158-15
Perfect score: 909
Sequence: 1 MSGLGRSRGGRSRVDQER.....SPALPGLKLSADQVALVYST 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262191 seqs, 70875818 residues

Total number of hits satisfying chosen parameters: 262191

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_AA_New.*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	909	100.0	166	6	US-10-293-816-6
2	909	100.0	293	6	US-10-268-951-22
3	909	100.0	293	6	US-10-258-368-1
4	909	100.0	293	6	US-10-293-816-2
5	904	99.4	301	6	US-10-258-368-12
6	881	96.9	404	6	US-10-258-368-15
7	851	71.6	366	6	US-10-258-368-6
8	490.5	54.0	334	6	US-10-258-368-8
9	204	22.4	34	1	PCT-US02-34376-14
10	204	22.4	34	6	US-10-281-053-14
11	201	22.1	33	1	PCT-US02-34376-13
12	201	22.1	33	6	US-10-281-053-13
13	97.5	10.7	1548	6	US-10-180-903-2
14	88	9.7	195	6	US-10-094-886-174
15	88	9.7	195	6	US-10-094-886-176
16	87.5	9.6	463	5	US-09-906-777B-285
17	87.5	9.6	463	5	US-09-904-011C-285
18	87.5	9.6	463	5	US-09-665-350B-285
19	87.5	9.6	463	6	US-10-131-813A-360
20	87.5	9.6	463	6	US-10-131-819A-360
21	87.5	9.6	463	6	US-10-131-823A-360
22	87.5	9.6	463	6	US-10-131-824A-360
23	87.5	9.6	463	6	US-10-131-826A-360
24	87.5	9.6	463	6	US-10-131-829A-360
25	87.5	9.6	463	6	US-10-125-926A-360
26	87.5	9.6	463	6	US-10-127-829A-360

ALIGNMENTS

RESULT 1
US-10-293-816-6
; Sequence 6 Application US/10293816
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/10/293,816
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-816-6

Query Match 100.0%; Score 909; DB 6; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.2e-78;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSGLGRSRGGRSRVDQERFPQGLWTGVAMRSCPEQYWDPLLTGTCMSCKTICNHQSQR 60
Db 1 MSGLGRSRGGRSRVDQERFPQGLWTGVAMRSCPEQYWDPLLTGTCMSCKTICNHQSQR 60

Qy 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCSICGQHPKQCAIFCENKLRSPVNLPPELRR 120
Db 61 TCAAFCSRSLSCRKEQGFYDHLRLDCISCSICGQHPKQCAIFCENKLRSPVNLPPELRR 120

Qy 121 QRSGEVENNSDNGRYQGLHRGSEASPALPGLKLSADQVALVYST 166
Db 121 QRSGEVENNSDNGRYQGLHRGSEASPALPGLKLSADQVALVYST 166

RESULT 2
US-10-268-951-22
; Sequence 22 Application US/10268951
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P2

```
/ CURRENT APPLICATION NUMBER: US/10/268,951
/ CURRENT FILING DATE: 2002-10-11
/ PRIOR APPLICATION NUMBER: 10/082,260
/ PRIOR FILING DATE: 2002-02-26
/ PRIOR APPLICATION NUMBER: 09/879,919
/ PRIOR FILING DATE: 2001-06-14
/ PRIOR APPLICATION NUMBER: 08/815,783
/ PRIOR FILING DATE: 1997-03-12
/ PRIOR APPLICATION NUMBER: 60/328,401
/ PRIOR FILING DATE: 2001-10-12
/ PRIOR APPLICATION NUMBER: 60/293,812
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,978
/ PRIOR FILING DATE: 2001-03-23
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/254,875
/ PRIOR FILING DATE: 2000-12-13
/ PRIOR APPLICATION NUMBER: 60/241,952
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/211,537
/ PRIOR FILING DATE: 2000-06-15
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO: 22
/ LENGTH: 293
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-268-951-22
```

```
Query Match
Best Local Similarity 100.0%; Score 909; DB 6; Length 293;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHOSQR 60
DB 1 MSGLSRRRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHOSQR 60
QY 61 TCAAFCRSLSCRKEQKGFYDHLIRDCISCAISICGQHPKOCAYFCENKLRSPVNLPEELRR 120
DB 61 TCAAFCRSLSCRKEQKGFYDHLIRDCISCAISICGQHPKOCAYFCENKLRSPVNLPEELRR 120
QY 121 QRSGEVNNSDNSGRYQGLEHHRGSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLEHHRGSEASPALPGLKLSADQVALVYST 166
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```
RESULT 3
US-10-258-368-1
/ Sequence 1, Application US/10258368
/ GENERAL INFORMATION:
/ APPLICANT: Ambrose, Christine
/ APPLICANT: Thompson, Jeffrey
/ APPLICANT: Schneider, Pascal
/ APPLICANT: Renner, Paul
/ TITLE OF INVENTION: Taci As As Anti-Tumor Agent
/ FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
/ CURRENT APPLICATION NUMBER: US/10/258,368
/ CURRENT FILING DATE: 2002-10-21
/ PRIOR APPLICATION NUMBER: USSN 60/199,946
/ PRIOR FILING DATE: 2000-04-27
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO: 1
/ LENGTH: 293
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-258-368-1
```

```
Query Match
Best Local Similarity 100.0%; Score 909; DB 6; Length 293;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 MSGLSRRRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHOSQR 60
DB 1 MSGLSRRRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHOSQR 60
QY 61 TCAAFCRSLSCRKEQKGFYDHLIRDCISCAISICGQHPKOCAYFCENKLRSPVNLPEELRR 120
DB 61 TCAAFCRSLSCRKEQKGFYDHLIRDCISCAISICGQHPKOCAYFCENKLRSPVNLPEELRR 120
QY 121 QRSGEVNNSDNSGRYQGLEHHRGSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLEHHRGSEASPALPGLKLSADQVALVYST 166
```

```
RESULT 4
US-10-293-816-2
/ Sequence 2, Application US/10293816
/ GENERAL INFORMATION:
/ APPLICANT: Bram, Richard J.
/ APPLICANT: Von Bulow, Gotz
/ TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
/ FILE REFERENCE: 44158/254623
/ CURRENT APPLICATION NUMBER: US/10/293,816
/ CURRENT FILING DATE: 2002-11-12
/ PRIOR APPLICATION NUMBER: US 09/782,857
/ PRIOR FILING DATE: 2001-02-14
/ PRIOR APPLICATION NUMBER: US 09/290,333
/ PRIOR FILING DATE: 1999-04-12
/ PRIOR APPLICATION NUMBER: US 08/810,572
/ PRIOR FILING DATE: 1997-03-03
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 2
/ LENGTH: 293
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-293-816-2
```

```
Query Match
Best Local Similarity 100.0%; Score 909; DB 6; Length 293;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHOSQR 60
DB 1 MSGLSRRRGSRVDOERFPQGLMTGVAMRSCPEEQYWDPLLTGTCMSCKTICNHOSQR 60
QY 61 TCAAFCRSLSCRKEQKGFYDHLIRDCISCAISICGQHPKOCAYFCENKLRSPVNLPEELRR 120
DB 61 TCAAFCRSLSCRKEQKGFYDHLIRDCISCAISICGQHPKOCAYFCENKLRSPVNLPEELRR 120
QY 121 QRSGEVNNSDNSGRYQGLEHHRGSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLEHHRGSEASPALPGLKLSADQVALVYST 166
```

```
RESULT 5
US-10-258-368-12
/ Sequence 12, Application US/10258368
/ GENERAL INFORMATION:
/ APPLICANT: Ambrose, Christine
/ APPLICANT: Thompson, Jeffrey
/ APPLICANT: Schneider, Pascal
/ APPLICANT: Renner, Paul
/ TITLE OF INVENTION: Taci As As Anti-Tumor Agent
/ FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
/ CURRENT APPLICATION NUMBER: US/10/258,368
/ CURRENT FILING DATE: 2002-10-21
/ PRIOR APPLICATION NUMBER: USSN 60/199,946
/ PRIOR FILING DATE: 2000-04-27
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO: 12
```



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; LENGTH: 301
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-12

Query Match      99.4%; Score 904; DB 6; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2  SGLGRSRRGSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMCKTICNHQSORT 61
Db  10 SGLGRSRRGSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMCKTICNHQSORT 69
QY  62 CAAFCRSLSCRKEQKGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRRQ 121
Db  70 CAAFCRSLSCRKEQKGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRRQ 129
QY  122 RSQGEVNNSDNSGRYQGLEHRRGSEASPALPGLKLSADQVALVYST 166
Db  130 RSQGEVNNSDNSGRYQGLEHRRGSEASPALPGLKLSADQVALVYST 174

RESULT 6
US-10-258-368-15
; Sequence 15, Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; APPLICANT: Rennert, Paul
; TITLE OF INVENTION: Taci As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT APPLICATION NUMBER: US/10/258,368
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/10/258,368
; PRIOR FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-15

Query Match      96.9%; Score 881; DB 6; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.2e-75;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  MSGLGSRRRGSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMCKTICNHQSOR 60
Db  18 MSGLGSRRRGSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMCKTICNHQSOR 77
QY  61 TCAAFCRSLSCRKEQKGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRR 120
Db  78 TCAAFCRSLSCRKEQKGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNLPPELRR 137
QY  121 QRSQGEVNNSDNSGRYQGLEHRRGSEASPALPGLKLSADQV 160
Db  138 QRSQGEVNNSDNSGRYQGLEHRRGSEASPALPGLKLSADQV 177

RESULT 7
US-10-258-368-6
; Sequence 6, Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; APPLICANT: Rennert, Paul
; TITLE OF INVENTION: Taci As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT APPLICATION NUMBER: US/10/258,368
; CURRENT FILING DATE: 2002-10-21
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; PRIOR APPLICATION NUMBER: USSN 60/199,946
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-6

Query Match      71.6%; Score 651; DB 6; Length 366;
Best Local Similarity 100.0%; Pred. No. 5.8e-54;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  MSGLGSRRRGSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMCKTICNHQSOR 60
Db  24 MSGLGSRRRGSRVDOERFPQGLWTGVAMRSCPEEQYWDPLLTGTCMCKTICNHQSOR 83
QY  61 TCAAFCRSLSCRKEQKGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNL 115
Db  84 TCAAFCRSLSCRKEQKGFYDHLRLDCISCASICGQHPKQCAFCENKLRSPVNL 138

RESULT 8
US-10-258-368-8
; Sequence 8, Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; APPLICANT: Rennert, Paul
; TITLE OF INVENTION: Taci As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT APPLICATION NUMBER: US/10/258,368
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: USSN 60/199,946
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-8

Query Match      54.0%; Score 490.5; DB 6; Length 334;
Best Local Similarity 92.6%; Pred. No. 7.9e-39;
Matches 88; Conservative 1; Mismatches 1; Indels 5; Gaps 2;

QY  25 LW----TGVAMRSCPEEQYWDPLLTGTCMCKTICNHQSORTCAAFCRSLSCRKEQKGFYD 80
Db  13 LWVPGSTG-DVRSCPEEQYWDPLLTGTCMCKTICNHQSORTCAAFCRSLSCRKEQKGFYD 71
QY  81 HLLRDCISASICGQHPKQCAFCENKLRSPVNL 115
Db  72 HLLRDCISASICGQHPKQCAFCENKLRSPVNL 106

RESULT 9
PCT-US02-34376-14
; Sequence 14, Application PC/TUS0234376
; GENERAL INFORMATION:
; APPLICANT: Zhang, Gongyi
; APPLICANT: Shu, Hong-Bing
; APPLICANT: Liu, Yingfang
; APPLICANT: Xu, Liangguo
; TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
; FILE REFERENCE: Modified
; FILE OF INVENTION: 2879-86-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/34376
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,106
; PRIOR FILING DATE: 2001-10-24
```

```
; PRIOR APPLICATION NUMBER: 60/348,962
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/354,966
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/403,364
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 14
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-34376-14
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```
Query Match 22.4%; Score 204; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 71 CRKEQGFYDHLRDCISCSICGHPKQCAFC 104
Db 1 CRKEQGFYDHLRDCISCSICGHPKQCAFC 34
```

```
RESULT 10
US-10-281-053-14
; Sequence 14, Application US/10281053
; GENERAL INFORMATION:
; APPLICANT: Zhang, Gongyi
; APPLICANT: Shu, Hong-Bing
; APPLICANT: Liu, Yingfang
; APPLICANT: Xu, Liangguo
; TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
; FILE REFERENCE: 2879-86
; CURRENT APPLICATION NUMBER: US/10/281,053
; PRIOR FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,106
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/348,962
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/354,966
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/403,364
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 14
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-281-053-14
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```
Query Match 22.4%; Score 204; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 71 CRKEQGFYDHLRDCISCSICGHPKQCAFC 104
Db 1 CRKEQGFYDHLRDCISCSICGHPKQCAFC 34
```

```
RESULT 11
PCT-US02-34376-13
; Sequence 13, Application PC/TUS0234376
; GENERAL INFORMATION:
; APPLICANT: Zhang, Gongyi
; APPLICANT: Shu, Hong-Bing
; APPLICANT: Liu, Yingfang
; APPLICANT: Xu, Liangguo
; TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
; TITLE OF INVENTION: Modified Proteins and Methods Related Thereto
; FILE REFERENCE: 2879-86-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/34376
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```
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,106
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/348,962
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/354,966
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/403,364
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 13
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-34376-13
```

```
Query Match 22.1%; Score 201; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.3e-12;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 34 CPEEQYWDPLGTGCMSCKTICNHQSORTCAFC 66
Db 1 CPEEQYWDPLGTGCMSCKTICNHQSORTCAFC 33
```

```
RESULT 12
US-10-281-053-13
; Sequence 13, Application US/10281053
; GENERAL INFORMATION:
; APPLICANT: Zhang, Gongyi
; APPLICANT: Shu, Hong-Bing
; APPLICANT: Liu, Yingfang
; APPLICANT: Xu, Liangguo
; TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
; FILE REFERENCE: 2879-86
; CURRENT APPLICATION NUMBER: US/10/281,053
; PRIOR FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,106
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/348,962
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/354,966
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/403,364
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 13
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-281-053-13
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```
Query Match 22.1%; Score 201; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.3e-12;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 34 CPEEQYWDPLGTGCMSCKTICNHQSORTCAFC 66
Db 1 CPEEQYWDPLGTGCMSCKTICNHQSORTCAFC 33
```

```
RESULT 13
US-10-180-903-2
; Sequence 2, Application US/10180903
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: SPC6 SERINE PROTEASE GENE DISRUPTIONS,
; TITLE OF INVENTION: AND COMPOSITIONS AND METHODS RELATED THERETO
; FILE REFERENCE: R-720
; CURRENT APPLICATION NUMBER: US/10/180,903
```

```
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/300,978
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/324,820
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1548
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-180-903-2

Query Match      10.7%; Score 97.5; DB 6; Length 1548;
Best Local Similarity 30.2%; Pred. No. 0.45;
Matches 29; Conservative 12; Mismatches 32; Indels 23; Gaps 7;

QY 14 RVDDQ--EERFPQGLWTGVAMRSCPEEQYWDPLLG-TCMSCKTICN-----HQSQTCAAF 65
DB 627 RADKHGQERF---LYHGECLNCPVGHY--PAKGHITCLPCDNCCLYNPHICRMSGY 681

QY 66 -----CRSLSCRKQKGYDHLRLDLCISCASIC 93
DB 682 VIIPNHTCQKLECR--QGEFQDSEYECMPCBEGC 715

RESULT 14
US-10-094-886-174
; Sequence 174, Application US/10094886
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Vernet, Corine A.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier, Raymond J., Jr.
; APPLICANT: Miller, Charles
; APPLICANT: Casman, Stacie
; APPLICANT: Pena, Carol
; APPLICANT: Gangolli, Esha
; APPLICANT: Gusev, Vladimir
; APPLICANT: Smithson, Glennda
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Gerlach, Valerie
; APPLICANT: Pochart, Pascal
; APPLICANT: Fernandes, Elma
; APPLICANT: Shinkets, Richard
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderne, Steven
; APPLICANT: Larocheille, William
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-290 B
; CURRENT APPLICATION NUMBER: US/10/094,886
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,182
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/288,052
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/318,510
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/274,281
```

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; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/314,018
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,849
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/296,693
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/313,626
; PRIOR FILING DATE: 2001-08-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: Patentin 2.1
; SEQ ID NO 174
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-886-174

Query Match      9.7%; Score 88; DB 6; Length 195;
Best Local Similarity 26.0%; Pred. No. 0.54;
Matches 39; Conservative 15; Mismatches 50; Indels 46; Gaps 10;

QY 28 GVAMRSCPEEQYWD--PLLGTCMSCKTICNHQSQTCAAFCSLSCKRKEQKFYDHL--- 82
DB 55 GVCLLSSCPGSGYGYTRYDINKTKCKADCD-----TC--FNKNF-CTKCKSGFYHLGKC 106

QY 83 LRDC-----ISCASI-----CGOHPKOCAY--FCENKLRSPV----- 112
DB 107 LDCNCPGLEANNHTMECVSIVHCEVSEWNPSPCTKKGTCGFKRGTTETRVREIIQHPSA 166

QY 113 --NLPPELRRQSRGEVNNSDNSGRYOGLE 140
DB 167 KGNLCPTNETRKTCTVORKKQCKGE-RGLE 195

RESULT 15
US-10-094-886-176
; Sequence 176, Application US/10094886
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Vernet, Corine A.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier, Raymond J., Jr.
; APPLICANT: Miller, Charles
; APPLICANT: Casman, Stacie
; APPLICANT: Pena, Carol
; APPLICANT: Gangolli, Esha
; APPLICANT: Gusev, Vladimir
; APPLICANT: Smithson, Glennda
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Gerlach, Valerie
; APPLICANT: Pochart, Pascal
; APPLICANT: Fernandes, Elma
; APPLICANT: Shinkets, Richard
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderne, Steven
; APPLICANT: Larocheille, William
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-290 B
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Tue Jan 7 10:36:50 2003

us-09-855-158-15.rapn

Page 6

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; CURRENT APPLICATION NUMBER: US/10/094,886
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,182
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/288,052
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/318,510
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/314,018
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,849
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/296,693
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/313,626
; PRIOR FILING DATE: 2001-08-21
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: Patentin 2.1
; SEQ ID NO: 176
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-886-176
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Query Match          9.7%; Score 88; DB 6; Length 195;
Best Local Similarity 26.0%; Pred. No. 0.54; 50; Indels 46; Gaps 10;
Matches 39; Conservative 15; Mismatches 50; Indels 46; Gaps 10;

QY 28 GVMRSGPTEQYWD--PLGTGMSCKTICNHSQRTCAAFCSLSCKRQSKFYDHL--- 82
DB 55 GVCSSCPGSGYGTGRYPDINKCTKCRACD-----TC--FNKNF--CTKCKSGFYHLHGKC 106
QY 83 LRDC-----ISCASI-----CGQHPRQCAV--PCENKLRSPV----- 112
DB 107 LDNCPEGLNANHMTMECVSIHCEVSEWNPSPCTGKKGKGTGRTETRVREIIQHPSA 166
QY 113 --NLPELRORSGEVENNSDNGRYGLE 140
DB 167 KGNLCPTNETRKCTVQRKKCKQGE--RGLE 195
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Search completed: January 7, 2003, 09:54:18
Job time : 22.6341 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:31:39 ; Search time 24.0125 Seconds
(without alignments)
371.797 Million cell updates/sec

Title: US-09-855-158-16

Perfect score: 405
Sequence: 1 CPBEQWPLLTGTCMSCKTI.....DCISCASICGHPKQCAFC 67

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
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21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	393	97.0	166	19 AAW75785	Human lymphocyte s
2	393	97.0	166	23 AAE15494	Human TACI extrace
3	393	97.0	265	22 AAE09244	Human TACI splice
4	393	97.0	291	23 AAU10949	Human AGP-3 recept
5	393	97.0	293	19 AAW75783	Human lymphocyte s
6	393	97.0	293	21 AAB36312	Human neutrokine-a
7	393	97.0	293	21 AAY94000	A transmembrane ac
8	393	97.0	293	22 AAE09240	Human TACI protein
9	393	97.0	293	22 AAY71914	Human tumour necro
10	393	97.0	293	23 AAU99512	Human TACI-Ig Fc

11	393	97.0	293	23 ABB81488	Human TACI recepto
12	393	97.0	293	23 AA014130	Human transmembran
13	393	97.0	293	23 AAU75408	Tumour necrosis fa
14	393	97.0	293	23 AAE15493	Human transmembran
15	393	97.0	293	23 AAU09800	Human AGP-3 relate
16	393	97.0	342	23 AAU14135	Protein of N-termi
17	393	97.0	334	23 AA014133	Protein of hTACI (
18	393	97.0	386	23 AA014132	Protein of hTACI (
19	393	97.0	357	23 AAE15498	Human TACI-immunog
20	393	97.0	404	23 AA014136	Protein of a compl
21	313	77.3	59	23 AAE15500	Human TACI cystein
22	256	63.2	249	21 AAY94006	A murine znf4, a
23	204	50.4	34	23 AAE15496	Human TACI cystein
24	204	50.4	38	23 AAU10952	Human AGP-3 recept
25	204	50.4	247	21 AAY93998	Human BR43x2, an i
26	201	49.6	33	23 AAE15495	Human TACI cystein
27	201	49.6	37	23 AAU10951	Human AGP-3 recept
28	84.5	20.9	220	22 AAB65001	Human secreted pro
29	76.5	18.9	325	19 AAW53240	Homo sapiens vascu
30	76.5	18.9	325	22 AAY97572	Human VEGF-D prote
31	76.5	18.9	354	19 AAW49036	Human vegf2 growt
32	76.5	18.9	354	19 AAW53241	Homo sapiens vascu
33	76.5	18.9	354	19 AAW44293	Human vascular end
34	76.5	18.9	354	21 AAB10649	Human VEGD protein
35	76.5	18.9	354	21 AAB29049	Human VEGF-D prote
36	76.5	18.9	354	21 AAY70750	Human prepro-vascu
37	76.5	18.9	354	21 AAY70983	Human vascular end
38	76.5	18.9	354	22 AAU08441	Polypeptide for hu
39	76.5	18.9	354	22 AAB70685	Human vascular end
40	76.5	18.9	354	22 AAY97573	Human VEGF-D1 prot
41	76.5	18.9	354	22 AAB37606	Human VEGF-D; Hom
42	76.5	18.9	620	18 AAW14994	Human c-fos, induce
43	76	18.8	177	21 AAY17467	Human Rank-like pr
44	76	18.8	173	22 AAU03118	Composite protein
45	76	18.8	197	21 AAB01421	Human TANGO 140-2.

ALIGNMENTS

RESULT 1
AAW75785
ID AAW75785 standard; Protein; 166 AA.
XX
AC AAW75785;
XX
DT 18-JAN-1999 (first entry)
XX
DE Human lymphocyte surface receptor extracellular domain.
XX
KW TACI; transmembrane activator and CAML-interactor;
KW calcium signal-modulating cyclophilin ligand; human
KW lymphocyte surface receptor; human B-cell; B lymphocyte;
KW infection; cancer; rheumatoid arthritis; autoimmune disease;
KW glomerulonephritis; immunosuppressive; graft versus host disease;
KW transplant rejection; therapy; signal transduction.
XX
OS Homo sapiens.
XX
PN WO9839361-A1.
XX
PD 11-SEP-1998.
XX
PF 03-MAR-1998; 98WO-US04270.
XX
PR 03-MAR-1997; 97US-0810572.
XX
PA (STUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
PI Bram RJ, Von Bulow G;
XX
DR WPI; 1998-506346/43.
DR N-PSDB; AAV57330.

XX New isolated transmembrane activator protein - used to develop
PT products for treating e.g. infections, cancers, autoimmune and
PT inflammatory conditions, transplant rejection or graft-versus-host
PT disease
XX
PS Claim 8; Page 73; 89pp; English.
XX This is the amino acid sequence of the N-terminal, i.e. the
CC extracellular, domain of novel human transmembrane activator and
CC CAML-interactor (TACI) protein (see AAM75783). TACI is a lymphocyte
CC receptor protein that is involved in the calcium activation pathway.
CC It is normally present in B-lymphocytes, and to a much lesser extent
CC in immature T-lymphocytes, and can therefore be targeted to
CC specifically regulate B cell responses without affecting T cell
CC activity. The extracellular domain of TACI functions as a binding
CC site for a ligand that stimulates the activation of the cell by
CC inducing the binding of the C-terminal portion (see AAM75784) of
CC TACI to the N-terminal domain of CAML. A recombinant form of the
CC extracellular portion of TACI acts as a dominant-negative or
CC blocking agent and acts to suppress the immune system. It can be
CC used to treat or prevent autoimmune disease, graft rejection or
CC graft versus host disease. The extracellular region is also used
CC in a claimed method for identifying a ligand for TACI, in which
CC binding of a candidate molecule is determined by detecting cellular
CC activation of the AP-1, CAMP or NF-KB pathway, of NF-AT
CC transcription factor, or of NF-AT dependent transcription.
XX
SQ Sequence 166 AA;
Query Match 97.0%; Score 393; DB 19; Length 166;
Best Local Similarity 94.4%; Pred. No. 7,7e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 1 CPEEQYWDPLLTGTCMSCKTICNHOSQRTCAFC-----CRKEQKGFYDHLRDCISCSASIC 56
DB 34 CPEEQYWDPLLTGTCMSCKTICNHOSQRTCAFCRSLSCKEKGKFDHLRDCISCSASIC 93
QY 57 GQHPKQCAVFC 67
DB 94 GQHPKQCAVFC 104
RESULT 2
AAE15494
ID AAE15494 standard; Protein; 166 AA.
XX
AC AAE15494;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human TACI extracellular domain.
XX
DE Human; transmembrane activator and intracellular CAML interactor; TACI;
KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.
XX
OS Homo sapiens.
XX
PN WO200187979-A2.
XX
PD 22-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-US15567.
XX
PR 12-MAY-2000; 2000US-204039P.
XX 27-JUN-2000; 2000US-214591P.
PR 14-MAY-2001; 2001US-0214591.

XX (AMGE-) AMGEN INC.
XX
XX The11 LE, Yu G;
XX
XX WPI; 2002-066686/09.
XX
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor
PT family ligand
XX
PS Claim 1; Fig 12A; 94pp; English.
XX
CC The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering
CC a specific binding partner for APRIL (870, a tumour necrosis factor-TNF
CC family ligand), having the consensus sequence region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma), hyperendia, Crohn's
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease), colitis) scleroderma, autoimmune disease (multiple
CC sclerosis), rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human TACI protein extracellular domain.
XX
SQ Sequence 166 AA;
Query Match 97.0%; Score 393; DB 23; Length 166;
Best Local Similarity 94.4%; Pred. No. 7,7e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 1 CPEEQYWDPLLTGTCMSCKTICNHOSQRTCAFC-----CRKEQKGFYDHLRDCISCSASIC 56
DB 34 CPEEQYWDPLLTGTCMSCKTICNHOSQRTCAFCRSLSCKEKGKFDHLRDCISCSASIC 93
QY 57 GQHPKQCAVFC 67
DB 94 GQHPKQCAVFC 104
RESULT 3
AAE09244
ID AAE09244 standard; Protein; 265 AA.
XX
AC AAE09244;
XX
DT 19-NOV-2001 (first entry)
XX
DE Human TACI splice variant protein.
XX
DE Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
KW TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KW psoriasis.
XX
OS Homo sapiens.
XX
PN WO200160397-A1.
XX
PD 23-AUG-2001.
XX
PF 28-NOV-2000; 2000WO-US32378.
XX
PR 16-FEB-2000; 2000US-0182938.

```

PR 22-AUG-2000; 2000US-0226986.
XX (GETH ) GENENTECH INC.
XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
XX Yan M;
XX WPI; 2001-541628/60.
XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
XX activity, for treating autoimmune disorders and cancer, comprises
XX exposing the cells to TALL-1 or APRIL polypeptide agonists or
XX antagonists -
XX Example 1; Fig 6; 160pp; English.
XX The invention relates to methods of using one or more agonists or
XX antagonists to modulate the activity of the members of TNF (tumour
XX necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
XX e.g. TACI or BCMA. The method is useful for treating pathological
XX conditions or diseases associated with increased TALL-1 and APRIL
XX expression or activity. TALL-1 and APRIL antagonists are used to
XX block the interaction between APRIL and TALL-1 with TACI or BCMA.
XX They are useful for treating a mammal suffering from cancer such
XX as leukaemia, lymphoma, myeloma, cancers of lung and colon and
XX autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
XX psoriasis and lupus erythematosus. The present sequence is human
XX TACI splice variant protein.
XX Sequence 265 AA;
XX
XX Query Match 97.0%; Score 393; DB 22; Length 265;
XX Best Local Similarity 94.4%; Pred. No. 1.2e-32;
XX Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
XX
XX QY 1 CPBEQYWDPLLGTCMSCKTICNHQSORTCAAFCSLSCREQKGFYDHLRLDCISCASIC 56
XX Db 34 CPBEQYWDPLLGTCMSCKTICNHQSORTCAAFCSLSCREQKGFYDHLRLDCISCASIC 93
XX
XX QY 57 GQHPKQCAVFC 67
XX Db 94 GQHPKQCAVFC 104
XX
XX RESULT 4
XX AAU10949
XX ID AAU10949 standard; Protein; 291 AA.
XX AC AAU10949;
XX
XX DT 12-MAR-2002 (first entry)
XX DE Human AGP-3 receptor extracellular domain.
XX
XX KW Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;
XX dermatological; neuroprotective; nootropic; immunomodulator; metabolic;
XX antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever;
XX antiParkinsonian; antiparotatic; vasotropic; antibacterial; asthma;
XX AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor;
XX mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder;
XX rheumatoid arthritis; graft-versus-host disease; Crohn's disease;
XX pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease;
XX diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia;
XX multiple sclerosis; Parkinson's disease; transgenic animal.
XX
XX OS Homo sapiens.
XX
XX PN WO200185782-A2.
XX
XX PD 15-NOV-2001.
XX
XX PF 12-FEB-2001; 2001WO-US04568.
XX

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PR 11-FEB-2000; 2000US-181800P.
XX (AMGE-) AMGEN INC.
XX Boyle WJ, Hsu H;
XX WPI; 2002-049441/06.
XX Composition, useful for identifying modulator of receptor for treating
XX asthma and glomerulonephritis, comprises AGP-3 (tumour necrosis factor
XX ligand family member) receptor and encoding nucleic acids -
XX Claim 1; Fig 18; 124pp; English.
XX
XX The invention relates to a composition (I) comprising AGP-3 receptor
XX (tumour necrosis factor ligand family member) related protein (II)
XX attached to a vehicle protein. (I) is useful for modulating AGP-3-related
XX activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in
XX assays to identify cells and tissues that express AGP-3R or proteins
XX related to AGP-3R-related protein and for identifying compounds
XX (agonists or antagonists) that interact with AGP-3R proteins. (II) is
XX also useful for identifying intracellular proteins that interact with
XX the respective cytoplasmic domains by yeast two-hybrid screening
XX process. (II) is involved in B cell growth, survival and activation
XX particularly in lymph node, spleen, and Peyer's patches. AGP-3R
XX agonists and antagonists identified using (II) are used for modulating
XX B cell response and are used to treat diseases characterised by
XX inflammatory processes or deregulated immune response such as
XX rheumatoid arthritis, graft-versus-host disease, Crohn's disease,
XX lupus etc. (II) is also useful in the production of hybridoma cells
XX which are derived from B cells which involves treating the hybridoma
XX cells with (II). (II) is useful in the treatment of inflammatory
XX conditions of joints, e.g., rheumatoid arthritis, osteoarthritis, etc.
XX (II), its agonists or antagonists are useful for treating acute
XX pancreatitis, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,
XX asthma, atherosclerosis, cachexia/anorexia, diabetes, fever,
XX glomerulonephritis, inflammatory bowel disease, ischaemic injury, septic
XX including cerebral ischaemia, multiple myeloma, multiple sclerosis,
XX osteoporosis, Parkinson's disease, pain, reperfusion injury, septic
XX shock, etc. The nucleic acids are also useful for developing transgenic
XX animals expressing (II), which are useful for producing the polypeptides
XX and for the study of in vivo biological activity. The present sequence
XX represents the amino acid sequence of human AGP-3 extracellular domain.
XX
XX Sequence 291 AA;
XX
XX Query Match 97.0%; Score 393; DB 23; Length 291;
XX Best Local Similarity 94.4%; Pred. No. 1.3e-32;
XX Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
XX
XX QY 1 CPBEQYWDPLLGTCMSCKTICNHQSORTCAAFCSLSCREQKGFYDHLRLDCISCASIC 56
XX Db 34 CPBEQYWDPLLGTCMSCKTICNHQSORTCAAFCSLSCREQKGFYDHLRLDCISCASIC 93
XX
XX QY 57 GQHPKQCAVFC 67
XX Db 94 GQHPKQCAVFC 104
XX
XX RESULT 5
XX AAU75783
XX ID AAU75783 standard; Protein; 293 AA.
XX AC AAU75783;
XX
XX DT 18-JAN-1999 (first entry)
XX DE Human lymphocyte surface receptor TACI.
XX
XX KW TACI; transmembrane activator and CAML-interactor;
XX calcium signal-modulating cyclophilin ligand; human;
XX lymphocyte surface receptor; human; B-cell; B lymphocyte;
XX infection; cancer; rheumatoid arthritis; autoimmune disease;

```


ID AAY94000 standard; Protein; 293 AA.
AC AAY94000;
XX
XX
DT 20-OCT-2000 (first entry)
XX
XX
DE A transmembrane activator and CAML-interactor (TACI).
XX
XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
KW ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
KW renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;
KW immune response; immunosuppression; graft rejection; joint pain;
KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
KW renal artery stenosis; occlusion; cholesterol; renal emboli.
XX
OS Homo sapiens.
XX
PN WO200040716-A2.
XX
PD 13-JUL-2000.
XX
XX 07-JAN-2000; 2000WO-US00396.
XX
XX 07-JAN-1999; 99US-0226533.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
XX Gross JA, Xu W, Madden K, Yee DP;
PI WPI; 2000-452538/39.
DR N-PSDB; AAA58558.
XX
XX Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
PT renal disease, graft versus host disease, and inflammation, comprises
PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide -
XX
XX Disclosure; Page 149-150; 175pp; English.
XX
XX The present sequence represents a human transmembrane activator and
CC CAML-interactor (TACI) receptor. TACI is a tumour necrosis factor (TNF)
CC receptor. The extracellular domains of BR43x2 (an isoform of TACI), TACI
CC or BCMA (a related B cell protein) receptor contain a cysteine rich
CC domain, and are used for inhibiting ztnf4 activity. ztnf4 is a TNF
CC ligand. They may also be used for inhibiting BR43x2, TACI or BCMA
CC receptor-ligand engagement associated with activated or resting B
CC lymphocytes, effector T-cells, or with antibody production. The
CC antibody production is associated with an autoimmune disease selected
CC from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis
CC and rheumatoid arthritis. The ztnf4 activity and BR43x2, TACI or BCMA
CC receptor-ligand engagement is associated with asthma, bronchitis,
CC emphysema, end stage renal failure, glomerulonephritis, vasculitis,
CC nephritis, pyelonephritis, renal neoplasms, multiple myelomas, lymphomas,
CC light chain neuropathy, amyloidosis, moderating immune response,
CC immunosuppression, graft rejection, graft versus host disease,
CC inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint
CC pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA
CC polypeptides, fusions, antibodies, agonists or antagonists can be used
CC to treat hypertension, renal artery stenosis, or occlusion, and
XX cholesterol or renal emboli.
XX
SQ Sequence 293 AA;
Query Match 97.0%; Score 393; DB 21; Length 293;
Best Local Similarity 94.4%; Pred. No. 1.3e-32;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 1 CPBEQYWDPLLTGTCMSCKTICNHQSORTCAAFCSLSCRKEQKGFYDHLRLDTCISCASIC 56
|||||

Db 34 CPBEQYWDPLLTGTCMSCKTICNHQSORTCAAFCSLSCRKEQKGFYDHLRLDTCISCASIC 93
QY 57 GQHPKQCAAYFC 67
|||||
Db 94 GQHPKQCAAYFC 104
|||||
RESULT 8
AAE09240
ID AAE09240 standard; Protein; 293 AA.
XX
AC AAE09240;
XX
XX 19-NOV-2001 (first entry)
DT
XX Human TACI protein.
DE
XX Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
KW TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KW psoriasis.
XX
XX Homo sapiens.
XX
XX WO200160397-A1.
PN
XX 23-AUG-2001.
PD
XX
XX 28-NOV-2000; 2000WO-US32378.
PF
XX 16-FEB-2000; 2000US-0182938.
PR
XX 22-AUG-2000; 2000US-0226596.
PR
XX (GETH) GENENTECH INC.
PA
XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
PI Yan W;
XX
XX WPI; 2001-541628/60.
DR N-PSDB; AADI5901.
XX
XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
PT activity, for treating autoimmune disorders and cancer, comprises
PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
PT antagonists -
XX
XX Example 1; Fig 1; 160pp; English.
XX
XX The invention relates to methods of using one or more agonists or
CC antagonists to modulate the activity of the members of TNF (tumour
CC necrosis factor), especially TALL-1, APRIL and TNF receptor (TNFR)
CC e.g. TACI or BCMA. The method is useful for treating pathological
CC conditions or diseases associated with increased TALL-1 and APRIL
CC expression or activity. TALL-1 and APRIL antagonists are used to
CC block the interaction between APRIL and TALL-1 with TACI or BCMA.
CC They are useful for treating a mammal suffering from cancer such
CC as leukaemia, lymphoma, myeloma, cancers of lung and colon and
CC autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
CC psoriasis and lupus erythematosus. The present sequence is human
CC TACI protein.
XX
XX
SQ Sequence 293 AA;
Query Match 97.0%; Score 393; DB 22; Length 293;
Best Local Similarity 94.4%; Pred. No. 1.3e-32;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 1 CPBEQYWDPLLTGTCMSCKTICNHQSORTCAAFCSLSCRKEQKGFYDHLRLDTCISCASIC 56
|||||

DB 94 GQHPKQCAVFC 104

RESULT 9
AA71914
ID AA71914 standard; Protein; 293 AA.
XX
AC AA71914;
XX
DT 26-MAR-2001 (first entry)
XX
DE Human tumour necrosis factor receptor (TACI) protein.
XX
KW Human; transmembrane activator and CAML interactor; TACI;
KW tumour necrosis factor receptor; TNF; autoimmune disease; diabetes;
KW calcium-signal modulating cyclophilin ligand; CAML; viral infection;
KW neutrokin alpha polypeptide; TACI-Ligand; TACI-L; cytosolic; therapy;
KW neuroprotective; antidiabetic; antiviral; antiinflammatory; tumour;
KW antiaerthritic; antipneumatic; immunosuppressive; multiple sclerosis;
KW rheumatoid arthritis; graft rejection; inflammation; cell proliferation;
KW cell death; immunoglobulin E-mediated allergic reaction; IGE.
XX
OS Homo sapiens.
XX
FH Key
FH Domain
FT 2..166 Extracellular domain
FT /label= Extracellular domain
FT /note= "Binds with amino acids 123-285 of extracellular
FT domain of TACI-L"

XX WO200067034-A1.
XX
XX 09-NOV-2000.
XX
XX 14-APR-2000; 2000WO-US10282.
XX
XX 30-APR-1999; 99US-0302863.
XX
XX (IMMU) IMMUNEX CORP.
XX
XX Goodwin RG, Din WS;
XX
XX WPI; 2001-016005/02.
XX
XX DR N-PSDB; AAD02006.
XX
XX Use of new interactions between tumour necrosis factor receptors (TNF) and TACI ligands to screen candidate molecules for determining agonist and antagonist interactions which are used for treating inflammation -
XX
XX Claim 10; Fig 1b; 46pp; English.
XX
XX The present sequence is a human tumour necrosis factor receptor (TACI)
XX protein. TACI (transmembrane activator and calcium-signal modulating
XX cyclophilin ligand (CAML)-interactor) forms a complex with neutrokin
XX alpha polypeptide (TACI-Ligand). The antagonist or agonist of
XX TACI/TACI-L complex is useful for modulating an intracellular signalling
XX cascade mediated by TACI/TACI-L complex. Antagonists of TACI/TACI-L
XX complex are used to inhibit the interaction between TACI and TACI-L for
XX therapeutic purposes to treat tumour and tumour metastasis and to combat
XX various autoimmune diseases e.g. multiple sclerosis and diabetes, as
XX well as other disorders, such as viral infection, rheumatoid arthritis,
XX graft rejection, and immunoglobulin (Ig) E-mediated allergic reactions
XX and inflammation. The interaction is used to study cellular processes
XX associated with tumour necrosis factor (TNF)-receptors such as immune
XX regulation, cell proliferation, cell death and inflammatory responses.
XX The interaction between the extracellular region of TACI and TACI-L can
XX be used to further develop understanding of which cell types TACI-L
XX acts upon.
XX
XX Sequence 293 AA;
XX
XX Query Match 97.0%; Score 393; DB 22; Length 293;
XX Best Local Similarity 94.4%; Pred. No. 1.3e-32;

Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 1 CPEQYMPRLGTCTGCTCTCHQSORTCAPC-----CRKQGFYHLLADPCLSCASC 56
DB 34 CPEQYMPRLGTCTGCTCTCHQSORTCAPC-----CRKQGFYHLLADPCLSCASC 93
QY 57 GQHPKQCAVFC 67
DB 94 GQHPKQCAVFC 104

RESULT 10
AAU99512
ID AAU99512 standard; Protein; 293 AA.
XX
AC AAU99512;
XX
DT 07-OCT-2002 (first entry)
XX
DE Human TACI-IgG Fc fusion protein.
XX
KW Human; tumour necrosis factor; TNF delta; pulmonary system disorder;
KW immunoglobulin production; B-cell proliferation; immune system disorder;
KW autoimmune disease; cancer; lymphoproliferative disorder; pain;
KW microbial infection; parasitic infection; bone disease; atherosclerosis;
KW cardiovascular disease; neurodegenerative disease; wound healing;
KW graft versus host disease; hematopoietic cell disorder; nephritis;
KW transmembrane activator and CAML-interactor; TACI; TNF epsilon; IgG;
KW immunoglobulin G; Fc portion.
XX
XX Homo sapiens.
XX
XX OS
XX
XX US2002064829-A1.
XX
XX 30-MAY-2002.
XX
XX 14-JUN-2001; 2001US-0879919.
XX
XX 14-MAR-1996; 96US-016812P.
XX
XX 15-JUN-2000; 2000US-211537P.
XX
XX 23-OCT-2000; 2000US-241952P.
XX
XX 13-DEC-2000; 2000US-254875P.
XX
XX 16-MAR-2001; 2001US-276248P.
XX
XX 23-MAR-2001; 2001US-277978P.
XX
XX 25-MAY-2001; 2001US-293499P.
XX
XX 12-MAR-1997; 97US-0815763.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Yu G, Ni J, Gentz RL, Dillon PJ;
XX
XX WPI; 2002-556722/59.
XX
XX Novel human multimeric tumour necrosis factor delta or epsilon protein
XX useful for treating disease or disorder of immune system such as
XX autoimmune disease, immunodeficiency, or cancer of immune system -
XX
XX Example 29; Page 125; 143pp; English.
XX
XX The present invention relates to the isolation of human tumour necrosis
XX factor (TNF) delta and TNF epsilon proteins, and the polynucleotide
XX sequences encoding them. The proteins are useful for modulating
XX immunoglobulin production or for modulating proliferation of B-cells.
XX The sequences of the invention are useful for treating diseases or
XX disorders of the immune system. Such disorders include autoimmune
XX diseases (e.g. systemic lupus erythematosus (SLE), acquired
XX immunodeficiency syndrome (AIDS)), cancers of the immune system
XX (e.g. chronic lymphocytic leukaemia (CLL), multiple myeloma,
XX non-Hodgkin's lymphoma or Hodgkin's disease), lymphoproliferative
XX disorders, microbial infections (e.g. viral, bacterial), parasitic
XX infections, nephritis, bone disease (e.g. osteoporosis), atherosclerosis,
XX pain, cardiovascular disorders (e.g. myocardial infarction, stroke),
XX neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's

CC disease), graft versus host disease, wound healing, haematopoietic cell
 CC disorders (e.g. anaemia), inflammatory disorders (e.g. asthma),
 CC diseases or disorders associated with various mucous membranes of the
 CC body (e.g. mucositis), and disorders of the pulmonary system. The
 CC proteins are also useful as a vaccine adjuvant that enhances immune
 CC responsiveness to specific antigens. The present sequence for human
 CC transmembrane activator and CAML-interactor (TACI)-immunoglobulin G
 CC (IgG) Fc fusion protein is used in the examples of the present
 CC invention.

XX Sequence 293 AA;

Query Match 97.0%; Score 393; DB 23; Length 293;
 Best Local Similarity 94.4%; Pred. NO. 1.3e-32;
 Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 CPEQYWDPLLTGTCMSCKTICNHQSORTCAAFCSRLSCRKEQKQFYDHLRLDCISCASIC 56

DB 34 CPEQYWDPLLTGTCMSCKTICNHQSORTCAAFCSRLSCRKEQKQFYDHLRLDCISCASIC 93

QY 57 GQHPKQCAAYFC 67

DB 94 GQHPKQCAAYFC 104

RESULT 11

AB581488
 ID ABB81488 standard; Protein; 293 AA.

AC ABB81488;

DT 02-SEP-2002 (first entry)

DE Human TACI receptor related protein SEQ ID NO:8.

XX Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;
 XX immunosuppressive; dermatological; antiinflammatory; antidiabetic;
 XX neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
 XX nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
 XX autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
 XX multiple sclerosis; insulin dependent diabetes mellitus; asthma;
 XX rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
 XX glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
 XX pylonephritis; renal neoplasm; multiple myeloma; amyloidosis;
 XX light chain neuropathy; hypertension; large vessel disease;
 XX graft-versus host disease; graft rejection; Crohn's disease.

XX Homo sapiens.

XX WO200238766-A2.

PD 16-MAY-2002.

XX 05-NOV-2001; 2001WO-US47018.

XX 07-NOV-2000; 2000US-246449P.

PR 20-DEC-2000; 2000US-257131P.

PR 28-JUN-2001; 2001US-301715P.

PR 29-AUG-2001; 2001US-315565P.

XX (ZYMO) ZYMOGENETICS INC.

XX Gross JA, Xu W, Henne RM, Grant FJ;

DR WPI; 2002-508212/54.

XX Novel isolated human tumor necrosis factor receptor polypeptide, termed
 PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end
 PT stage renal failure or renal disease and lymphoma

XX Disclosure; Page 136-137; 154pp; English.

XX The present invention describes a human tumour necrosis factor receptor

CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,
 CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
 CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
 CC activities, and can be used in gene therapy. (I) can be used for
 CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
 CC (e.g. ZTNF4), for treating disorders and diseases associated with B
 CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
 CC inhibiting the proliferation of tumour cells. (I) is useful for treating
 CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
 CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
 CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
 CC leukaemia, nephritis, and pyelonephritis, and for treating renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
 CC amyloidosis, hypertension, large vessel disease, graft-versus host
 CC disease, graft rejection and Crohn's disease. (I) is useful for
 CC modulating the immune system, for regulating B cell responses and
 CC development, for modulating development of other cells, antibody
 CC production and cytokine production, and for modulating T and B cell
 CC communication. The present sequence represents a protein which is
 CC given in the exemplification of the present invention.

XX Sequence 293 AA;

Query Match 97.0%; Score 393; DB 23; Length 293;
 Best Local Similarity 94.4%; Pred. NO. 1.3e-32;

Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 CPEQYWDPLLTGTCMSCKTICNHQSORTCAAFCSRLSCRKEQKQFYDHLRLDCISCASIC 56

DB 34 CPEQYWDPLLTGTCMSCKTICNHQSORTCAAFCSRLSCRKEQKQFYDHLRLDCISCASIC 93

QY 57 GQHPKQCAAYFC 67

DB 94 GQHPKQCAAYFC 104

RESULT 12

AAO14130
 ID AAO14130 standard; Protein; 293 AA.

AC AAO14130;

XX 02-MAY-2002 (first entry)

XX Human transmembrane activator CAML interactor protein (TACI).

XX Human transmembrane activator CAML interactor protein; TACI; cytostatic;
 XX cell proliferation; tumour; vulnery; renal cell cancer; mastocytoma;
 XX Kaposi's sarcoma; breast; ovarian carcinoma; rectal; throat; melanoma;
 XX colon; bladder; mammary adenocarcinoma; gastrointestinal; hyperplasia;
 XX pharyngeal squamous cell; stomach; cellular hyperproliferation; pannus;
 XX scleroderma; rheumatoid arthritis; scarring; liver; lung fibrosis;
 XX uterine.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 1..114

FT /label= Extracellular_domain

XX WO200181417-A2.

XX 01-NOV-2001.

XX 27-APR-2001; 2001WO-US40626.

XX 27-APR-2000; 2000US-199946P.

XX (BIOJ) BIOGEN INC.

XX (APOT-) APOTEC R & D SA.

XX Ambrose C, Thompson J, Schneider P, Rennert P;

XX WPI: 2002-062027/08.
 DR N-PSDB; AAK98726.
 XX
 PT Treating mammary for condition associated with undesired cell
 PT proliferation e.g., solid tumour or reducing solid tumour size located in
 PT mammary comprises administering transmembrane activator CAML interactor
 PT protein reagent -
 XX
 XX Claim 8; Fig 1; 42pp; English.
 XX
 XX This sequence represents the human transmembrane activator CAML
 CC interactor protein (TACI). The invention relates to treating a mammal for
 CC a condition associated with undesired cell proliferation (e.g. a solid
 CC tumour, or reducing the size of a solid tumour located on or in a mammal)
 CC comprising administering a transmembrane activator CAML interactor
 CC protein (TACI) reagent. The TACI reagent has cytostatic and vulnary
 CC activity. Treating a mammal (e.g. human, cow, horse, dog, mouse, rat or
 CC cat) for a condition associated with undesired cell proliferation (e.g.
 CC cancer such as renal cell cancer, Kaposi's sarcoma, breast cancer,
 CC sarcoma, ovarian carcinoma, rectal cancer, throat cancer, melanoma, colon
 CC cancer, bladder cancer, mastocytoma, lung cancer, mammary adenocarcinoma,
 CC pharyngeal squamous cell carcinoma, gastrointestinal cancer or stomach
 CC cancer). The method is also useful for treating cellular
 CC hyperproliferation (hyperplasia) such as scleroderma, pannus formation in
 CC rheumatoid arthritis, post-surgical scarring and lung, liver and uterine
 CC fibrosis. The TACI reagent of the invention can extend mean survival time
 CC of a mammal by 25% as compared to the mean survival time of a mammal in
 CC the absence of administering the TACI reagent. The TACI reagent also
 CC reduces the size of the tumour by 25% or more.
 CC
 XX Sequence 293 AA;
 XX
 XX Query Match 97.0%; Score 393; DB 23; Length 293;
 XX Best Local Similarity 94.4%; Pred. No. 1.3e-32;
 XX Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 XX
 QY 1 CPEEYWPDLGTGCMSCRTICNHOSORTCAFC---CRKEQKGFYDHLDRDCISCASIC 56
 DB 34 CPEEYWPDLGTGCMSCRTICNHOSORTCAFCRSLSCKEKGKFDHLDRDCISCASIC 93
 QY 57 GQHPKQCAVFC 67
 DB 94 GQHPKQCAVFC 104
 XX
 XX RESULT 13
 XX AAU75408 standard; Protein; 293 AA.
 XX
 XX AAU75408;
 XX
 DT 09-APR-2002 (first entry)
 XX
 XX Tumour necrosis factor (TNF) receptor TACI-FC fusion.
 XX
 XX Tumour necrosis factor; TNF; cytostatic; arteriosclerosis;
 KW analgesic; cerebroprotective; neurotropic; neuroprotective; hepatotropic;
 KW immunoglobulin production; B cell proliferation; immunosuppressive;
 KW HIV; human immunodeficiency virus; autoimmune disease; immunodeficiency;
 KW Sjogren's syndrome; systemic lupus erythematosus; Hodgkin's disease;
 KW common variable immunodeficiency; CVID; non-Hodgkin's lymphoma; AIDS;
 KW acquired immunodeficiency; cancer; multiple myeloma; CLL;
 KW chronic lymphocytic leukaemia; lymphoproliferative disorder;
 KW bacterial infection; viral infection; osteoporosis; atherosclerosis;
 KW pain; cardiovascular disorder; stroke; allergy; Alzheimer's disease;
 KW neurodegenerative disease; inflammation; liver disease; cirrhosis;
 KW cardiomyopathy; diabetes; psoriasis; glomerulonephritis;
 KW ulcerative colitis; angiodenesis; septic shock; wound healing;
 KW tumour necrosis factor receptor; TACI; immunoglobulin; IgG.
 XX
 XX Homo sapiens.
 OS Synthetic.

XX WO200196528-A2.
 XX
 XX 20-DEC-2001.
 XX
 XX 14-JUN-2001; 2001WO-US19026.
 XX
 XX 15-JUN-2000; 2000US-211537P.
 XX 23-OCT-2000; 2000US-241952P.
 XX 13-DEC-2000; 2000US-254875P.
 XX 16-MAR-2001; 2001US-276248P.
 XX 23-MAR-2001; 2001US-277978P.
 XX 25-MAY-2001; 2001US-293499P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Yu G, Ni J, Gentz RL, Dillon PJ, Hilbert D;
 XX WPI: 2002-130727/17.
 XX N-PSDB; ABR13415.
 XX
 XX Novel multimeric human tumour necrosis factor delta or epsilon protein
 PT useful for treating cancer, immune system disorders, infection,
 PT cardiovascular disorders, liver disease, cardiomyopathy, diabetes and
 PT psoriasis -
 XX
 XX Example 29; Page 341-342; 344pp; English.
 XX
 XX The invention describes a multimeric human tumour necrosis factor (TNF)
 CC delta or epsilon protein (I). (I) or a composition containing them (II)
 CC are useful for modulating immunoglobulin production or proliferation of B
 CC cells. (I) or (II) is useful for treating a disease or disorder of the
 CC immune system, preferably an autoimmune disease (e.g. Sjogren's syndrome,
 CC systemic lupus erythematosus or common variable immunodeficiency (CVID));
 CC an immunodeficiency e.g. acquired immunodeficiency syndrome (AIDS);
 CC cancer of the immune system (e.g. Hodgkin's disease, non-Hodgkin's
 CC lymphoma, multiple myeloma and chronic lymphocytic leukaemia (CLL)); in
 CC the diagnosis and treatment or prevention of cancer, lymphoproliferative
 CC disorder, bacterial and viral infections, osteoporosis, atherosclerosis,
 CC pain, cardiovascular disorders (e.g. stroke), allergy, inflammation,
 CC neurodegenerative disease (e.g. Alzheimer's disease), liver disease (e.g.
 CC cirrhosis), cardiomyopathy, diabetes, asthma, psoriasis, septic shock,
 CC glomerulonephritis, ulcerative colitis, arteriosclerosis; for promoting
 CC angiogenesis and wound healing; as a diagnostic research reagent; as an
 CC agent to target and kill cells expressing a TNFdelta and/or TNFepsilon
 CC receptor; in apoptosis of transformed cell lines; mediation of cell
 CC activation and proliferation; and as an immunogen to produce (II). (II)
 CC is useful to purify, detect and target (I). for measuring levels of (I)
 CC in biological samples, for immunophenotyping samples, and to treat,
 CC inhibit or prevent diseases and disorders associated with aberrant
 CC expression and/or activity of (I). This is the amino acid sequence of a
 CC fusion protein of tumour necrosis factor receptor TNFRI and immunoglobulin
 CC G (Igg) crystallisation fragment, described in the method of the
 CC invention.
 XX
 XX Sequence 293 AA;
 XX
 XX Query Match 97.0%; Score 393; DB 23; Length 293;
 XX Best Local Similarity 94.4%; Pred. No. 1.3e-32;
 XX Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 XX
 QY 1 CPEEYWPDLGTGCMSCRTICNHOSORTCAFC---CRKEQKGFYDHLDRDCISCASIC 56
 DB 34 CPEEYWPDLGTGCMSCRTICNHOSORTCAFCRSLSCKEKGKFDHLDRDCISCASIC 93
 QY 57 GQHPKQCAVFC 67
 DB 94 GQHPKQCAVFC 104
 XX
 XX RESULT 14
 XX ABR15493 standard; Protein; 293 AA.
 XX
 XX ABR15493

XX AAE15493;
AC
XX 12-MAR-2002 (first entry)
DT
XX Human transmembrane activator and intracellular CAML interactor protein.
DE
XX Human; transmembrane activator and intracellular CAML interactor; TACI;
KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Region 34..66
FT /note= "Cysteine-rich consensus region"
FT Region 71..104
FT /note= "Cysteine-rich consensus region"
FT Domain 167..186
FT /label= Transmembrane_domain
XX
XX WO200187979-A2.
DN
XX 22-NOV-2001.
PD
XX 14-MAY-2001; 2001WO-US15567.
XX
XX 12-MAY-2000; 2000US-204039P.
PR 27-JUN-2000; 2000US-214591P.
PR 14-MAY-2001; 2001US-0214591.
XX
XX (AMGE-) AMGEN INC.
PA
XX Theall LE, Yu G;
PI
XX WPI; 2002-066686/09.
DR
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor
PT family ligand
XX
XX Disclosure; Fig 12A; 94pp; English.
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering
CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human TACI protein.
XX
XX Sequence 293 AA;

Query Match 97.0%; Score 393; DB 23; Length 293;
Best Local Similarity 94.4%; Pred. No. 1.3e-32;

Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 1 CPSEQYWDPLLTGTCMSCKTICNHOSQRTCAAF-----CRKEQGFYDHLRLDCISCASIC 56
DB 34 CPSEQYWDPLLTGTCMSCKTICNHOSQRTCAAF-----CRKEQGFYDHLRLDCISCASIC 93
QY 57 GOHPKQCAAYFC 67
DB 94 GOHPKQCAAYFC 104
RESULT 15
AAU09900
ID AAU09900 standard; Protein; 293 AA.
XX
AC AAU09900;
XX
DT 12-MAR-2002 (first entry)
XX Human AGP-3 related protein receptor.
DE
XX Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;
KW dermatological; neuroprotective; neotropic; immunomodulator; metabolic;
KW antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever;
KW antiparkinsonian; antipsoriatic; vasotropic; antibacterial; asthma;
KW AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor;
KW mesenteric lymph node; AGP-3; inflammatory disease; immune disorder;
KW rheumatoid arthritis; graft-versus-host disease; Crohn's disease;
KW pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease;
KW diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia;
KW multiple sclerosis; Parkinson's disease; transgenic animal.
XX
OS Homo sapiens.
XX WO200185782-A2.
XX
XX 15-NOV-2001.
XX
XX 12-FEB-2001; 2001WO-US04568.
XX
XX 11-FEB-2000; 2000US-181800P.
PR
XX (AMGE-) AMGEN INC.
PA
XX Boyle WJ, Hsu H;
PI
XX WPI; 2002-049441/06.
DR N-FSD5; AAS18558.
XX
XX Composition, useful for identifying modulator of receptor for treating
PT asthma and glomerulonephritis, comprises AGP-3 (tumour necrosis factor
PT ligand family member) receptor and encoding nucleic acids -
XX
XX Disclosure; Page 117-119; 124pp; English.
XX
XX The invention relates to a composition (I) comprising AGP-3 receptor
CC (tumour necrosis factor ligand family member) related protein (II)
CC attached to a vehicle protein. (I) is useful for modulating AGP-3-related
CC activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in
CC assays to identify cells and tissues that express AGP-3 or proteins
CC related to AGP-3-related protein and for identifying compounds
CC (agonists or antagonists) that interact with AGP-3 proteins. (II) is
CC also useful for identifying intracellular proteins that interact with
CC the respective cytoplasmic domains by yeast two-hybrid screening
CC process. (II) is involved in B cell growth, survival and activation
CC particularly in lymph node, spleen, and Peyer's patches. AGP-3
CC agonists and antagonists identified using (II) are used for modulating
CC B cell response and are used to treat diseases characterised by
CC inflammatory processes or deregulated immune responses such as
CC rheumatoid arthritis, graft-versus-host disease, Crohn's disease,
CC lupus, etc. (II) is also useful in the production of hybridoma cells
CC which are derived from B cells, which involves treating the hybridoma
CC cells with (II). (II) is useful in the treatment of inflammatory

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us-09-855-158-16.rag

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CC conditions of joints, e.g., rheumatoid arthritis, osteoarthritis, etc.
CC (II), its agonists or antagonists are useful for treating acute
CC pancreatitis, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,
CC asthma, atherosclerosis, cachexia/anorexia, diabetes, fever,
CC glomerulonephritis, inflammatory bowel disease, ischemic injury
CC including cerebral ischemia, multiple myeloma, multiple sclerosis,
CC osteoporosis, Parkinson's disease, pain, reperfusion injury, septic
CC shock, etc. The nucleic acids are also useful for generating transgenic
CC animals expressing (II), which are useful for producing the polypeptides
CC and for the study of in vivo biological activity. The present sequence
CC represents the amino acid sequence of human AGP-3 related protein
XX receptor.

SQ Sequence 293 AA;

Query Match

97.0%; Score 393; DB 23; Length 293;

Best Local Similarity 94.4%; Pred. No. 1.3e-32;

Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY	1	CPEEQYWDPLGTGWSCKTICNHQSORTCAFC---	CRKEQGFYDHLRDCISCASIC	56
DB	34	CPEEQYWDPLGTGWSCKTICNHQSORTCAFCRSLS	CRKEQGFYDHLRDCISCASIC	93
QY	57	GOHPKQCAVFC		67
DB	94	GOHPKQCAVFC		104

Search completed: January 7, 2003, 09:37:29
Job time : 25.0125 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:35:04 ; Search time 9.57143 Seconds
(without alignments)
672.941 Million cell updates/sec

Title: US-09-855-158-16

Perfect score: 405
Sequence: 1 CPBEQYWDPLLGTCMSCKTI.....DCISCASICGHPKQCAAYFC 67

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR_73:*

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	81.5	20.1	1299	2	T43251	furin (EC 3.4.21.75) - fall armyworm
2	80	19.8	1208	2	H59834	hypothetical prote
3	77	19.0	2864	2	I28626	variant-specific s
4	75	18.5	1548	2	S34583	serine proteinase
5	74.5	18.4	962	2	JC5571	subtilisin-like pr
6	74.5	18.4	969	1	A39490	subtilisin-like pr
7	74.5	18.4	975	2	JC5570	subtilisin-like pr
8	71.5	17.7	773	2	I46059	beta-1 integrin su
9	71.5	17.7	932	2	I52527	PACE4A - mouse (fr
10	71.5	17.7	1680	2	A43434	furin (EC 3.4.21.7
11	71	17.5	108	2	AD0715	conserved hypothet
12	70	17.3	1124	1	I58388	protein-tyrosine k
13	69.5	17.2	798	2	S01659	integrin beta-1 ch
14	69.5	17.2	799	1	IQMSFB	fibronectin recept
15	69	17.0	899	2	G02428	subtilisin-like pr
16	69	17.0	915	2	JG6148	subtilisin-like pr
17	68.5	16.9	501	2	I61512	TNF receptor assoc
18	68	16.8	1339	2	JC4387	epidermal growth f
19	67.5	16.7	146	2	S46368	STIG1 protein - co
20	67.5	16.7	2233	2	T28669	surface protein 51
21	67.5	16.7	3084	1	MMWSA	laminin alpha-1 ch
22	67	16.5	1210	2	AS3183	epidermal growth f
23	67	16.5	1751	1	MGUHM	laminin alpha-2 ch
24	66.5	16.4	184	2	S43486	B-cell maturation
25	66.5	16.4	937	2	I53282	gene PAC84 protein
26	66	16.3	248	2	T03869	hypothetical prote
27	66	16.3	1119	2	A88481	protein C16A3.6 [i
28	66	16.3	1122	2	I54237	protein-tyrosine k
29	66	16.3	1123	1	JN0712	protein-tyrosine k

30 66 16.3 1125 1 JH0771 protein-tyrosine k
31 66 16.3 1210 1 GQHUE epidermal growth f
32 65.5 16.2 202 2 T50635 hypothetical prote
33 65.5 16.2 210 2 T33697 hypothetical prote
34 65.5 16.2 843 2 A27131 epidermal growth f
35 65.5 16.2 1173 2 B97208 pyruvate ferredoxi
36 65 16.0 270 2 T27786 hypothetical prote
37 65 16.0 572 2 T29880 hypothetical prote
38 65 16.0 799 2 JC4126 integrin beta olig
39 65 16.0 915 2 B48225 probable propotei
40 65 16.0 1342 2 A36223 kinase-related tra
41 65 16.0 3106 1 S53868 laminin alpha-2 ch
42 64.5 15.9 279 2 JG0164 LIM protein, FHL4
43 64.5 15.9 798 2 A28193 variant-specific s
44 64.5 15.9 3006 2 T28625 integrin beta-1 ch
45 64 15.8 97 2 S34769 eclosion hormone -

ALIGNMENTS

RESULT 1
T43251
furin (EC 3.4.21.75) - fall armyworm
N;Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serin
C;Species: Spodoptera frugiperda (fall armyworm)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C;Accession: T43251
R;Cleplik, M.; Klenk, H.
submitted to the EMBL Data Library, January 1996
A;Description: Cloning and functional characterization of FURIN from Spodoptera frugiper
A;Reference number: Z22368
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1299 <CIE>
A;Cross-references: EMBL:Z68888; NID:gl167859; PID:e219690; PIDN:CAA93116.1
A;Experimental source: clone Sfurin 6; ovary
C;Function:
A;Description: responsible for the endoproteolytic processing of proproteins with specif
C;Keywords: hydrolase; serine proteinase

Query Match 20.1%; Score 81.5; DB 2; Length 1299;
Best Local Similarity 30.1%; Pred No. 2.2;
Matches 22; Conservative 5; Mismatches 33; Indels 13; Gaps 3;

QY 1 CPBEQYWDPLLGTCMSCKTICNHQSQTCAA----FCRKEQKGFYDHLRDCISCASIC 56
Db 1116 CLGSQYDAYSCTCRSCDASC-----RTCSGPGQFCTTCSRPLRIDRLANNQCVPCCSER 1170

QY 57 G-----QHPKQCAAY 65
Db 1171 GVTNSTPPTDCCH 1183

RESULT 2
H69834
hypothetical protein yhjQ - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C;Accession: H69834
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Bouilliet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmsen, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
Kech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel
Y, M.; Oгава, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Poh, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Scoffone, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipar, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
 A:Author: Yoshikawa, H.F.; Zamboni, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: H69834
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-108 <KUN>
 A:Cross-references: GB:299109; GB:AL009126; NID:92633260; PID:CA12900.1; PID:e1183062;
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yhjO

Query Match 19.8%; Score 80; DB 2; Length 108;
 Best Local Similarity 22.6%; Pred. No. 0.59;
 Matches 24; Conservative 7; Mismatches 25; Indels 50; Gaps 4;

QY 4 EOYMDLLGTCMSCKTICNH-----OSQTCAPFC----- 33
 DB 2 EOYSEACIACIDCMKACHCFTKCLSESVQHLSGCIPLDRECADICALAVKAMQTDSP 61
 QY 34 -----CRKEQGF-YDHLRDCISCASIGQHPRKOC 63
 DB 62 FMKEIATLCADICEACGTGCGHNDH---COACAKCFTCAEQC 103

RESULT 3
 T8626
 Variant-specific surface protein 2 - malaria parasite (Plasmodium falciparum)
 C:Species: Plasmodium falciparum
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
 C:Accession: T28626
 R:Su, X.Z.; Heatwole, V.M.; Wertheimer, S.P.; Guinea, F.; Herfel, J.A.; Peterson, D.S.
 Cell 82, 89-100, 1995
 A:Title: The large diverse gene family var encodes proteins involved in cytoadherence an
 A:Reference number: Z20487; MUID:95330813; PMID:7606788
 A:Accession: T28626
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-2664 <SUX>
 A:Cross-references: EMBL:L40609; NID:g886376; PID:g886378; PID:AAA75398.1
 C:Genetics:
 A:Introns: 2197/3
 A>Note: var-2

Query Match 19.0%; Score 77; DB 2; Length 2664;
 Best Local Similarity 44.7%; Pred. No. 9.5;
 Matches 17; Conservative 4; Mismatches 9; Indels 8; Gaps 2;

QY 32 FCCRKEQGFYDHLRDCISCAS-----ICGQHPKOC 63
 DB 1031 FC-KEOSRLYELRLDCGSCCTGCKNNDKCAKCDKOC 1066

RESULT 4
 S34583
 serine proteinase (EC 3.4.21.-) PC6B - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
 C:Accession: S34583
 R:Nakagawa, T.; Murakami, K.; Nakayama, K.
 FEBS Lett. 327, 165-171, 1993
 A:Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a
 A:Reference number: S34583; MUID:93327934; PMID:8335106
 A:Accession: S34583
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1548 <NAK>
 A:Cross-references: GB:D17583; NID:9407344; PID:BA04507.1; PID:DL005033; PID:g440374
 C:Keywords: hydrolase, serine proteinase

Query Match 18.5%; Score 75; DB 2; Length 1548;
 Best Local Similarity 25.0%; Pred. No. 10;

Matches 21; Conservative 5; Mismatches 34; Indels 24; Gaps 3;
 QY 1 CPEBYMDPLGTCMSCKTICNHQ-----QRTCAFCCKRQGRKYPD 43
 DB 1152 CAAYEMDEGSHRCOPCKKCSRCGSEEDQCTCPRTFLNTTCVKEC---PEGHTD 1208

QY 44 HLRLDCISCASIC---GQHPKOC 63
 DB 1209 KDSQCIVLCHSSCRTPGPHSMQC 1232

RESULT 5
 JC5571
 subtilisin-like proteinase (EC 3.4.21.-) PACE4 precursor, splice form E-II -
 C:Species: Homo sapiens (man)
 C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
 C:Accession: JC5571
 R:Mori, K.; Kii, S.; Tsuji, A.; Nagahama, M.; Imamaki, A.; Hayashi, K.; Akamatsu, T.; N
 J. Biochem. 121, 941-948, 1997
 A:Title: A novel human PACE4 isoform, PACE4E is an active processing protease containin
 A:Reference number: JC5570; MUID:97335942; PMID:9192737
 A:Accession: JC5571
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-962 <MOB>
 A:Cross-references: DBJ:D87994; NID:g2330550; PID:BA021792.1; PID:g2330551
 A:Experimental source: brain cerebellum
 C:Comment: This enzyme is a processing protease and responsible for processing of vario
 ch it is retained intracellularly.
 C:Genetics:
 A:Gene: GDB:PACE4
 A:Cross-references: GDB:131390; OMIM:167405
 A:Map position: 15q26-15q26
 C:Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
 C:Keywords: glycoprotein; hydrolase; serine proteinase
 F:1-62/Domain: signal sequence #status predicted <SIG>
 F:63-149/Domain: propeptide #status predicted <PRO>
 F:156-434/Domain: subtilisin homology <SBT>
 F:938-954/Domain: hydrophobic cluster #status predicted <HCL>
 F:205-246,347,420/Active site: Asp, His, Asn, Ser #status predicted
 F:259/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.4%; Score 74.5; DB 2; Length 962;
 Best Local Similarity 27.8%; Pred. No. 8.4;
 Matches 15; Conservative 9; Mismatches 23; Indels 7; Gaps 3;

QY 14 CMSCKT-ICNHQRTCAFCCKRQGFYDHLRDCISC---ASIGQHPKOC 63
 DB 751 CUSCRGPFYHDEMTCTVLC---PAGFYADESQNCKLCKHPCKKCYDEPKC 801

RESULT 6
 A39490
 subtilisin-like proteinase (EC 3.4.21.-) PACE4 precursor, splice form A - hu
 N:Alternate names: Kexin homolog
 C:Species: Homo sapiens (man)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Mar-2000
 C:Accession: A39490
 R:Kiefer, M.C.; Tucker, J.E.; Joh, R.; Landsberg, K.E.; Saltman, D.; Barr, P.J.
 DNA Cell Biol. 10, 757-769, 1991
 A:Title: Identification of a second human subtilisin-like protease gene in the fee/fps
 A:Reference number: A39490; MUID:92075167; PMID:1741956
 A:Accession: A39490
 A:Molecule type: mRNA
 A:Residues: 1-969 <KIB>
 A:Cross-references: GB:M80482; NID:g189531; PID:AAA59998.1; PID:g189532
 C:Genetics:
 A:Gene: GDB:PACE4
 A:Cross-references: GDB:131390; OMIM:167405
 A:Map position: 15q26-15q26
 C:Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
 C:Keywords: alternative splicing; hydrolase; serine proteinase
 F:150-963/Product: serine proteinase PACE4 #status predicted <SIG>

F:196-434/Domain: subtilisin homology <SBT>
F:205,246,420/Active site: Asp, His, Ser #status predicted

Query Match 18.4%; Score 74.5; DB 1; Length 969;
Best Local Similarity 27.8%; Pred. No. 8.4;
Matches 15; Conservative 9; Mismatches 23; Indels 7; Gaps 3;

QY 14 CMCKT-ICNHQSQRTCAAFCCRKEQGFYDHLRLDRCISC---ASICGQHPKQC 63
DB 764 CLSCRRGFYHHQEMTCTVTLCTLC---PAGFYADESQKNCLKCHPSCKKCVDEPEKC 814

RESULT 7
JCS570
subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form E-I - H
C:Species: Homo sapiens (man)
C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C:Accession: JCS570
R:Mori, K.; Kii, S.; Tsuji, A.; Nagahama, M.; Imamaki, A.; Hayashi, K.; Akamatsu, T.; Na
J. Biochem. 121, 941-948, 1997
A:Title: A novel human PACE4 isoform. PACE4E is an active processing protease containing
A:Reference number: JCS570; MUID:97335942; PMID:9192737
A:Accession: JCS570
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-975 <MOR>
A:Cross-references: DBJ:D87993; NID:g2330548; PIDN:BAA21791.1; PID:g2330549
A:Experimental source: brain cerebellum
C:Comment: This enzyme is a processing protease and responsible for processing of various
ch it is retained intracellularly.
C:Genetics:
A:Gene: GDB:PACE4
A:Cross-references: GDB:131390; OMIM:167405
A:Map position: 15q26-15q26
C:Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C:Keywords: alternative splicing; glycoprotein; hydrolase; serine proteinase
F:1-62/Domain: signal sequence #status predicted <SIG>
F:63-149/Domain: propeptide #status predicted <PRO>
F:196-434/Domain: subtilisin homology <SBT>
F:952-968/Domain: hydrophobic cluster #status predicted <HCL>
F:205,246,347,420/Active site: Asp, His, Asn, Ser #status predicted
F:259/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 18.4%; Score 74.5; DB 2; Length 975;
Best Local Similarity 27.8%; Pred. No. 8.4;
Matches 15; Conservative 9; Mismatches 23; Indels 7; Gaps 3;

QY 14 CMCKT-ICNHQSQRTCAAFCCRKEQGFYDHLRLDRCISC---ASICGQHPKQC 63
DB 764 CLSCRRGFYHHQEMTCTVTLCTLC---PAGFYADESQKNCLKCHPSCKKCVDEPEKC 814

RESULT 8
I46059
beta-1 integrin subunit - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Aug-1999
C:Accession: I46059
R:MacLaren, L.A.; Wildeman, A.G.
Biol. Reprod. 53, 153-165, 1995
A:Title: Fibronectin receptors in preimplantation development: cloning, expression, and
A:Reference number: I46059; MUID:95399478; PMID:7545439
A:Accession: I46059
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-773 <MAC>
A:Cross-references: EMBL:U10865; NID:q520520; PIDN:AAA80571.1; PID:q520521
C:Superfamily: integrin beta chain; laminin-type EGF-like homology

Query Match 17.7%; Score 71.5; DB 2; Length 773;
Best Local Similarity 32.8%; Pred. No. 14;
Matches 21; Conservative 7; Mismatches 29; Indels 7; Gaps 4;

QY 8 DPLIGT--CMCKT-TCNHQSQRTCAAFCCRKEQGFYDHLRLDRCISCASICGQHPK--Q 62
DB 568 DCSLIGTSCMAVNGQICNGRGVCECGA--CKCTDPRKPGPTCEMCTCLGVCVAHKECVQ 625

QY 63 CAYF 66
DB 626 CRAP 629

RESULT 9
I52527
PACE4A - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
C:Accession: I52527
R:Hosaka, M.; Murakami, K.; Nakayama, K.
Biomed. Res. 15, 383-390, 1994
A:Title: PACE4A is a ubiquitous endoprotease that has similar but not identical substrates
A:Reference number: I52527
A:Accession: I52527
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-932 <RES>
A:Cross-references: GB:D50060; NID:g769700; PIDN:BAA08777.1; PID:g769701
C:Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
F:172-410/Domain: subtilisin homology <SBT>

Query Match 17.7%; Score 71.5; DB 2; Length 932;
Best Local Similarity 29.6%; Pred. No. 16;
Matches 16; Conservative 7; Mismatches 24; Indels 7; Gaps 3;

QY 14 CMCKT-ICNHQSQRTCAAFCCRKEQGFYDHLRLDRCISC---ASICGQHPKQC 63
DB 727 CLSCRRGFYHHQEMTCTVTLCTLC---PAGFYADESQRLCHPSCKKCVDEPEKC 777

RESULT 10
A43434
furin (EC 3.4.21.75) 2 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Mar-2000
C:Accession: A43434
R:Reboerck, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, E.;
J. Biol. Chem. 267, 17208-17215, 1992
A:Title: Cloning and functional expression of Dfurin2, a subtilisin-like proprotein proc
A:Reference number: A43434; MUID:92381036; PMID:1512259
A:Accession: A43434
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1680 <ROE>
A:Cross-references: GB:M94375; NID:gl57461; PID:gl57462
A:Note: sequence extracted from NCBI backbone (NCBIN:111933, NCBIP:111934)
C:Genetics:
A:Gene: FlyBase:Fur2
A:Cross-references: FlyBase:FBN0004598
C:Superfamily: subtilisin homology
C:Keywords: hydrolase; serine proteinase; transmembrane protein
F:409-652/Domain: subtilisin homology <SBT>
F:418,457,638/Active site: Asp, His, Ser #status predicted

Query Match 17.7%; Score 71.5; DB 2; Length 1680;
Best Local Similarity 32.1%; Pred. No. 23;
Matches 18; Conservative 6; Mismatches 23; Indels 9; Gaps 3;

QY 1 CPBQYWDPLLGTCMCKTICNHQSQRTC---AAFCCRKEQGFYDHLRLDRCISC 52
DB 1387 CLSQYVYDTSATCKTC-----HDSCSRSGPGQFCKGCVPPPLHLDQLNSQCVSC 1437

RESULT 11
AD0715
conserved hypothetical protein STY1859 [imported] - Salmonella enterica subsp. enterica
C:Species: Salmonella enterica subsp. enterica serovar typhi

A>Note: this species has also been called *Salmonella typhi*
C.Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C.Accession: A00715
R.Parthill J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Mole, S.; O'Gaora, P.
Nature 413, 846-852, 2001.
A.Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A>Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
A.Reference number: A0502; PMID:1167608
A.Accession: A00715
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-108 <PAR>
A.Cross-references: GB:AL51382; PIDN:CAD02093.1; PID:g16502928; GSPDB:GN00176
C.Genetics:
A.Gene: STY1859

Query Match 17.5%; Score 71; DB 2; Length 108;
Best Local Similarity 32.3%; Pred. No. 4.2;
Matches 21; Conservative 5; Mismatches 19; Indels 20; Gaps 5;
DB 59 EESYQKL---CRLCADIC-----KCAECARHD---HDH---CQNCARAC---SQ 98
QY 3 EEOYWPDLGTGCMSCRTICNHOSORTCAFCCKREQGFYDHLRDCISCAISCGHPKQ 62
DB 59 EESYQKL---CRLCADIC-----KCAECARHD---HDH---CQNCARAC---SQ 98
QY 63 CAYFC 67
DB 99 CADAC 103

RESULT 12
158388
Protein-tyrosine kinase (EC 2.7.1.112), receptor type tek precursor - human
C.Species: Homo sapiens (man)
C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C.Accession: I58388
R.Ziegler, S.F.; Bird, T.A.; Scherlinger, J.A.; Schooley, K.A.; Baum, P.R.
Oncogene 8, 663-670, 1993
A>Title: Molecular cloning and characterization of a novel receptor protein tyrosine kin
A.Reference number: I58388; MUID:93173509; PMID:8382358
A.Accession: I58388
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Cross-references: GB:L06139; NID:9292823; PIDN:AAA61139.1; PID:9292824
C.Genetics:
A.Gene: GDB:TEK
A.Cross-references: GDB:344185; OMIM:600221
A.Map position: 9p21-9p21
C.Function:
A.Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C.Superfamily: protein-tyrosine kinase, receptor type Ite; EGF homology; fibronectin ty
C.Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosph
F:1-22/Domain: signal sequence #status predicted <SIG>
F:123-1124/Product: protein-tyrosine kinase predicted <IM>
F:123-1024/Domain: immunoglobulin homology <IM1>
F:135-137/Region: cell attachment (R-G-D) motif
F:211-251/Domain: EGF homology <EG1>
F:255-298/Domain: EGF homology <EG2>
F:302-340/Domain: EGF homology <EG3>
F:364-426/Domain: immunoglobulin homology <IM2>
F:447-527/Domain: fibronectin type III repeat homology <FN3A>
F:542-625/Domain: fibronectin type III repeat homology <FN3B>
F:638-720/Domain: fibronectin type III repeat homology <FN3C>
F:752-772/Domain: transmembrane #status predicted <TM>
F:822-1099/Domain: protein kinase #status predicted <KIN>
F:830-838/Region: protein kinase ATP-binding motif
F:140-158-399, 428, 464, 560, 596, 649, 691/Binding site: carbohydrate (Asn) (covalent) #statu
F:855, 872, 964/Active site: Lys, Glu, Asp #status predicted

Query Match 17.3%; Score 70; DB 1; Length 1124;
Best Local Similarity 26.4%; Pred. No. 25;

Matches 24; Conservative 4; Mismatches 37; Indels 26; Gaps 3;
QY 3 EEOYDP---LLGTGM-----SCRTICN-HOSORTCAFCCKR 36
DB 212 EAKXKRGPECNHLCSTACMNNGVCHEDTGECICPRGMATCEACALHFRGRTCKRCGQ 271
QY 37 EOGKEVDHLRDCISCAISCGHPKQCAVFC 67
DB 272 ECKSYVFCFLPDPYGCSCATGMKGLQCNAC 302

RESULT 13
S01659
Integrin beta-1 chain precursor - mouse
C.Species: Mus musculus (house mouse)
C.Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 20-Aug-1999
C.Accession: S01659
R.Tominaga, S.I.
FEBS Lett. 238, 315-319, 1988
A>Title: Murine mRNA for the beta-subunit of integrin is increased in BALB/c-3T3 cells
A.Reference number: S01659; MUID:89005707; PMID:3262537
A.Accession: S01659
A.Molecule type: mRNA
A.Residues: 1-798 <TOM>
A.Cross-references: EMBL:Y00769; NID:952721; PIDN:CAA68738.1; PID:952722
A>Note: the authors translated the codon ATT for residue 696 as Leu
C.Superfamily: integrin beta chain; laminin-type EGF-like homology
C.Keywords: cell adhesion; cytoskeleton; duplication; heterodimer; membrane protein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-798/Product: integrin beta-1 chain #status predicted <MAT>

Query Match 17.2%; Score 69.5; DB 2; Length 798;
Best Local Similarity 29.3%; Pred. No. 22;
Matches 17; Conservative 8; Mismatches 28; Indels 5; Gaps 3;
QY 12 GTCMCK-TICNHOSORTCAFCCKREQGFYDHLRDCISCAISCGHPK--QCAVFC 66
DB 597 GPLASNGQICNGRIGCEGA--CKCTPKRGPGTCCTGTCGACAHKEVCQCRAP 652

RESULT 14
IYM5FB
fibronectin receptor beta chain precursor - mouse
C.Species: Mus musculus (house mouse)
C.Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-Jul-1999
C.Accession: P0104; B60597
R.Holers, V.M.; Ruff, T.G.; Parks, D.L.; McDonald, J.A.; Ballard, L.L.; Brown, E.J.
J. Exp. Med. 169, 1589-1605, 1989
A>Title: Molecular cloning of a murine fibronectin receptor and its expression during i
for histocompatibility complex class II.
A.Reference number: P0104; MUID:89235580; PMID:2523953
A.Accession: P0104
A.Molecule type: mRNA
A.Residues: 1-799 <HOL>
A.Cross-references: GB:X15202; GB:Y00818; NID:950986; PIDN:CAA33372.1; PID:g762977
A.Experimental source: strain BALB/c
A.Note: the cDNA clone was missing the first nucleotide of Met-1
R.Rybeck, R.P.; Madonald-Bravo, H.; Zerial, M.; Bravo, R.
Exp. Cell Res. 180, 537-545, 1989
A>Title: Coordinate induction of fibronectin, fibronectin receptor, tropomyosin, and ac
A.Reference number: A60597; MUID:89121031; PMID:2521606
A.Accession: B60597
A.Status: nucleic acid sequence not shown; not compared with conceptual translation
A.Molecule type: mRNA
A.Residues: 596-799 <RYS>
C.Comment: The receptor is a heterodimer of alpha and beta chains.
C.Superfamily: integrin beta chain; laminin-type EGF-like homology
C.Keywords: cell adhesion; duplication; glycoprotein; heterodimer; receptor; transmembr
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-799/Product: fibronectin receptor beta chain #status predicted <MAT>
F:21-729/Domain: extracellular #status predicted <EXT>
F:730-752/Domain: transmembrane #status predicted <TRA>
F:753-799/Domain: intracellular #status predicted <INT>

F:50,94,97,212,269,363,406,417,482,521,585,670/Binding site: carbohydrate (Asn) (covalent)

Query Match 17.2%; Score 69.5; DB 1; Length 799;
 Best Local Similarity 29.3%; Pred. No. 22;
 Matches 17; Conservative 8; Mismatches 28; Indels 5; Gaps 3;
 QY 12 GTCMSCK-TICHQSQRTCAAFCCCKEKGKFDYHLRLDCISCASICGQHPK--QCAIFY 66
 Db 598 GPCLASNGQICNGRIGCEGA--CKTDPKFGPTCCTCQTLGVCAEHKEVCQCRAF 653

RESULT 15

G02428
 subtilisin-like proprotein convertase (EC 3.4.21.-) 5 precursor - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Mar-2000
 C:Accession: G02428
 R:Reudelhuber, T.L.
 submitted to the EMBL Data Library, February 1996
 A:Reference number: H01242
 A:Accession: G02428
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-899 <REU>
 A:Cross-references: EMBL:U49114; NID:gl218057; PIDN:AAA91807.1; PID:gl218058
 C:Gene: PCS
 C:Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
 C:Keywords: hydrolase, serine proteinase
 F:148-386/Domain: subtilisin homology <SBT>

Query Match 17.0%; Score 69; DB 2; Length 899;
 Best Local Similarity 26.0%; Pred. No. 27;
 Matches 19; Conservative 7; Mismatches 23; Indels 24; Gaps 5;

QY 1 CPEDQYWDPLLTGTCMSCKTICNHQSQRTCAAF--C--CRK-----EQGKFYD 43
 Db 710 CPDGSYQDTKKNLCRKSENC-----KTCTEPHNTCTCRDGLSLQGSRCVSCDGRYFN 764
 QY 44 HLLRDCISCASIC 56
 Db 765 G--QDCQPCHRFC 775

Search completed: January 7, 2003, 09:41:19
 Job time : 10.5714 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:31:59 ; Search time 5.03759 Seconds
(without alignments)
551.635 Million cell updates/sec

Title: US-09-855-158-16

Perfect score: 405

Sequence: 1 CPBEQYWDPLGLTCTMCKTI.....DCISCASICGHPKQCAAYFC 67

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	393	97.0	293	T13X_HUMAN	O14836 homo sapien
2	256	63.2	249	T13X_MOUSE	O94835 mus musculu
3	86.5	21.4	971	BECK_MOUSE	O92011 mus musculu
4	84.5	20.9	971	RECK_HUMAN	O95980 homo sapien
5	76.5	18.9	354	VEGD_HUMAN	O93915 homo sapien
6	76	18.8	297	XEDA_HUMAN	Q94945 homo sapien
7	75	18.5	1877	PK5_MOUSE	Q94592 mus musculu
8	74.5	18.4	969	PAC4_HUMAN	P29122 homo sapien
9	71.5	17.7	773	ITB1_BOVIN	P53712 bos taurus
10	71.5	17.7	1680	FUR2_DROME	P30432 drosophila
11	70	17.3	1124	TIE2_HUMAN	Q02763 homo sapien
12	69.5	17.2	798	TIE2_MOUSE	P09055 mus musculu
13	69	17.0	913	PK5_HUMAN	Q92824 homo sapien
14	68.5	16.9	501	TRA2_MOUSE	P39429 mus musculu
15	67.5	16.7	3084	LMA1_MOUSE	P19137 mus musculu
16	67	16.5	1210	EGFR_MOUSE	Q01279 mus musculu
17	67	16.5	3110	LMA2_HUMAN	P24043 homo sapien
18	66.5	16.4	184	TR17_HUMAN	Q02223 homo sapien
19	66.5	16.4	798	ITB1_FELCA	P53713 felis silve
20	66.5	16.4	937	PAC4_RAT	Q63415 rattus norv
21	66	16.3	60	MT_ICTPU	Q93571 ictalurus p
22	66	16.3	1122	TIE2_MOUSE	Q02858 mus musculu
23	66	16.3	1210	EGFR_HUMAN	P00533 homo sapien
24	65.5	16.2	60	MT_GADMO	P51902 gadus morhu
25	65.5	16.2	358	VEGD_MOUSE	P97946 mus musculu
26	65.5	16.2	1426	EGFR_DROME	P04412 drosophila
27	65	16.0	739	ITB1_RAT	P49134 rattus norv
28	65	16.0	1339	ERB3_HUMAN	Q62799 rattus norv
29	65	16.0	1342	ERB3_HUMAN	P21860 homo sapien
30	65	16.0	1696	1 PK5_BRACL	Q9PJ15 branchiosto
31	65	16.0	1877	1 PK5_RAT	P41413 rattus norv
32	65	16.0	2569	1 LMA3_MOUSE	Q61789 mus musculu
33	65	16.0	3106	1 LMA2_MOUSE	Q06075 mus musculu

34	64.5	15.9	443	1	FBL4_MOUSE	Q9evj9 mus musculu
35	64.5	15.9	798	1	ITB1_XENLA	P12606 xenopus lae
36	64	15.8	97	1	ECLH_DROME	Q07892 drosophila
37	64	15.8	119	1	ANTA_HAEGH	P16242 haementeria
38	64	15.8	1125	1	TIE2_BOVIN	Q06807 bos taurus
39	63.5	15.7	388	1	SH4_HUMAN	Q13839 homo sapien
40	63.5	15.7	400	1	LMB_HIKME	Q25092 hirudo medi
41	63.5	15.7	2482	1	WVF_PIG	Q28833 sus scrofa
42	63	15.6	474	1	TR1B_MOUSE	P25119 mus musculu
43	63	15.6	819	1	MTFC_HABIN	P71397 haemophilus
44	62.5	15.4	60	1	MTA_THERC	P52721 thermarces
45	62.5	15.4	388	1	SH4_CAVPO	O70528 cavia porce

ALIGNMENTS

RESULT 1
T13X_HUMAN
ID T13X_HUMAN STANDARD; PRT; 293 AA.
AC O14836;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE tumor necrosis factor receptor superfamily member 13B (Transmembrane activator and CAML interactor).
GN TNFRSF13B OR TACI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=97458245; PubMed=9311921;
RA von Buelow G.-U., Bram R.J.;
RT "NF-AT activation induced by a CAML-interacting member of the tumor necrosis factor receptor superfamily.";
RL Science 278:138-141(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RX Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP FUNCTION
RX MEDLINE=20519647; PubMed=10956646;
RA Gan Y., Bressette D., Carrell J.A., Kaufman T., Feng P., Taylor K., Wu Y., Cho Y.H., Garcia A.D., Gollatz E., Dimke D., Lafleur D., Migone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J., Olsen H.S., Kanakaraj P., Moore P.A., Baker K.P.;
RT "Tumor necrosis factor (TNF) receptor superfamily member TACI is a high affinity receptor for TNF family members APRIL and BLYS.";
RL J. Biol. Chem. 275:35478-35485(2000).
RN [4]
RP FUNCTION.
RX MEDLINE=21170294; PubMed=10973284;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M., McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M., Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating humoral immunity.";
RL Nat. Immunol. 1:252-256(2000).
RN [5]
RP FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAPF/BLYS that binds both ligands with similar high affinity. Mediates calcineurin-dependent activation of NF-AT, as well as activation of NF-kappa-B and AP-1 involved in the stimulation of B- and T-cell function and the regulation of humoral immunity.
RN [6]
RP SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal domain of CAML with its C-terminus.
RN [7]
RP TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small intestine and peripheral blood leukocytes. Expressed in resting B-

cells and activated T-cells, but not in resting T-cells.
 CC - SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
 CC - CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.
 CC -----
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 CC -----
 CC EMBL, AF023614; AAC51790.1; -
 CC EMBL, BC028072; AAH28072.1; -
 CC GenBank, U00001; U00001.1; -
 CC MIM: 604907; -
 CC InterPro: IPR001368; TNFR_C6.
 CC PROSITE, PS00652; TNFR_NGFR_1; 1.
 CC PROSITE, PS00650; TNFR_NGFR_2; FALSE NEG.
 CC Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;
 CC Repeat.
 CC DOMAIN 1 165 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 166 186 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 CC (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC REPEAT 33 67 TNFR-CYS 1.
 CC REPEAT 70 104 TNFR-CYS 2.
 CC DISULFID 34 47 BY SIMILARITY.
 CC DISULFID 47 62 BY SIMILARITY.
 CC DISULFID 50 62 BY SIMILARITY.
 CC DISULFID 54 66 BY SIMILARITY.
 CC DISULFID 71 86 BY SIMILARITY.
 CC DISULFID 89 100 BY SIMILARITY.
 CC DISULFID 93 104 BY SIMILARITY.
 CC CAROXYD 128 128 N-LINKED (GLCNAC...) (POTENTIAL).
 CC CYS 251 251 P -> D (IN REF. 2).
 CC SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;
 CC
 CC Query Match 97.0%; Score 393; DB 1; Length 293;
 CC Best Local Similarity 94.4%; Pred. No. 66-34;
 CC Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 CC
 CC QY 1 CEEQYWDPLGTGCMSCKTIQNHQSORTCAAF-CKRKGKPYDHLRDCISGASIC 56
 CC 34 CEEQYWDPLGTGCMSCKTIQNHQSORTCAAFCRSLCKRKGKPYDHLRDCISGASIC 93
 CC DB
 CC QY 57 GQHPKOCAYFC 67
 CC 94 GQHPKOCAYFC 104
 CC DB
 CC
 CC RESULT 2
 CC T13X MOUSE STANDARD; PRT; 249 AA.
 CC ID T13X MOUSE
 CC AC 09RT35; 09DB23; 249 AA.
 CC DT 15-JUN-2002 (Rel. 41, Created)
 CC DT 15-JUN-2002 (Rel. 41, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
 CC activator and CAML interactor).
 CC GN TNFRSF13B OR TAC1.
 CC OS Mus musculus (Mouse).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC OX NCBI_TaxId=10090;
 CC RN SEQUENCE FROM N.A.
 CC RP Tissue=Spleen;
 CC RX MEDLINE=2117254; PubMed=1081172;
 CC RA Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A.,
 CC Dixit V.M.,
 CC "Identification of a receptor for Blys demonstrates a crucial role in
 CC humoral immunity.";
 CC Nat. Immunol. 1:37-41 (2000).
 CC RT

RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6J; Tissue=Lung;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai T., Shnagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Yukitani Y., Kono H., Adachi U., Fukuda I.,
 RA Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasuyama T., Saito K.,
 RA Kato K., Matsuda H.A., Ashburner M., Balasov S., Casavant T.,
 RA Fleischmann J., Gaasterland P., Glaser C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nakado I., Pesole G., Quackenbush J.,
 RA Schmitt L.W., Stead E., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barin G.,
 RA Blake J., Botfield D., Boujra N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaez P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohetsuki S.,
 RA Hayashizaki Y.,
 RA "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690 (2001).
 RL [3]
 RP FUNCTION.
 RX MEDLINE=20341628; PubMed=10860535;
 RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
 RA Thellin L.E., Colombero A., Solovjev I., Lee F., McCabe S., Elliott R.,
 RA Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,
 RA Meng S.-Y., Boyle W.J., Heu H.,
 RA "TRAC1 is a TRAF-interacting receptor for TRAF-1, a tumor necrosis
 RA factor family member involved in B cell regulation.";
 RL J. Exp. Med. 192:1137-1143 (2000).
 RL [4]
 RP FUNCTION.
 RX MEDLINE=21322748; PubMed=11429548;
 RA Wang H., Marsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,
 RA Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.,
 RA "TRAC1-11gand interactions are required for T cell activation and
 RA collagen-induced arthritis in mice.";
 RL Nat. Immunol. 2:632-637 (2001).
 CC - FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TAL1/BAFF/Blys
 CC that binds both ligands with similar high affinity. Mediates
 CC calcineurin-dependent activation of NF-AT, as well as activation
 CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
 CC cell function and the regulation of humoral immunity (by
 CC similarity).
 CC - SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
 CC domain of CAMLg with its C-terminus (by similarity).
 CC - SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC - SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
 CC -----
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 CC -----
 CC EMBL, AF257673; AAC00081.1; -
 CC EMBL, AF257673; AAC00081.1; -
 CC MGD, MGI:1889411; TNFR_NGFR_1; 1.
 CC PROSITE, PS00652; TNFR_NGFR_1; 1.
 CC PROSITE, PS00652; TNFR_NGFR_2; 2.
 CC Receptor; Immune response; Signal-anchor; Transmembrane; Repeat.
 CC DOMAIN 1 128
 CC TRANSMEM 129 149
 CC CYTOPLASMIC (POTENTIAL).
 CC REPEAT 5 38
 CC REPEAT 42 76
 CC

FT DISULFID 6 19 BY SIMILARITY.
 FT DISULFID 22 34 BY SIMILARITY.
 FT DISULFID 26 38 BY SIMILARITY.
 FT DISULFID 43 58 BY SIMILARITY.
 FT DISULFID 61 72 BY SIMILARITY.
 FT DISULFID 65 76 BY SIMILARITY.
 FT CONFLICT 137
 FT CONFLICT 137 I -> F (IN REF. 2).
 SQ SEQUENCE 249 AA; 26947 MW; CB2F2D61C2931D81 CRC64;

Query Match 63.2%; Score 256; DB 1; Length 249;
 Best Local Similarity 57.7%; Pred. No. 7.8e-20;
 Matches 41; Conservative 11; Mismatches 15; Indels 4; Gaps 1;

QY 1 CPBEQYWDPLGLTGMCKTICNHQSORTCAAF-----CRKEQKGYDHLRLDCISCASIC 56
 ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 Db 6 CPKQYWDSSRKSCVSCALTCSSQRTCTDCKFNCRKQGRYYDHLGLGVSCDSTC 65

QY 57 GQHPKQCAVFC 67
 ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 Db 66 TQHPQCAHFC 76

RESULT 3
 RECK_MOUSE STANDARD; PRT; 971 AA.

AC Q9Z0U1;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Reversion-inducing cysteine-rich protein with Kazal motifs precursor (mRECK).
 GN RECK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99007295; PubMed=9789069;
 RA Takahashi C., Sheng Z., Horan T.P., Kitayama H., Maki M., Hitomi K.,
 RA Kitaura Y., Takai S., Sasahara R.M., Horimoto A., Ikawa Y.,
 RA Ratzkin B.J., Arakawa T., Noda M.;
 RT "Regulation of matrix metalloproteinase-9 and inhibition of tumor
 invasion by the membrane-anchored glycoprotein RECK.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:13221-13226(1998).
 CC -!- FUNCTION: Negatively regulates matrix metalloproteinase-9 (MMP-9)
 by suppressing MMP-9 secretion, and by direct inhibition of its
 enzymatic activity. RECK down-regulation by oncogenic signals may
 facilitate tumor invasion and metastasis. Appears to also
 regulate MMP-2 and MT1-MMP, which are involved in cancer
 progression (By similarity).
 CC -!- SUBUNIT: Interacts with MMP-9.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -!- DEVELOPMENTAL STAGE: In E10.5 embryos the RECK protein is widely
 expressed in mesenchymal tissues and is relatively abundant in the
 marginal zone of the neural tube and large blood vessels such as
 the aorta.
 CC -!- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; A2006960; BAA34061.1; -
 DR WGD; MG1; 1855698; RECK.
 DR InterPro; IPR0023350; Kazal.
 DR Pfam; PF00050; Kazal; 2.
 DR SMART; SM00280; KAZAL; 2.
 DR PROSITE; PS00282; KAZAL; 1.

KW Signal; Glycoprotein; GPI-anchor; Serine protease inhibitor;
 KW Membrane; Anti-oncogene; Repeat.
 FT CHAIN 1 22 POTENTIAL.
 FT CHAIN 23 942 REVERSION-INDUCING CYSTEINE-RICH PROTEIN
 WITH KAZAL MOTIFS.
 FT PROPEP 943 971 REMOVED IN MATURE FORM (POTENTIAL).
 FT LIPID 942 942 GPI-ANCHOR (POTENTIAL).
 FT DOMAIN 633 677 KAZAL-LIKE 1.
 FT DOMAIN 704 750 KAZAL-LIKE 2 (DEGENERATE).
 FT DOMAIN 751 787 KAZAL-LIKE 3 (DEGENERATE).
 FT DOMAIN 37 338 5 X KNOT REPEATS.
 FT REPEAT 37 84 KNOT 1.
 FT REPEAT 104 141 KNOT 2.
 FT REPEAT 151 197 KNOT 3.
 FT REPEAT 216 263 KNOT 4.
 FT REPEAT 292 338 KNOT 5.
 FT DISULFID 635 654 BY SIMILARITY.
 FT DISULFID 633 658 BY SIMILARITY.
 FT DISULFID 643 677 BY SIMILARITY.
 FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 971 AA; 106134 MW; 2FC8EBE38A20F86D CRC64;

Query Match 21.4%; Score 86.5; DB 1; Length 971;
 Best Local Similarity 26.8%; Pred. No. 0.077;
 Matches 26; Conservative 8; Mismatches 28; Indels 35; Gaps 6;

QY 1 CPEE--QYWDPL-----LGTC-----MSCKTICNHQSORTCAAFCCRKE 37
 ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 Db 74 CPETWVEIWSMNSLPGVFKKSDGWGLGCCELAIGLECRACKQACKQASKNDISKVRKE 133

QY 38 QGKFYDHLRLDCIS-----CASICGQHPKQCAVFC 67
 ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 Db 134 ---YENALFSCISRNEMSGSVCCSVAGHH-TNCREFC 165

RESULT 4
 RECK_HUMAN STANDARD; PRT; 971 AA.

AC O95980; OSW37;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Reversion-inducing cysteine-rich protein with Kazal motifs precursor (hRECK) (Suppressor of tumorigenicity 15) (STI15).
 GN RECK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND N-GLYCOSYLATION.
 RX TISSUE=Fibroblast;
 RX MEDLINE=99007295; PubMed=9789069;
 RA Takahashi C., Sheng Z., Horan T.P., Kitayama H., Maki M., Hitomi K.,
 RA Kitaura Y., Takai S., Sasahara R.M., Horimoto A., Ikawa Y.,
 RA Ratzkin B.J., Arakawa T., Noda M.;
 RT "Regulation of matrix metalloproteinase-9 and inhibition of tumor
 invasion by the membrane-anchored glycoprotein RECK.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:13221-13226(1998).
 CC -!- FUNCTION: Negatively regulates matrix metalloproteinase-9 (MMP-9)
 by suppressing MMP-9 secretion and by direct inhibition of its
 enzymatic activity. RECK down-regulation by oncogenic signals may
 facilitate tumor invasion and metastasis. Appears to also
 regulate MMP-2 and MT1-MMP, which are involved in cancer
 progression.
 CC -!- SUBUNIT: Interacts with MMP-9.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -!- DEVELOPMENTAL STAGE: In E10.5 embryos the RECK protein is widely
 expressed in mesenchymal tissues and is relatively abundant in the
 marginal zone of the neural tube and large blood vessels such as
 the aorta.
 CC -!- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; A2006960; BAA34061.1; -
 DR WGD; MG1; 1855698; RECK.
 DR InterPro; IPR0023350; Kazal.
 DR Pfam; PF00050; Kazal; 2.
 DR SMART; SM00280; KAZAL; 2.
 DR PROSITE; PS00282; KAZAL; 1.

```

CC -|- SUBUNIT: Interacts with MMP-9.
CC -|- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -|- TISSUE SPECIFICITY: Expressed in various tissues and untransformed
CC cells. It is undetectable in tumor-derived cell lines and
CC oncogenically transformed cells.
CC -|- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D50406; BAA34060.1; -.
DR EMBL; AL158830; CAD1384.1; -.
DR Genew; HGNC:11345; RECK.
DR MIM; 605227; -.
DR HSSP; P80424; IAN1.
DR InterPro; IPR002350; Kazal.
DR SMART; SM00280; KAZAL; 3.
DR SMART; SM00011; VWC def: 1.
DR PROSITE; PS00282; KAZAL; 1.
DR Signal; Glycoprotein; GPI-anchor; Serine protease inhibitor;
DR Membrane; Anti-oncogene; Repeat.
FT SIGNAL 1 92
FT CHAIN 23 942
FT FT REPEAT
FT FT PROPEP 943 971
FT FT LIPID 942 942
FT FT DOMAIN 632 677
FT FT DOMAIN 708 750
FT FT DOMAIN 753 787
FT FT DOMAIN 37 338
FT FT DOMAIN 37 84
FT FT REPEAT 104 141
FT FT REPEAT 151 197
FT FT REPEAT 216 263
FT FT REPEAT 292 338
FT FT DISULFID 635 654
FT FT DISULFID 633 658
FT FT CARBOHYD 643 677
FT FT CARBOHYD 39 39
FT FT CARBOHYD 86 86
FT FT CARBOHYD 200 200
FT FT CARBOHYD 297 297
FT FT CARBOHYD 352 352
FT SEQUENCE 971 AA, 106456 MW, 173D47D6AE6F834 CRC64;

Query Match 20.9%; Score 84.5; DB 1; Length 971;
Best Local Similarity 25.8%; Pred. No. 0.12; 27; Indels 35; Gaps 6;
Matches 25; Conservative 10; Mismatches

QY 1 CPEE--QYWDPL-----IGTC-----MSCKTICNHSQRTCAFCCKRE 37
DB 74 CPEIWEIWNCKMNSLPGVFKSGDGVNGVGGCCCLALALECRQCKQASSKNDISKVCRK 133
QY 38 OGKPYDHLRLDCIS-----CASICGHPKQCAVFC 67
DB 134 ---YENALFSCISRNEMSGVCCSYAGHH-TNCREVC 165

RESULT 5
VEGCD HUMAN STANDARD; PRT; 354 AA.
ID VEGD HUMAN
AC 043915;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
DE growth factor) (FIGF).
GN FIGF OR VEGFD.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=9734918; PubMed=9205122;
RA Yamada Y., Nezu U.-I., Shimane M., Hirata Y.;
RT "Molecular cloning of a novel vascular endothelial growth factor,
RT VEGF-D.";
RL Genomics 42:483-488(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=98140120; PubMed=9479493;
RA Rocchigiani M., Lestingi M., Luddi A., Orlandini M., Franco B.,
RA Rossi E., Ballabio A., Zuffardi O., Oliviero S.;
RT "Human FIGF: cloning, gene structure, and mapping to chromosome Xp22.1
RT between the FIGA and the GRP genes.";
RL Genomics 47:207-216(1998).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=9818549; PubMed=9435229;
RA Achen M.G., Jeltsch M., Kukk E., Maekinen T., Vitale A., Wilks A.F.,
RA Altalo K., Stacker S.A.;
RT "Vascular endothelial growth factor D (VEGF-D) is a ligand for the
RT tyrosine kinases VEGF receptor 2 (Flk1) and VEGF receptor 3 (Flt4).";
RL Proc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).
RN [4]
RP PROCESSING, AND SEQUENCE OF 89-94; 100-105 AND 206-213.
RX MEDLINE=20011413; PubMed=10542246;
RA Stacker S.A., Stevers K.L., Caesar C., Vitale A., Domagala T.,
RA Nice E.C., Koufal S., Simpson R.J., Moritz R., Karpen T.,
RA Altalo K., Achen M.G.;
RT "Biosynthesis of vascular endothelial growth factor-D involves
RT proteolytic processing which generates non-covalent homodimers.";
RL J. Biol. Chem. 274:32127-32136(1999).
RN [5]
RP FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis
RN and endothelial cell growth, stimulating their proliferation and
RN migration and also has effects on the permeability of blood
RN vessels. May function in the formation of the venous and lymphatic
RN vascular systems during embryogenesis, and also in the maintenance
RN of differentiated lymphatic endothelium in adults. Binds and
RN activates VEGFR-2 (Flk1) and VEGFR-3 (Flt4) receptors.
RN -|- SUBUNIT: Homodimer; non-covalent and antiparallel.
RN -|- SUBCELLULAR LOCATION: Secreted.
RN -|- TISSUE SPECIFICITY: Highly expressed in lung, heart, small
RN intestine and fetal lung, and at lower levels in skeletal muscle,
RN colon, and pancreas.
RN -|- PTM: Undergoes a complex proteolytic maturation which generates a
RN variety of processed secreted forms with increased activity toward
RN VEGFR-3 and VEGFR-5. VEGF-D first form an antiparallel homodimer
RN linked by disulfide bonds before secretion. The fully processed
RN VEGF-D is composed mostly of two VEGF homology domains (VHDS)
RN bound by non-covalent interactions.
RN -|- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
RN -----
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RN or send an email to license@isb-sib.ch).
RN -----
DR EMBL; D89630; BAA24264.1; -.
DR EMBL; Y12863; CAA73370.1; -.
DR EMBL; Y12864; CAA73371.1; -.
DR EMBL; Y12865; CAA73371.1; JOINED.
DR EMBL; Y12866; CAA73371.1; JOINED.
DR EMBL; Y12867; CAA73371.1; JOINED.
DR EMBL; Y12868; CAA73371.1; JOINED.

```


RC STRAIN=ICR; TISSUE=Intestine;
RX MEDLINE=93327934; PubMed=8335106;
RA Nakagawa T., Murakami K., Nakayama K.;
RT "Identification of an isoform with an extremely large Cys-rich region
of PC5, a kex2-like processing endoprotease.";
RL FEBS Lett. 327:165-171(1993).
[2]
RN SEQUENCE FROM N.A. (ISOFORM PCSA).
RP TISSUE=Brain, and Intestine;
RC MEDLINE=93224489; PubMed=8468318;
RA Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,
Nakayama K.;
RT "Identification and functional expression of a new member of the
mammalian Kex2-like processing endoprotease family: Its striking
structural similarity to PACE4.";
RL J. Biochem. 113:132-135(1993).
[3]
RN SEQUENCE FROM N.A. (ISOFORM PCSA).
RP TISSUE=Adrenal cortex;
RC MEDLINE=93342056; PubMed=8341687;
RA Lusson J., Vleau D., Hamelin J., Day R., Chretien M., Seidah N.G.;
RT "cDNA structure of the mouse and rat subtilisin/kexin-like PC5: a
candidate proprotein convertase expressed in endocrine and
nonendocrine cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
[4]
RN PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.
RP DE BIE I., Marcinkiewicz M., Matile D., Lazure C., Nakayama K.,
Bendayan M., Seidah N.G.;
RT "The isoforms of proprotein convertase PC5 are sorted to different
subcellular compartments.";
RL J. Cell Biol. 135:1261-1275(1996).
[5]
RN DEVELOPMENTAL EXPRESSION.
RP MEDLINE=96293359; PubMed=8698833;
RA Christan D.B., Califen M., Robertson E.J.;
RT "SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone
morphogenetic proteins at distinct sites during embryogenesis.";
RL J. Cell Biol. 134:181-191(1996).
[6]
RN DEVELOPMENTAL EXPRESSION.
RP MEDLINE=97436919; PubMed=2921583;
RA Rancourt S.L., Rancourt D.E.;
RT "Murine subtilisin-like proteinase SPC6 is expressed during embryonic
implantation, somitogenesis, and skeletal formation.";
RL Dev. Genet. 21:75-81(1997).
CC -I- FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPEPTASE ACTIVITY
WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE
OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF. MAY BE RESPONSIBLE
FOR THE MATURATION OF GASTROINTESTINAL PEPTIDES. MAY BE INVOLVED
IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA THE ACTIVATION
OF GROWTH FACTORS.
CC CC
CC -I- CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
PROPEPTEINS BY CLEAVAGE OF ARG-XAA-YAA-ARG-|-ZAA BONDS, WHERE XAA
CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
CC CC
CC -I- SUBCELLULAR LOCATION: PCSA IS SECRETED THROUGH THE REGULATED
SECRETORY PATHWAY. PCSB IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO
A PARACENTRIAL POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH
EARLY ENDOSOMES.
CC CC
CC -I- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS: PCSB/LONG (SHOWN HERE)
AND PCSA/SHORT ARE PRODUCED BY ALTERNATIVE SPLICING.
CC CC
CC -I- TISSUE SPECIFICITY: PCSA IS EXPRESSED IN MOST TISSUES BUT IS MOST
ABUNDANT IN THE TESTIS AND ADRENALS. PCSB IS EXPRESSED IN THE
INTESTINE, ADRENALS AND LUNG BUT NOT IN THE BRAIN.
CC CC
CC -I- DEVELOPMENTAL STAGE: HEAVILY EXPRESSED THROUGHOUT THE EMBRYO,
EXCEPT IN THE DEVELOPING NEUROUS SYSTEM, THE KIDS AND THE LIVER,
BUT MARKEDLY UPREGULATED AT DISCRETE SITES DURING DEVELOPMENT. AT
E6.5, PROMINENT EXPRESSION OBSERVED IN DIFFERENTIATING DECIDUA.
CC CC
CC AT E7.5, INTENSE EXPRESSION IN EXTRAMEMBRYONIC ENDODERM, ANIONIC AND
NASCENT MESODERM. AT 8.5, ABUNDANT EXPRESSION IN SOMITES AND YOLK
SAC FOLLOWED BY A CONFINANT EXPRESSION TO DERMATOTOME COMPARTMENT. BETWEEN
E9.5 AND E11.5, ABUNDANT EXPRESSION IN AER (THICKENED ECTODERMAL

CC		CELLS OF LIMB BUDS) . AT E12.5, EXPRESSION IN THE LIMBS IS CONFINED TO THE CONDENSING MESENCHYM SURROUNDING THE CARTILAGE. AT THIS STAGE, STRONG EXPRESSION ALSO DETECTED IN VERTEBRAL AND FACIAL CARTILAGE PRIMORDIA AND IN THE MUSCLE OF THE TONGUE. AT E16.5, ABUNDANT EXPRESSION IN EPITHELIAL CELLS OF THE INTESTINAL VILLI.
CC		ISOFORM A IS MOST ABUNDANT AT ALL STAGES BUT SIGNIFICANT LEVELS OF ISOFORM B OCCUR AT E12.5.
CC	-1-	DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE ASSISTING THE FOLDING OF THE ZMOGEN WITHIN THE ENDOPLASMIC RETICULUM.
CC	-1-	DOMAIN: AC 1 AND AC 2 (CLUSTERS OF ACIDIC AMINO ACIDS) CONTRAIN SORTING INFORMATION. AC 1 DIRECTS TGN LOCALIZATION AND INTERACTS WITH THE TGN SORTING PROTEIN PALS-1.
CC	-1-	SIMILARITY: BELONGS TO PERTIDASE FAMILY S8.
CC	-1-	SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
CC		-----
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/isb-sib.ch) .
CC		-----
DR	EMBL; D17583;	BAA04507.1; ;
DR	EMBL; D12619;	BAA02143.1; ;
DR	EMBL; L14932;	AAA74636.1; ;
DR	PfR; JX0248;	JX0248.
DR	PfR; A48225;	A48225.
DR	HSSP; Q99405;	1MPT.
DR	MEROPS;	S08_076; ;
DR	MGD; MGI:97515;	PCsk5.
DR	InterPro; IPR000561;	EGF-like.
DR	InterPro; IPR002174;	Furin-like.
DR	InterPro; IPR002684;	p domain.
DR	InterPro; IPR000209;	Peptidase_S8.
DR	Pfam; PF00082;	peptidase_S8; 1.
DR	Pfam; PF01483;	p_subtilisin.
DR	PRINTS; PR00723;	SBRTILISIN.
DR	PRODOM; PD000717;	p_domain; 1.
DR	SMART; SM00161;	EGF_3.
DR	SMART; SM00001;	EGF-like; 2.
DR	SMART; SM00261;	FU; 22.
DR	PROSITE; PS00136;	SUBTILASE_ASP; 1.
DR	PROSITE; PS00137;	SUBTILASE_HIS; 1.
DR	PROSITE; PS00138;	SUBTILASE_CSR; 1.
KW	Hydrolase;	Serine protease; Glycoprotein; Zymogen; Signal;
KW	Cleavage on pair of basic residues;	Repeat; Alternative splicing;
KV	Transmembrane.	
FT	SIGNAL	1
FT	PROPEP	35
FT	CHAIN	117
FT		
FT	DOMAIN	117
FT	TRANSMEM	1768
FT	DOMAIN	1790
FT	DOMAIN	1877
FT	DOMAIN	117
FT	DOMAIN	452
FT	DOMAIN	464
FT	DOMAIN	602
FT	DOMAIN	638
FT	DOMAIN	1753
FT	DOMAIN	1825
FT	DOMAIN	1844
FT	DOMAIN	1856
FT	SITE	116
FT	SITE	117
FT	ACT_SITE	521
FT	ACT_SITE	523
FT	ACT_SITE	173
FT	ACT_SITE	214
FT	ACT_SITE	388
FT	CABOARD	227
FT	CABOARD	383
FT	CABOARD	383
FT	CABOARD	667
FT	CABOARD	754
FT	CABOARD	804
FT	CABOARD	854
FT	CABOARD	854
FT	CABOARD	951
FT		
FT	DOMAIN	117
FT	TRANSMEM	1768
FT	DOMAIN	1790
FT	DOMAIN	1877
FT	DOMAIN	117
FT	DOMAIN	452
FT	DOMAIN	464
FT	DOMAIN	602
FT	DOMAIN	638
FT	DOMAIN	1753
FT	DOMAIN	1825
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FT	DOMAIN	1856
FT	SITE	116
FT	SITE	117
FT	ACT_SITE	521
FT	ACT_SITE	523
FT	ACT_SITE	173
FT	ACT_SITE	214
FT	ACT_SITE	388
FT	CABOARD	227
FT	CABOARD	383
FT	CABOARD	383
FT	CABOARD	667
FT	CABOARD	754
FT	CABOARD	804
FT	CABOARD	854
FT	CABOARD	854
FT	CABOARD	951
FT		
FT	DOMAIN	117
FT	TRANSMEM	1768
FT	DOMAIN	1790
FT	DOMAIN	1877
FT	DOMAIN	117
FT	DOMAIN	452
FT	DOMAIN	464
FT	DOMAIN	602
FT	DOMAIN	638
FT	DOMAIN	1753
FT	DOMAIN	1825
FT	DOMAIN	1844
FT	DOMAIN	1856
FT	SITE	116
FT	SITE	117
FT	ACT_SITE	521
FT	ACT_SITE	523
FT	ACT_SITE	173
FT	ACT_SITE	214
FT	ACT_SITE	388
FT	CABOARD	227
FT	CABOARD	383
FT	CABOARD	383
FT	CABOARD	667
FT	CABOARD	754
FT	CABOARD	804
FT	CABOARD	854
FT	CABOARD	854
FT	CABOARD	951
FT		
FT	DOMAIN	117
FT	TRANSMEM	1768
FT	DOMAIN	1790
FT	DOMAIN	1877
FT	DOMAIN	117
FT	DOMAIN	452
FT	DOMAIN	464
FT	DOMAIN	602
FT	DOMAIN	

FT CARBOHYD 1016 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1220 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1317 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1317 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1523 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1711 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1733 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 878 GSYDDQGHCHQCEASCAKCMGPTQDCISCPVTRVLD -->
 FT ATEESWAEAGFCMLVKKNLCKQKVLQQLCKCTCTFQG
 FT (IN ISOFORM PCSA).
 FT VARSPLIC 916 1877 MISSING (IN ISOFORM PCSA).
 SQ SEQUENCE 1877 AA; 203287 MW; EC850E2DF20EA1C3 CRC64;
 Query Match 18.5%; Score 75; DB 1; Length 1877;
 Best Local Similarity 25.0%; Pred. No. 2;
 Matches 21; Conservative 5; Mismatches 34; Indels 24; Gaps 3;
 QY 1 CPBEQYWDPLLGTCMCKTICNHQS-----QRTCAAFCCRKEQCKFYD 43
 DB 1481 CAAVEYWDGSHRCQPCCHKKCSGFSBQCYTCPTRETLNTICVKEC---PEGYHTD 1537
 QY 44 HLLRDCISASIC-----GOHPKQC 63
 DB 1538 KDSQCVLCHSSCRCTCEGPHSMQC 1561
 RESULT 8
 ID PAC4 HUMAN STANDARD; PRT; 969 AA.
 AC Q29122; Q15099; Q15100; Q9UEJ1; Q9UEJ2; Q9UEJ7; Q9UEJ8; Q9UEJ9;
 AC Q9UEG7; Q9Y4G9; Q9Y4H0; Q9Y4H1;
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Paired basic amino acid cleaving enzyme 4 precursor (BC 3.4.21.-.)
 DE (Subtilisin/kexin-like protease PACE4) (Subtilisin-like proprotein
 DE convertase 4) (SPC4).
 GN PAC4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN SEQUENCE FROM N.A. (ISOFORMS PACE4A-I AND PACE4B).
 RC TISSUE=Hepatosoma, and Kidney;
 RX MEDLINE=92075167; PubMed=1741956;
 RA Kiefer M.C., Tucker J.E., Joh R., Landsberg K.E., Saltman D.,
 RA Bart P.J.;
 RA "Identification of a second human subtilisin-like protease gene in
 RT the feg/fps region of chromosome 15.";
 RL DNA Cell Biol. 10:757-769(1991).
 RN SEQUENCE FROM N.A. (ISOFORMS PACE4C AND PACE4D).
 RC TISSUE=Placenta;
 RX MEDLINE=94235049; PubMed=8179631;
 RA Tsuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.,
 RA Matsuda Y.;
 RT "Identification of novel cDNAs encoding human kexin-like protease,
 RT PACE4 isoforms.";
 RL Biochem. Biophys. Res. Commun. 200:943-950(1994).
 RN ERRATUM.
 RP MEDLINE=95071480; PubMed=7980617;
 RX Tsuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.,
 RA Matsuda Y.;
 RT "Identification of novel cDNAs encoding human kexin-like protease,
 RT PACE4 isoforms.";
 RL Biochem. Biophys. Res. Commun. 204:1381-1382(1994).
 RN SEQUENCE FROM N.A. (ISOFORM PACE4A-II).
 RC TISSUE=Placenta;
 RA Mori K., Imamaki A., Kii S., Nagamune H., Nagahama M., Tsuji A.,
 RA Matsuda Y.;
 RT "Identification of a novel PACE4 isoform, PACE4E.";

Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 [5] SEQUENCE FROM N.A. (ISOFORMS PACE4E-I AND PACE4E-II).
 RN TISSUE=Cerebellum;
 RX MEDLINE=97335942; PubMed=9192737;
 RA Mori K., Kii S., Tsuji A., Nagahama M., Imamaki A., Hayashi K.,
 RA Akamatsu T., Nagamune H., Matsuda Y.;
 RT "A novel human PACE4 isoform, PACE4E is an active processing protease
 RT containing a hydrophobic cluster at the carboxy terminus.";
 RL J. Biochem. 121:941-948(1997).
 [6] SEQUENCE FROM N.A. (ISOFORMS PACE4A-I; A-II; CS; D; E-I; E-II).
 RN MEDLINE=98021085; PubMed=9378725;
 RX Tsuji A., Hine C., Tamai Y., Yonemoto K., Mori K., Yoshida S.,
 RA Bando M., Sakai E., Mori K., Akamatsu T., Matsuda Y.;
 RT "Genomic organization and alternative splicing of human PACE4 (SPC4),
 RT kexin-like processing endoprotease.";
 RL J. Biochem. 122:438-452(1997).
 [7] ALTERNATIVE SPLICING (ISOFORM PACE4CS).
 RN MEDLINE=97064242; PubMed=8906861;
 RX Zhong M., Benjannet S., Lazure C., Munzer S., Seidah N.G.;
 RT "Functional analysis of human PACE4-A and PACE4-C isoforms:
 RT identification of a new PACE4-CS isoform.";
 RL FEBS Lett. 396:31-36(1996).
 [8] CHARACTERIZATION.
 RN MEDLINE=99233559; PubMed=10215603;
 RX Sucic J.F., Moehring J.M., Innocencio N.M., Luchini J.W.,
 RA Moehring T.J.;
 RT "Endoprotease PACE4 is Ca2+-dependent and temperature-sensitive and
 RT can partly rescue the phenotype of a furin-deficient cell strain.";
 RL Biochem. J. 339:639-647(1999).
 [9] PROCESSING.
 RN MEDLINE=98408849; PubMed=9738469;
 RX Nagahama M., Taniguchi T., Hashimoto E., Imamaki A., Mori K.,
 RA Tsuji A., Matsuda Y.;
 RT "Biosynthetic processing and quaternary interactions of proprotein
 RT convertase SPC4 (PACE4).";
 RL FEBS Lett. 434:155-159(1998).
 CC -!- FUNCTION: LIKELY TO REPRESENT AN ENDOPEPTIDASE ACTIVITY WITHIN THE
 CC CONSTITUTIVE SECRETORY PATHWAY, WITH UNIQUE RESTRICTED
 CC DISTRIBUTION IN BOTH NEUROENDOCRINE AND NON-NEUROENDOCRINE TISSUES
 CC AND CAPABLE OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF.
 CC -!- CATALYTIC ACTIVITY. RELEASE OF MATURE PROTEINS FROM THEIR
 CC PROPEPTIDES BY CLEAVAGE OF ARG-XAA-YAA-ARG-1-ZAA BONDS,
 CC WHERE XAA CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
 CC -!- COFACTOR: PACE4A IS PROBABLY CALCIUM-DEPENDENT.
 CC -!- SUBUNIT: THE PACE4A-1 PRECURSOR PROTEIN SEEMS TO EXIST IN THE
 CC RETICULUM ENDOPLASMIC AS BOTH A MONOMER AND A DIMER-SIZED COMPLEX
 CC WHEREAS MATURE PACE4A-1 EXISTS ONLY AS A MONOMER, SUGGESTING THAT
 CC PROPEPTIDE CLEAVAGE AFFECTS ITS TERTIARY OR QUATERNARY STRUCTURE.
 CC -!- SUBCELLULAR LOCATION: PACE4A-I AND PACE4A-II ARE SECRETED. PACE4C
 CC AND PACE4CS ARE NOT SECRETED AND REMAIN PROBABLY IN ZYMOGEN FORM
 CC IN ENDOPLASMIC RETICULUM. PACE4E-I AND PACE4E-II ARE RETAINED
 CC INTRACELLULARLY PROBABLY THROUGH A HYDROPHOBIC CLUSTER IN THEIR C-
 CC TERMINUS. PACE4B MIGHT BE SECRETED.
 CC -!- ALTERNATIVE PRODUCTS: 8 ISOFORMS; PACE4A-I/PACE4 (SHOWN HERE),
 CC PACE4A-II, PACE4B/PACE4.1, PACE4C, PACE4CS, PACE4D, PACE4E-I AND
 CC PACE4E-II; ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORMS PACE4B,
 CC C, CS AND D MIGHT BE ENZYMATICALLY INACTIVE.
 CC -!- TISSUE SPECIFICITY: EACH PACE4 ISOFORM EXHIBITS A UNIQUE
 CC RESTRICTED DISTRIBUTION. PACE4A-I IS EXPRESSED IN HEART, BRAIN,
 CC PLACENTA, LUNG, SKELETAL MUSCLE, KIDNEY, PANCREAS, BUT AT
 CC COMPARATIVELY HIGHER LEVELS IN THE LIVER. PACE4A-II IS AT LEAST
 CC EXPRESSED IN PLACENTA. PACE4B WAS ONLY FOUND IN THE EMBRYONIC
 CC KIDNEY CELL LINE FROM WHICH IT WAS ISOLATED. PACE4C AND PACE4D ARE
 CC EXPRESSED IN PLACENTA. PACE4E-I IS EXPRESSED IN CEREBELLUM,
 CC PLACENTA AND PITUITARY. PACE4E-II IS AT LEAST PRESENT IN
 CC CEREBELLUM.
 CC -!- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
 CC ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC

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EMBL; U10865; AAA80571.1; -
HSSP; P05106; 1JUV2.
InterPro; IPR000561; EGF-like.
InterPro; IPR002369; Integrin_B.
InterPro; IPR001169; Integrin_beta_C.
InterPro; IPR003659; Plexin-like.
Pfam; PF00362; Integrin_B; 1.
ProDom; PD001811; Integrin_B; 1.
SMART; SM00001; EGF-like; 1.
SMART; SM00187; INB; 1.
SMART; SM00423; PSI; 1.
PROSITE; PS00243; INTEGRIN_BETA; 3.
PROSITE; PS00222; EGF_1; UNKNOWN 2.
Intergrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
Repeat; Phosphorylation.
NON_TER 1
DOMAIN <1 705
TRANSMEM 706 728
DOMAIN 729 >773
DOMAIN 117 355
DOMAIN 443 612
REPEAT 443 492
REPEAT 493 536
REPEAT 537 575
REPEAT 576 612
DISULFID 4 441
DISULFID 12 22
DISULFID 15 52
DISULFID 25 41
DISULFID 184 190
DISULFID 238 278
DISULFID 378 392
DISULFID 412 433
DISULFID 439 443
DISULFID 454 466
DISULFID 463 502
DISULFID 468 477
DISULFID 479 493
DISULFID 508 513
DISULFID 510 545
DISULFID 515 530
DISULFID 532 537
DISULFID 551 556
DISULFID 553 584
DISULFID 558 567
DISULFID 569 576
DISULFID 590 595
DISULFID 592 638
DISULFID 597 607
DISULFID 610 613
DISULFID 617 626
DISULFID 623 700
DISULFID 642 676
MOD_RES 760 760
CARBOHYD 27 27
CARBOHYD 71 71
CARBOHYD 74 74
CARBOHYD 189 199
CARBOHYD 246 246
CARBOHYD 340 340
CARBOHYD 383 383
CARBOHYD 394 394
CARBOHYD 458 458
CARBOHYD 497 497
CARBOHYD 561 561
CARBOHYD 646 646
NON_TER 773 773
SEQUENCE 773 AA; 85322 MW; 54340866CE157195 CRC64;

Query Match 17.7%; Score 71.5; DB 1; Length 773;
Best Local Similarity 32.8%; Pred. No. 2.3; 29; Indels 7; Gaps 4;
Matches 21; Mismatches 7; Indels 7; Gaps 4;
QY 8 DPLLGT-CMSCK-TICNHQSORTCAFCRCRKEQKFFDYDHLRLDTCISASICGQHPK-Q 62
DB 568 DCSLGTSTCMVANGQICNGRVCCEGA--CKCTDFPQPTCEMCTCLGVCAEHEKCVQ 625

QY 63 CAYF 66
DB 626 CRAF 629

RESULT 10

FUR2_DROME
ID FUR2_DROME STANDARD; PRT: 1680 AA.
AC P30432;
DT 01-APR-1993 (rel. 25, Created)
DT 01-APR-1993 (rel. 25, Last sequence update)
DT 15-JUL-1998 (rel. 36, Last annotation update)
DE Furin-like protease 2 precursor (EC 3.4.21.75) (Furin 2).
GN FUR2
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_taxid=7227;
[1]
SEQUENCE FROM N.A.
MEDLINE=92381036; PubMed=1512259; Pauli I.G.L., Kurzik-Dumke U.,
Roebroek A.J.M., Creemers J.W.M., Leunissen J.A.F., van de Ven W.J.;
"Cloning and functional expression of Dfurn2, a subtilisin-like
proteolytic processing enzyme of Drosophila melanogaster with multiple
repeats of a cysteine motif.";
J. Biol. Chem. 267:17208-17215(1992).
CC - FUNCTION: FURIN IS LIKELY TO REPRESENT THE UBIQUITOUS ENDOPEPTIDASE
ACTIVITY WITHIN CONSTITUTIVE SECRETORY PATHWAYS AND CAPABLE OF
CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF (BY SIMILARITY).
CC - CATALYTIC ACTIVITY: Release of mature proteins from their
proteins by cleavage of Arg-Xaa-Yaa-Arg-|-Zaa bonds, where Xaa
can be any amino acid and Yaa is Arg or Lys. Releases albumin,
complement component C3 and von Willebrand factor from their
respective precursors.
CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8. FURIN SUBFAMILY.
CC
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or send an email to license@isb-sib.ch).

EMBL; M94375; AAA28551.1; -

PIR; A43434; A43434.

HSSP; Q99405; IMPT.

MEROPS; S08.049; -

FlyBase; FBgn0004598; Fur2.

InterPro; IPR000561; EGF-like.

InterPro; IPR002174; Furin-like.

InterPro; IPR002884; P domain.

InterPro; IPR000209; Peptidase_S8.

Pfam; PF00082; Peptidase_S8; 1.

Pfam; PF01483; P; PARTIAL.

PRINTS; PR00723; SUBTILISIN.

ProDom; PD000717; P domain; 1.

SMART; SM00181; EGF_1.

SMART; SM00261; FU_10.

PROSITE; PS00136; SUBTILASE ASP; 1.

PROSITE; PS00137; SUBTILASE_HIS; 1.

PROSITE; PS00136; SUBTILASE_SER; 1.

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Tue Jan 7 10:36:54 2003

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FT DOMAIN 771 1124 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 44 102 IGF-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 210 252 EGF-LIKE 1.
FT DOMAIN 254 299 EGF-LIKE 2.
FT DOMAIN 301 341 EGF-LIKE 3.
FT DOMAIN 370 424 IGF-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 444 536 FIBRONECTIN TYPE-III 1.
FT DOMAIN 541 634 FIBRONECTIN TYPE-III 2.
FT DOMAIN 638 732 FIBRONECTIN TYPE-III 3.
FT DOMAIN 824 1096 PROTEIN KINASE.
FT NP BIND 830 838 ATP (BY SIMILARITY).
FT BINDING 855 855 ATP (BY SIMILARITY).
FT ACT SITE 964 964 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 399 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 464 464 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 560 560 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 596 596 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 649 649 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD RES 691 691 PHOSPHORYLATION (AUTO-).
FT VARIANT 992 992 R -> W (IN VMCM1; ACTIVATING EFFECT).
FT VARIANT 849 849 Y -> S (IN VMCM1; ACTIVATING EFFECT).
FT VARIANT 897 897 /FTID=VAR_008716.
SQ SEQUENCE 1124 AA; 125810 MW; 65BC05D18FA4CCEC CRC64;

Query Match 17.3%; Score 70; DB 1; Length 1124;
Best Local Similarity 26.4%; Pred. No. 4.4;
Matches 24; Conservative 4; Mismatches 37; Indels 26; Gaps 3;

QY 3 BEQYWDPR---LLGTQV-----SCKTICN-HQSQRTCAAPCCRK 36
Db 212 EAQKQGECHLCTACNNVGVCHDTGECICPFGMGRTCEKACELHTFGRTCKERCSCGQ 271
QY 37 BQKFEYDHLRDCISACISGQHPKQCAVFC 67
Db 272 EGCKSYVFCPLDPFGCCSACATGWKGLQCNAC 302

RESULT 12
ITBI_MOUSE STANDARD; PRT; 798 AA.
AC P09055;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Integrin beta-1 precursor (Fibronectin receptor beta subunit)
DE (CD29 antigen) (Integrin VLA-4 beta subunit).
GN ITGB1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=89005707; PubMed=3262537;
RA Tomlinaga S.;
RT "Mice" mRNA for the beta-subunit of integrin is increased in
RT BALB/c-3T3 cells entering the G1 phase from the G0 state.";
RL FEBS Lett. 238:315-319(1988).
RN [2]
RP SEQUENCE OF 2-798 FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=89235580; PubMed=2523953;
RA Holers V.M.; Ruff T.G.; Parks D.L.; McDonald J.A.; Ballard L.L.;
RA Brown E.J.;
RT "Molecular cloning of a murine fibronectin receptor and its
RT expression during inflammation. Expression of VLA-5 is increased in
RT activated peritoneal macrophages in a manner discordant from major

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RT HISTOCOMPATIBILITY COMPLEX CLASS II.";
RL J. EXP. MED. 169:1589-1605(1989).
CC -1- FUNCTION. INTEGRINS ALPHA-1/BETA-1, ALPHA-2/BETA-1, ALPHA-10/BETA-1
CC 1/BETA-1 AND ALPHA-11/BETA-1 ARE RECEPTORS FOR COLLAGEN. INTEGRINS ALPHA-
CC 1/BETA-1 AND ALPHA-2/BETA-2 RECOGNIZE THE PROLINE-HYDROXYLATED
CC SEQUENCE G-P-G-E-R IN COLLAGEN. INTEGRINS ALPHA-2/BETA-1, ALPHA-
CC 3/BETA-1, ALPHA-4/BETA-1, ALPHA-5/BETA-1, ALPHA-8/BETA-1, ALPHA-
CC 10/BETA-1, ALPHA-11/BETA-1 AND ALPHA-V/BETA-1 ARE RECEPTORS FOR
CC FIBRONECTIN. ALPHA-4/BETA-1 RECOGNIZES ONE OR MORE DOMAINS WITHIN
CC THE ALTERNATIVELY SPLICED CS-1 AND CS-5 REGIONS OF FIBRONECTIN.
CC INTEGRIN ALPHA-5/BETA-1 IS A RECEPTOR FOR FIBRINOGEN. INTEGRIN
CC ALPHA-1/BETA-1, ALPHA-2/BETA-1, ALPHA-6/BETA-1 AND ALPHA-7/BETA-1
CC ARE RECEPTORS FOR LAMININ. INTEGRIN ALPHA-4/BETA-1 IS A RECEPTOR
CC FOR VCAM1 AND RECOGNIZES THE SEQUENCE Q-I-D-S IN VCAM1. INTEGRIN
CC ALPHA-9/BETA-1 IS A RECEPTOR FOR VCAM1, CYTOTACTIN AND
CC OSTEOPOINTIN. IT RECOGNIZES THE SEQUENCE A-E-I-D-G-I-E-L IN
CC CYTOTACTIN. INTEGRIN ALPHA-3/BETA-1 IS A RECEPTOR FOR EPLIGRIN
CC AND THROMBOSPONDIN. INTEGRIN ALPHA-V/BETA-1 IS A RECEPTOR FOR
CC VITRONECTIN. BETA-1 INTEGRINS RECOGNIZE THE SEQUENCE R-G-D IN A
CC WIDE ARRAY OF LIGANDS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-1
CC ASSOCIATES WITH EITHER ALPHA-1, ALPHA-2, ALPHA-3, ALPHA-4, ALPHA-
CC 5, ALPHA-6, ALPHA-7, ALPHA-8, ALPHA-9, ALPHA-10, ALPHA-11 OR
CC ALPHA-V.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
CC -1- SIMILARITY: CONTAINS 1 VWFA-LIKE DOMAIN.
CC
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CC -----
CC EMBL; Y00769; CAA68738.1; -.
CC EMBL; X15202; CAA33272.1; -.
CC PIR; F01004; IJMSPB.
CC PIR; S01659; S01659.
CC HSSP; P05106; IJ02.
CC MGD; MGI:96610; Itgb1.
CC InterPro; IPR000561; EGF-like.
CC InterPro; IPR002369; Integrin_B.
CC InterPro; IPR001169; Integrin_beta_C.
CC InterPro; IPR003659; Plexin-like.
CC InterPro; IPR002035; VWF A.
CC Pfam; PF00362; Integrin_B; 1.
CC PRINTS; PR01186; INTEGRINB.
CC PRODOM; PD001811; Integrin_B; 1.
CC SMART; SM000001; EGF_like; 1.
CC SMART; SM00187; INB; 1.
CC SMART; SM00423; PSI; 1.
CC SMART; SM00327; VWF; 1.
CC PROSITE; PS00243; INTEGRIN BETA; 3.
CC PROSITE; PS00022; EGF 1; UNKNOWN 2.
CC Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;
CC Repeat; Signal; Phosphorylation.
CC SIGNAL 1 20
CC CHAIN 21 798 INTEGRIN BETA-1.
CC DOMAIN 21 728 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 729 751 POTENTIAL.
CC DOMAIN 752 798 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 140 378 VWFA-LIKE.
CC DOMAIN 466 635 4 CYSTEINE-RICH TANDEM REPEATS.
CC REPEAT 466 515 I.
CC REPEAT 516 559 II.
CC REPEAT 560 598 III.
CC REPEAT 599 635 IV.
CC DISULFID 27 464 BY SIMILARITY.
CC DISULFID 35 45 BY SIMILARITY.
CC DISULFID 38 75 BY SIMILARITY.
CC DISULFID 48 64 BY SIMILARITY.

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FT DISULFID 207 213 BY SIMILARITY.
 FT DISULFID 261 301 BY SIMILARITY.
 FT DISULFID 401 415 BY SIMILARITY.
 FT DISULFID 435 691 BY SIMILARITY.
 FT DISULFID 462 466 BY SIMILARITY.
 FT DISULFID 477 489 BY SIMILARITY.
 FT DISULFID 486 525 BY SIMILARITY.
 FT DISULFID 491 500 BY SIMILARITY.
 FT DISULFID 502 516 BY SIMILARITY.
 FT DISULFID 531 568 BY SIMILARITY.
 FT DISULFID 538 553 BY SIMILARITY.
 FT DISULFID 558 560 BY SIMILARITY.
 FT DISULFID 574 579 BY SIMILARITY.
 FT DISULFID 576 607 BY SIMILARITY.
 FT DISULFID 581 590 BY SIMILARITY.
 FT DISULFID 592 599 BY SIMILARITY.
 FT DISULFID 613 618 BY SIMILARITY.
 FT DISULFID 615 661 BY SIMILARITY.
 FT DISULFID 620 630 BY SIMILARITY.
 FT DISULFID 633 636 BY SIMILARITY.
 FT DISULFID 640 723 BY SIMILARITY.
 FT DISULFID 646 699 BY SIMILARITY.
 FT DISULFID 783 783 BY SIMILARITY.
 FT MOD_RES 50 50 PHOSPHORYLATION (BY SIMILARITY).
 FT CARBOHYD 94 94 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 363 363 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 417 417 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 520 520 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 584 584 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 385 385 E -> P (IN REF. 2).
 FT CONFLICT 392 392 G -> A (IN REF. 2).
 FT CONFLICT 443 445 IKI -> HSKL (IN REF. 2).
 SQ SEQUENCE 798 AA; 88231 MW; 26788F70A16856 CRC64;
 Query Match 17.2%; Score 69.5; DB 1; Length 798;
 Best Local Similarity 29.3%; Pred. No. 3.8;
 Matches 17; Conservative 8; Mismatches 28; Indels 5; Gaps 3;

Cy 12 GTCMSCK-TICNHSORTCAFCCKRKGKPYDHLDRDSCISASIGQHPK--QCAVF 66
 Db 597 GPCIASNOGICNGRGICGCA--CKCTDPKRGQPTCTCTGCAHKEVCVQCRAF 652

RESULT 13
 PCK5_HUMAN STANDARD; PRT; 913 AA.
 AC 092824; Q13527; 40, Created
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Proteolysin convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
 DE (Proteolysin convertase PCS) (Subtilisin/kexin-like protease PCS)
 DE (Convertase PCS) (PC6) (hPC6).
 OS Homo sapiens (Human).
 GN PCS5 OR PCS5 OR PC6.
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NX NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RX MEDLINE=96353680; PubMed=8755538;
 RA Miranda L., Wolf J., Pichantes S., Duke R., Franzusoff A.;
 RT "Isolation of the human PC6 gene encoding the putative host protease
 for HIV-1 gp160 processing in CD4+ T lymphocytes.";

RL Proc. Natl. Acad. Sci. U.S.A. 93:7695-7700 (1996).
 RN [2]
 RP REVISIONS.
 RA Franzusoff A., Miranda L., Wolf J., Pichantes S., Lu Y., Duke R.;
 RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
 RV [3]
 RP SEQUENCE OF 15-913 FROM N.A.
 RA Reudelhuber T.L.;
 RL Submitted (FEB-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPEPTIDASE ACTIVITY
 CC WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE
 CC OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF.
 CC -1- CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
 CC PROTEINS BY CLEAVAGE OF ARG-XAA-YAA-ARG(-ZAA BONDS, WHERE XAA
 CC CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
 CC -1- SUBCELLULAR LOCATION: Secreted (by similarity).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS SEEMS TO BE PRODUCED BY
 CC ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN T-LYMPHOCYTES.
 CC -1- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
 CC ASSISTING THE FOLDING OF THE ZMOGEN WITHIN THE ENDOPLASMIC
 CC RETICULUM.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
 CC -1- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
 CC -----
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 CC BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION -
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 CC USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; U56387; AAC50643.2; -;
 DR EMBL; U48114; AAA91807.1; -;
 DR HSSP; Q99405; IMPT.
 DR MEROPS; S08.076; -; PCSK5.
 DR Genem; HGNC:8747; PCSK5.
 DR MIM; 600488; -;
 DR InterPro; IPR002174; Furin-like.
 DR InterPro; IPR002884; P_domain.
 DR InterPro; IPR000209; Peptidase_S8.
 DR Pfam; PF00082; Peptidase_S8; 1.
 DR Pfam; PF01483; P; PARTIAL.
 DR PRINTS; PR00723; SUBTILISIN.
 DR ProDom; PD000717; P_domain; 1.
 DR SMART; SM00261; FU_5.
 DR PROSITE; PS00136; SUBTILASE ASP; 1.
 DR PROSITE; PS00137; SUBTILASE HIS; 1.
 DR PROSITE; PS00138; SUBTILASE SER; 1.
 DR KX Hydrolyase, Serine protease, Glycoprotein; Zymogen; Signal;
 DR KW cleavage on pair of basic residues; Repeat.
 FT SIGNAL 1 32
 FT PROPEP 33 114
 FT CHAIN 115 913
 FT DOMAIN 115 454
 FT DOMAIN 462 600
 FT DOMAIN 636 913
 FT DOMAIN 114 115
 FT SITE 519 521
 FT ACT_SITE 171 171
 FT ACT_SITE 212 212
 FT ACT_SITE 386 386
 FT CARBOHYD 225 225
 FT CARBOHYD 381 381
 FT CARBOHYD 665 665
 FT CARBOHYD 752 752
 FT CARBOHYD 802 802
 FT CARBOHYD 852 852
 FT CONFLICT 116 116
 FT CONFLICT 121 121
 FT CONFLICT 511 511
 type 5.
 PROTEIN CONVERTASE SUBTILISIN/KEXIN
 CATALYTIC.
 HOMO B.
 CYS-RICH MOTIF (CRM) REGION.
 CLEAVAGE (AUTO-) (BY SIMILARITY).
 CELL ATTACHMENT SITE (BY SIMILARITY).
 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CHARGE RELAY SYSTEM (BY SIMILARITY).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 S -> F (IN REF. 3).
 V -> A (IN REF. 3).
 R -> A (IN REF. 3).


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FT CONFLICT 601 601 R -> O (IN REF. 3).
SQ SEQUENCE 913 AA; 101775 MW; 21389264CAD7546C CRC64;
Query Match 17.0%; Score 69; DB 1; Length 913;
Best Local Similarity 26.0%; Pred. No. 4.7;
Matches 19; Conservative 7; Mismatches 23; Indels 24; Gaps 5;

QY 1 CPEQYWDPLGTCMSCKTICNHOSQRTCAAF--C--CRK-----EQGFYD 43
Db 724 CPDGYQDTKKNLCRKCSENC-----KTCTEPHNTCECRDGLSLGSRCSVSCEDGRYFN 778
QY 44 HLRDCLSCASIC 56
Db 779 G--QDCPCCHRFC 789

RESULT 14
TRA2_MOUSE
ID TRA2_MOUSE STANDARD; PRT; 501 AA.
AC P194329;
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 13-JUN-2002 (Rel. 41, Last annotation update)
DE TNF receptor associated factor 2 (TRAF2).
GN TRAF2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94349371; PubMed=8069916;
RA Roche M., Wong S.C., Henzel W.J., Goeddel D.V.;
RT "A novel family of putative signal transducers associated with the
RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
RL Cell 78:681-692(1994).
CC -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
CC OF THE 75 KDa TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2) AND
CC ACTIVATES NF-KAPPA-B.
CC -1- SUBUNIT: HOMODIMER OR HETERODIMER OF TRAF1 AND TRAF2. THIS
CC HETEROCOMPLEX CAN BIND TO THE N-TERMINAL OF INHIBITOR OF APOPTOSIS
CC PROTEINS 1 AND 2 (IAPs) TO RECRUIT THEM TO THE TUMOR NECROSIS
CC FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 TRAF-TYPE ZINC FINGERS.
CC -----
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CC -----
DR EMBL; L35303; AAC37662.1; -
DR HSSP; L12351; 1HWT.
DR MGD; MGI:101835; Traf2.
DR InterPro; IPRO02083; MATH.
DR InterPro; IPRO03007; TRAF.
DR InterPro; IPRO01293; Znf-TRAF.
DR InterPro; IPRO01841; Znf-TRAF.
DR Pfam; PF00937; ZF-C3HC4_1.
DR Pfam; PF00917; MATH_1.
DR Pfam; PF02167; ZF-TRAF_2.
DR SMART; SM0061; MATH; 1.
DR SMART; SM00184; RING_1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00518; ZF_RING_2; 1.
DR PROSITE; PS01455; ZF-TRAF_2.
DR Zinc-finger; Coiled coil; Repeat.
FT ZN_RING 34 73 RING-TYPE.

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FT ZN_RING 124 180 TRAF-TYPE 1.
FT ZN_RING 177 233 TRAF-TYPE 2.
FT DOMAIN 298 348 COILED COIL (POTENTIAL).
SQ SEQUENCE 501 AA; 56026 MW; 043B391180365F10 CRC64;
Query Match 16.9%; Score 68.5; DB 1; Length 501;
Best Local Similarity 25.0%; Pred. No. 3.3;
Matches 19; Conservative 10; Mismatches 28; Indels 19; Gaps 5;

QY 1 CPEQYWDPLGTCMSCKTICNHOS---QRTCAAF-----CCRKE--QGFYDHLRD 48
Db 156 CPKRSLL-----SCQHCRAFCPSVHDLVHYECPKPLTCDGCGKKKIPRETFQDH-VRA 208
QY 49 CISCASICQHPKQCA 64
Db 209 CSKCRVLCRFHTVGC 224

RESULT 15
LMA1_MOUSE
ID LMA1_MOUSE STANDARD; PRT; 3084 AA.
AC P19137;
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Laminin alpha-1 chain precursor (Laminin A chain).
GN LMA1 OR LAMA-1 OR LAMA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=89034134; PubMed=3182802;
RA Sasaki M., Kleinman H.K., Huber H., Deutzmann R., Yamada Y.;
RT "Laminin, a multidomain protein. The A chain has a unique globular
RT domain and homology with the basement membrane proteoglycan and the
RT laminin B chains."
RL J. Biol. Chem. 263:16536-16544(1988).
RN [2]
RP SEQUENCE OF 1-339 FROM N.A.
RX MEDLINE=88225080; PubMed=3267223;
RA Hartl L., Oberhauser I., Deutzmann R.;
RT "The N terminus of laminin A chain is homologous to the B chains."
RL Eur. J. Biochem. 173:629-635(1988).
RN [3]
RP SEQUENCE OF 2538-3084 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=89030693; PubMed=3181157;
RA Deutzmann R., Huber J., Schmetz K.A., Oberhauser I., Hartl L.;
RT "Structural study of long arm fragments of laminin. Evidence for
RT repetitive C-terminal sequences in the A-chain, not present in the B-
RT chains."
RL Eur. J. Biochem. 177:35-45(1988).
CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration, and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end.
CC THE ALPHA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (HIS LAMININ) AND
CC LAMININ-3 (S-LAMININ).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
CC COMPONENT).
CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -1- DOMAIN: DOMAINS VI, IV AND G ARE GLOBAL.
CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC -1- SIMILARITY: CONTAINS 17 LAMININ EGF-LIKE DOMAINS.

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CC -1- SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.
CC -1- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
CC -----
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DR EMBL; J04064; AAA39410.1; -;
DR EMBL; X07737; CAA30561.1; -;
DR EMBL; X13459; CAA31807.1; -;
DR EMBL; M36775; AAA39406.1; -;
DR PIR; A31771; MMMA.
DR HSP; Q60675; IQUO.
DR MGD; MGI.99892; Lamal.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001896; LamNT.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR Pfam; PF00052; laminin_B; 2.
DR Pfam; PF00053; laminin_EGF; 15.
DR Pfam; PF00054; laminin_G; 5.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PD00011; EGF_LAMININ.
DR ProDom; PD002082; LamNT; 1.
DR ProDom; PD003031; Laminin_B; 2.
DR SMART; SM00180; EGF_Lam; 14.
DR SMART; SM00281; LamB; 2.
DR SMART; SM00282; LamG; 5.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 11.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01248; LAMININ TYPE EGF; 15.
DR PROSITE; PS50025; LAM G DOMAIN; 5.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 3084 LAMININ ALPHA-1 CHAIN.
FT MOD_RES 25 25 BLOCKED.
FT DOMAIN 25 276 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 277 333 LAMININ EGF-LIKE 1.
FT DOMAIN 334 403 LAMININ EGF-LIKE 2.
FT DOMAIN 404 460 LAMININ EGF-LIKE 3.
FT DOMAIN 461 509 LAMININ EGF-LIKE 4.
FT DOMAIN 510 519 LAMININ EGF-LIKE 5 (N-TERMINAL).
FT DOMAIN 520 715 LAMININ DOMAIN IV 1 (DOMAIN IV B).
FT DOMAIN 716 748 LAMININ EGF-LIKE 5 (C-TERMINAL).
FT DOMAIN 749 797 LAMININ EGF-LIKE 6.
FT DOMAIN 798 855 LAMININ EGF-LIKE 7.
FT DOMAIN 856 908 LAMININ EGF-LIKE 8.
FT DOMAIN 909 957 LAMININ EGF-LIKE 9.
FT DOMAIN 958 1004 LAMININ EGF-LIKE 10.
FT DOMAIN 1005 1050 LAMININ EGF-LIKE 11.
FT DOMAIN 1051 1096 LAMININ EGF-LIKE 12.
FT DOMAIN 1097 1156 LAMININ EGF-LIKE 13.
FT DOMAIN 1157 1166 LAMININ EGF-LIKE 14 (N-TERMINAL).
FT DOMAIN 1167 1368 LAMININ DOMAIN IV 2 (DOMAIN IV A).
FT DOMAIN 1369 1409 LAMININ EGF-LIKE 14 (C-TERMINAL).
FT DOMAIN 1410 1458 LAMININ EGF-LIKE 15.
FT DOMAIN 1459 1515 LAMININ EGF-LIKE 16.
FT DOMAIN 1516 1562 LAMININ EGF-LIKE 17.
FT DOMAIN 1564 2124 DOMAIN II AND I.
FT DOMAIN 2125 2305 LAMININ G-LIKE 1.
FT DOMAIN 2313 2489 LAMININ G-LIKE 2.
FT DOMAIN 2494 2680 LAMININ G-LIKE 3.
FT DOMAIN 2722 2894 LAMININ G-LIKE 4.
FT DOMAIN 2899 3079 LAMININ G-LIKE 5.
FT DOMAIN 1612 1820 COILED COIL (POTENTIAL).
FT DOMAIN 1869 1903 COILED COIL (POTENTIAL).
FT DOMAIN 1189 1286 COILED COIL (POTENTIAL).
FT DOMAIN 1287 1384 CELL ATTACHMENT SITE.
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FT CARBOHYD 1344 1344 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1414 1414 N-LINKED (GLCNAC. . .) (POTENTIAL).
Query Match 16.7%; Score 67.5; DB 1; Length 3084;
Best Local Similarity 33.3%; Pred. No. 18;
Matches 19; Conservative 4; Mismatches 17; Indels 17; Gaps 4;
QY 9 PLAGTCMCKTICNHSORTCAFCCKRKGKFDHLRDICISAS-ICGHPKQCA 64
DB 1402 PILAPCVPCN--CNNRSD-----VCDPETGK-----CISCARDHTSGDHCELCIA 1442

Search completed: January 7, 2003, 09:38:12
UOB time : 6.03759 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:34:29 : Search time 18.9749 Seconds
(Without alignments)
727.547 Million cell updates/sec

Title: US-09-855-158-16

Perfect score: 405
Sequence: 1 CPEQWYDPLIGTMSCKT.....DCISCASICGQHPKQCAVFC 67

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_21:
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81.5	20.1	1299	5 Q26489	Q26489 spodoptera
2	80	19.8	108	16 Q07571	Q07571 bacillus su
3	77	19.0	2664	5 Q26033	Q26033 plasmodium
4	76.5	18.9	783	5 P92163	P92163 eicosyloce
5	75.5	18.6	704	3 Q74567	Q74567 trichoderm
6	75	18.5	1069	5 Q9BPS2	Q9BPS2 bombyx moxi
7	74	18.3	723	11 Q9D2H5	Q9D2H5 mus musculu
8	71.5	17.7	213	11 Q9LE4	Q9LE4 mus musculu
9	71.5	17.7	214	11 Q8ROY1	Q8ROY1 mus musculu
10	71.5	17.7	296	11 Q35171	Q35171 mus musculu
11	71.5	17.7	932	11 Q62030	Q62030 mus musculu
12	71.5	17.7	1376	5 Q8S2S2	Q8S2S2 drosophila
13	71.5	17.7	1679	5 Q24301	Q24301 salmonella
14	71	17.5	108	16 Q8ZPY1	Q8ZPY1 salmonella
15	71	17.5	108	16 Q8ZC68	Q8ZC68 salmonella
16	71	17.5	210	4 Q9BYR0	Q9BYR0 homo sapien

17	71	17.5	761	6 Q95LQ2	Q95LQ2 macaca fasc
18	71	17.5	1023	4 Q9UL17	Q9UL17 homo sapien
19	71	17.5	1704	5 Q94446	Q94446 chironomus
20	70.5	17.4	1362	13 Q9PV24	Q9PV24 xenopus lae
21	70	17.3	598	11 Q8RI51	Q8RI51 mus musculu
22	70	17.3	1557	5 Q8WPK9	Q8WPK9 olkopleura
23	69.5	17.2	98	5 Q16933	Q16933 pseudomona
24	69.5	17.2	109	2 Q68643	Q68643 ancylostoma
25	69.5	17.2	166	4 Q9BYR3	Q9BYR3 homo sapien
26	69.5	17.2	271	5 Q9VU12	Q9VU12 drosophila
27	69	17.0	154	4 Q9BEP4	Q9BEP4 homo sapien
28	69	17.0	913	4 Q9BEP9	Q9BEP9 homo sapien
29	69	17.0	1137	4 Q9BOM7	Q9BOM7 homo sapien
30	69	17.0	1918	4 Q9BOM7	Q9BOM7 homo sapien
31	69	17.0	1925	4 Q9P2E3	Q9P2E3 homo sapien
32	68.5	16.9	1438	11 Q922M5	Q922M5 mus musculu
33	68.5	16.9	508	11 Q54896	Q54896 mus musculu
34	68	16.8	433	11 Q91ZM6	Q91ZM6 ratius norv
35	67.5	16.7	146	10 Q40579	Q40579 nicotiana t
36	67.5	16.7	772	10 Q9JUI8	Q9JUI8 arabidopsis
37	67.5	16.7	798	6 Q8SQC0	Q8SQC0 bos taurus
38	67.5	16.7	2232	5 Q94711	Q94711 paramacium
39	67	16.5	136	11 Q99PK1	Q99PK1 mus musculu
40	67	16.5	643	11 Q9ERVE	Q9ERVE mus musculu
41	67	16.5	655	11 Q9WVF5	Q9WVF5 mus musculu
42	67	16.5	1083	11 Q9QK24	Q9QK24 ratius sp.
43	67	16.5	1210	11 Q9EP98	Q9EP98 mus musculu
44	67	16.5	2108	13 Q98019	Q98019 gallus gall
45	66.5	16.4	133	16 Q8XS26	Q8XS26 ralsstonia s

ALIGNMENTS

RESULT 1

ID Q26489 PRELIMINARY; PRT; 1299 AA.

AC Q26489; 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Endoprotease furin.
 GN FURIN
 OS Spodoptera frugiperda (Fall armyworm).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 CC Noctuidae; Noctuidae; Amphipyrinae; Spodoptera.
 OX NCBI_TaxId=7108;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=SF9; Klenk H.;
 RT "Cloning and functional characterization of FURIN from Spodoptera
 frugiperda (Sf9) cells.";
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z68888; CA93116.1; -.
 DR HSSP; Q99405; IMPT.
 DR InterPro; IPR002174; Furin-like
 DR InterPro; IPR002093; Peptidase_S8.
 DR InterPro; IPR002884; P_domain.
 DR Pfam; PF01483; P_1.
 DR PRINTS; PR00723; SUBTILISIN.
 DR ProDom; PD000717; P_domain; 1.
 DR SMART; SM00261; FU; 10.
 DR PROSITE; PS00136; SUBTILASE_ASP; 1.
 DR PROSITE; PS00137; SUBTILASE_HIS; 1.
 DR PROSITE; PS00138; SUBTILASE_SER; 1.
 KW Protease.
 SQ
 Query Match 20.1%; Score 81.5; DB 5; Length 1299;
 Best Local Similarity 30.1%; Pred. No. 0.038;

Matches 22; Conservative 5; Mismatches 33; Indels 13; Gaps 3;

QY 1 CPBEQWDPGLTGMCKTICNHQSORTCAA-----FCRKGQKGYDHLRLDCISCSASIC 56
 Db 1116 CLGQYDQATSGFRCSDASC-----RTCSGQFSCTTCRPLRDRLNQCVPCCSER 1170
 QY 57 G-----QHPKQAY 65
 Db 1171 GVTNSTPTDCCH 1183

RESULT 2

ID O07571 PRELIMINARY; PRT; 108 AA.
 AC O07571;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypothetical protein yhjQ.
 GN yhjQ.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=168;
 RC Noback M.A., Terpatra P., Holsappel S., Venema G., Bron S.;
 RA Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=168;
 RC MEDLINE=98044013; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
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 Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Banchin A.;
 RT "The complete genome sequence of the gram-positive bacterium Bacillus
 subtilis.";
 RL Nature 390:249-256 (1997).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=168;
 RC Kunst F., Ogasawara N., Yoshikawa H., Banchin A.;
 RA Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 RL EMBL; Y14081; CAA74479.1; -;
 DR EMBL; Z99109; CAB12900.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 108 AA; 11839 MW; 78637689ABB0FD8F CRC64;

Query Match 19.8%; Score 80; DB 16; Length 108;
 Best Local Similarity 22.6%; Pred. No. 0.006;
 Matches 24; Conservative 7; Mismatches 25; Indels 50; Gaps 4;
 QY 4 EYWDPLLTGTCNSCKTICNH-----QSORTCAAF----- 33
 Db 2 EYSEACIEACIDCKACNHCFTKLEESVQHLSGCGIRLDRECDICALAVKAMQTDSP 61
 QY 34 -----CRKEQKGF-YDHLRLDCISCSASICGQHPKQC 63
 Db 62 FMKEICALCADICEACGTECGKHIDH-----CQACAKACFTCAEQ 103

RESULT 3

ID Q26033 PRELIMINARY; PRT; 2664 AA.
 AC Q26033;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Variant-specific surface protein.
 GN VAR-2.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=FCR3;
 RC MEDLINE=95330813; PubMed=7606788;
 RA Su X.Z., Heatwole V.M., Wertheimer S.P., Guinet P., Herrfeldt J.A.,
 Peterson D.S., Ravetch J.A., Wellem T.E.;
 RT "The large diverse gene family var encodes proteins involved in
 RT cytoadherence and antigenic variation of Plasmodium falciparum-
 RT infected erythrocytes.";
 RL Cell 82:89-100 (1995).
 DR EMBL; L40609; AAA75398.1; -;
 DR InterPro: IPR004258; Pfam: PF03011; Pfam: 2;
 DR Pfam: PF03011; Pfam: 2;
 SQ SEQUENCE 2664 AA; 302410 MW; 6EA2468511703091 CRC64;

Query Match 19.0%; Score 77; DB 5; Length 2664;

Best Local Similarity 44.7%; Pred. No. 0.28;
 Matches 17; Conservative 4; Mismatches 9; Indels 8; Gaps 2;

QY 32 FCRKEQKGFYDHLRLDCISCS-----ICGQHPKQC 63

Db 1031 FC--REQSLYELLRLDCGCTTGKCNNDKCAKCKQC 1066

RESULT 4

ID P92163 PRELIMINARY; PRT; 783 AA.
 AC P92163;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Integrin beta G subunit.
 OS Strongylocentrotus purpuratus (Purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinozoa;
 OC Echinozoa; Echinozoa; Echinacea; Echinacea; Strongylocentrotidae;
 OX NCBI_TaxID=7668;
 [1]
 RN SEQUENCE FROM N.A.
 RP Marsden M., Burke R.D.;
 RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RL -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- PTM: THE CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN DISULFIDE
 CC BONDS (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
 DR EMBL; U77584; AAB39739.1; -;
 DR EMBL; U77587; AAB39741.1; -;

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DR HSPB, P05106, 13V2.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR002365; Integrin B.
DR InterPro: IPR001869; Integrin beta_C.
DR InterPro: IPR003659; Plexin-like.
DR InterPro: IPR002035; VWF_A.
DR Pfam: PF00362; Integrin_B; 1.
DR Pfam: PD001811; Integrin_B; 1.
DR SMART: SM00001; EGF-like; 1.
DR SMART: SM00187; INB; 1.
DR SMART: SM00423; PSI; 1.
DR SMART: SM00327; VMA; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_2.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PROSITE: PS00243; INTEGRIN_BETA; 2.
DR Cell adhesion: Cytoskeleton; Glycoprotein; Integrin; Repeat;
KW Transmembrane.
SQ SEQUENCE 783 AA; 85530 MW; B045C6FED86FB2 CRC64;

Query Match 18.9%; Score 76.5; DB 5; Length 783;
Best Local Similarity 33.3%; Pred. No. 0.11; 24; Indels 5; Gaps 3;
Matches 19; Conservative 9; Mismatches 24;

QY 13 TCMSCKTICNHSORTCAFCRCRKGKRY-DHLRDCISCSICGQHPK-QCAYF 66
DB 592 TCMGDTICNGEVCICGE--CKNAGSYRGALCODCPTCSGQCSRMEEVCQCAF 646

RESULT 5
QY 074567 PRELIMINARY; PRT; 704 AA.
ID 074567
AC 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Q174 protein.
GN Q174.
OS Trichoderma harzianum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; mitosporic Hypocreales; Trichoderma.
OX NCBI_TaxID=5544;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CECT 2413; PubMed=9600944;
RX MEDLINE=9826335; Pintor-Toro J.A., Jose A., Llobell A., Benitez T.;
RA Rey M., Ohno S.A., "Unexpected homology between inducible cell wall protein of
RT filamentous fungi and BR3 salivary protein of the insect Chironomus.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:6212-6216(1998).
DR EMBL: X95671; CA64974.1; -.
DR InterPro: IPR000561; EGF-like.
DR PROSITE: PS01186; EGF_2; 1.
KW EGF-like domain; Glycoprotein.
SQ SEQUENCE 704 AA; 77925 MW; 63414BDDEC365EBC CRC64;

Query Match 18.6%; Score 75.5; DB 3; Length 704;
Best Local Similarity 28.6%; Pred. No. 0.13;
Matches 28; Conservative 9; Mismatches 20; Indels 41; Gaps 9;

QY 1 CPEQYWDPLGTGCMSCCK--TI-----CNH-----QSQRCAAFCCRKGKRYFDH 44
DB 509 CPDQYWD---GSKCACPYGTVDGKHCNDPCGKAHFPDSNCKCV---CNK-QSEVYDS 561
QY 45 LTRDCISCSICGQH-----PRQAYFC 67
DB 562 KSKTC-SCPD--GGYWDGSKCACPYGKWDGKQCVNRC 596

RESULT 6
QY 09B82 PRELIMINARY; PRT; 1069 AA.
AC 09B82
DT 01-JUN-2001 (TREMblrel. 17, Created)

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DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Laminin (Fragment).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Plekoyota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Bombycoidea; Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; Tissue=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Kono H., Adachi J., Fukuda S.,
RA Aikawa T., Hara A., Fukunishi Y., Kiyosawa H., Kondo S., Yamana K.I.,
RA Aizawa K., Izawa M., Nishi K., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batelov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuenl P., Lewis S., Matsuo Y., Nikaido I., Perle G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli P., de Bonaldi M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Kamiya M., Lee N.H.,
RA Gustinich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli S., Mombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

QY 1 CPEQYWDPLGTGCMSCCKTICNHSORTCAFCRCRKGKRYDHLRDCISCSICGQH 59
DB 257 CADNYGDPILRGCEKCE--CNENIDITKPGNC-----DYTGKCLQCLNTNGEH 305
QY 60 PKQC 63
DB 306 CDVC 309

RESULT 7
QY 09D2H5 PRELIMINARY; PRT; 723 AA.
ID 09D2H5
AC 09D2H5
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE 493048B16R1K protein.
GN 493048B16R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; Tissue=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Kono H., Adachi J., Fukuda S.,
RA Aikawa T., Hara A., Fukunishi Y., Kiyosawa H., Kondo S., Yamana K.I.,
RA Aizawa K., Izawa M., Nishi K., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batelov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuenl P., Lewis S., Matsuo Y., Nikaido I., Perle G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli P., de Bonaldi M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Kamiya M., Lee N.H.,
RA Gustinich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli S., Mombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

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RESULT 11
ID Q62030 PRELIMINARY; PRT; 932 AA.
AC Q62030
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE PACE4A (Fragment).
GN PCSK6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RA STRAIN=ICR; TISSUE=LIVER;
RA Nakayama K.;
RL Submitted (MAR-1995) to the EMBL/Genbank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=LIVER;
RA Hosaka M.; Murakami K.; Nakayama K.;
RA "PACE4A is a ubiquitous endoprotease that has similar but not
RA identical substrate specificity to other kex2-like processing
RA endoproteases."
RT Biomed. Res. 15:383-390(1994).
DR EMBL; D50060; BA08777.1; -.
DR HSSP; Q99405; IMPT.
DR MEROPS; S08.075; -.
DR MGDI; MG1:102897; PCsk6.
DR InterPro; IPR000561; EGF_1like.
DR InterPro; IPR002174; Furin_1like.
DR InterPro; IPR000209; Peptidase_S8.
DR InterPro; IPR002884; P_domain.
DR InterPro; IPR000822; ZnF_C2H2.
DR Pfam; PF01483; P; 1.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR ProDom; PD000717; P_domain; 1.
DR SMART; SM00181; EGF_2.
DR SMART; SM00261; FU; 5.
DR SMART; SM00001; EGF_1like; 1.
DR PROSITE; PS00136; SUBTILASE_ASP; 1.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 932 AA; 103310 MW; 15660179C8CAC72E CRC64;

Query Match 17.7%; Score 71.5; DB 11; Length 932;
Best Local Similarity 29.6%; Pred. No. 0.57; 24; Indels 7; Gaps 3;
Matches 16; Conservative 7; Mismatches 24;

QY 14 CMSGCT-ICNHQSORTCAFCCKRKGKFFDHLRDCISC--ASTCGQHPRKC 63
DB 727 CLSGRGFYHHEFTNCTVTLCT---PALVADBSQRLCLRHPCQKCVDEPEKC 777

RESULT 12
ID Q6S2S2 PRELIMINARY; PRT; 1376 AA.
AC Q6S2S2
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE L030182P.
GN Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

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RN SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M.; Brokstein P.; Hong L.; Aspayani A.; Carlson J.;
RA Champe M.; Chavez C.; Dorenek D.; Farnan D.; Fise E.;
RA George R.; Gonzalez M.; Guerin H.; Krommiller B.; Li P.; Liao G.;
RA Miranda A.; Mungall C.J.; Nunoo J.; Pacleb J.; Paragas V.; Park S.;
RA Patel S.; Phouanavong S.; Wan K.; Yu C.; Lewis S.F.; Rubin G.M.;
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY070553; AAL48024.1; -.
SQ SEQUENCE 1376 AA; 149716 MW; B6704BA89A3A88FB CRC64;

Query Match 17.7%; Score 71.5; DB 5; Length 1376;
Best Local Similarity 32.1%; Pred. No. 0.82; 23; Indels 9; Gaps 3;
Matches 18; Conservative 6; Mismatches 23;

QY 1 CPEEQYWDPLGTGMSCKTICNHQSORTC--APCRKKGKFF-DHLRDCISC 52
DB 1083 CLSQYVDTTSATCKTC---HDSGRSCFGPGQFCCKGCVPLHLDQINSQVSC 1133

RESULT 13
ID Q24301 PRELIMINARY; PRT; 1679 AA.
AC Q24301
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE FUR2 protein.
GN FUR2 OR DFUR2 OR CG4235 OR CG18734.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA MELLINE=20196006; PubMed=10731132;
RA Adams M.D.; Celniker S.E.; Holt R.A.; Evans C.A.; Gocayne J.D.;
RA Amanatides P.G.; Scherer S.E.; Li P.W.; Hoskins R.A.; Galle R.F.;
RA George R.A.; Lewis S.B.; Richards S.; Ashburner M.; Henderson S.N.;
RA Sutton G.G.; Wortman J.R.; Yandell M.D.; Zhang Q.; Chen L.X.;
RA Brandon R.C.; Rogers J.-H.C.; Blazey R.G.; Champe M.; Pfeiffer B.D.;
RA Wan K.H.; Doyle C.; Baxter E.G.; Helt G.; Nelson C.R.; Miklos G.L.G.;
RA April J.F.; Aspayani A.; An H.-J.; Andrews-Pfannkoch C.; Baldwin D.;
RA Ballow R.M.; Basu A.; Baxendale J.; Bayraktaroglu L.; Beasley E.M.;
RA Beeson K.Y.; Benos P.V.; Berman B.P.; Bhandari D.; Bolshakov S.;
RA Borkova D.; Botchan M.R.; Bouck J.; Brokstein P.; Brotlier P.;
RA Burris K.C.; Busam D.A.; Butler H.; Cadieu E.; Center A.; Chandra I.;
RA Cherry J.M.; Cawley S.; Dahlke C.; Davenport L.B.; Davies P.;
RA de Pablo B.; Delcher A.; Deng Z.; Mays A.D.; Dew I.; Dietz S.M.;
RA Dodson K.; Evans G.; Fouts D.E.; Drenth J.; Dugan-Rocha S.; Dunn P.;
RA Durbin K.J.; Evangelista C.C.; Ferraz C.; Ferreira S.; Fleischmann W.;
RA Foaier C.; Gabrielian A.E.; Garg N.S.; Gelbart W.M.; Glasser K.;
RA Glodde K.; Gong F.; Gorrell J.H.; Gu Z.; Guan P.; Harris M.;
RA Harris N.L.; Hartley D.; Heiman T.J.; Hernandez J.R.; Houck J.;
RA Hostin D.; Houston K.A.; Howard T.J.; Wei M.-H.; Ibegwam C.;
RA Jaiswal M.; Kalush F.; Kappen G.H.; Ke Z.; Kennison J.A.; Ketchum K.A.;
RA Kimmel B.E.; Kodira C.D.; Kraft C.; Kravitz S.; Kulp D.; Lai X.;
RA Laoko P.; Lei Y.; Levitsky A.A.; Li J.; Li Z.; Liang Y.; Lin X.;
RA Liu X.; Mattei B.; McIntosh T.C.; McLeod M.P.; McPherson D.;
RA Merkulov G.; Milshina N.V.; Mobarry C.; Morris J.; Moshrefi A.;
RA Mount S.M.; Moy M.; Murphy B.; Murphy L.; Muny D.M.; Nelson D.L.;
RA Nelson D.L.; Nelson K.A.; Nix K.; Pollard J.D.; Pui V.; Reese M.G.;
RA Palazzolo M.; Piatman K.A.; Pan S.; Sanders R.D.; Scheelers F.; Shen T.;
RA Reinert K.; Remington K.; Sanders R.D.; Scheelers F.; Shen T.;
RA Shue B.C.; Siden-Kiamos I.; Simpson M.; Skrupny M.P.; Smith T.;
RA Spter B.; Spradling A.C.; Stepien M.; Strong R.; Sun E.; Wang X.;
RA Svirskas R.; Tector C.; Turner R.; Venter E.; Wang A.H.; Wang X.;
RA Wang Z.-Y.; Wasserman D.A.; Weinstein G.M.; Weissbach J.;
RA Williams S.M.; Woodard T.; Worley K.C.; Wu D.; Yang S.; Yao Q.A.;

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Run on: January 7, 2003, 09:35:14 ; Search time 8.22807 Seconds
(without alignments)
239.587 Million cell updates/sec

Title: US-09-855-158-16

Perfect score: 405
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Searched: 262574 seqs, 2942322 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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- 4: /cgn2_6/prodata/1/1aa/6B_COMB.pep.*
- 5: /cgn2_6/prodata/1/1aa/PCIVS_COMB.pep.*
- 6: /cgn2_6/prodata/1/1aa/backfilest1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	393	97.0	166	2	US-08-810-572A-6
2	393	97.0	166	4	US-09-290-333-6
3	393	97.0	293	2	US-08-810-572A-2
4	393	97.0	293	4	US-09-290-333-2
5	76.5	18.9	325	4	US-08-915-795-3
6	76.5	18.9	354	4	US-08-915-795-5
7	74.5	18.4	969	2	US-08-284-941-2
8	74.5	18.4	969	2	US-08-447-642-2
9	74.5	18.4	969	4	US-09-236-503-2
10	74.5	18.4	969	5	PCT-US93-02147A-2
11	70	17.3	969	5	US-09-590-656-1
12	70	17.3	977	4	US-09-590-656-2
13	70	17.3	1124	1	US-08-333-674-2
14	70	17.3	1124	5	PCT-US93-06093-2
15	69.5	17.2	75	2	US-08-465-380-6
16	69.5	17.2	75	2	US-08-465-380-41
17	69.5	17.2	75	2	US-08-480-478-35
18	69.5	17.2	75	2	US-08-486-397-6
19	69.5	17.2	75	2	US-08-486-397-41
20	69.5	17.2	75	2	US-08-486-399-6
21	69.5	17.2	75	2	US-08-486-399-41
22	69.5	17.2	75	2	US-08-461-965-6
23	69.5	17.2	75	2	US-08-461-965-41
24	69.5	17.2	75	2	US-08-326-110A-35
25	69.5	17.2	75	2	US-08-634-641-6
26	69.5	17.2	75	2	US-08-634-641-41
27	69.5	17.2	75	3	US-09-249-471-6

28	69.5	17.2	75	3	US-09-249-471-41	Sequence 41, Appl
29	69.5	17.2	75	3	US-09-249-472-6	Sequence 6, Appl
30	69.5	17.2	75	3	US-09-249-472-41	Sequence 41, Appl
31	69.5	17.2	75	3	US-09-249-451-6	Sequence 6, Appl
32	69.5	17.2	75	3	US-09-249-451-41	Sequence 41, Appl
33	69.5	17.2	75	3	US-08-809-455-6	Sequence 6, Appl
34	69.5	17.2	75	3	US-08-809-455-41	Sequence 41, Appl
35	69.5	17.2	75	3	US-09-249-461-6	Sequence 6, Appl
36	69.5	17.2	75	3	US-09-249-461-41	Sequence 41, Appl
37	69.5	17.2	75	3	US-09-249-448-6	Sequence 6, Appl
38	69.5	17.2	75	3	US-09-249-448-41	Sequence 41, Appl
39	69.5	17.2	75	3	US-08-465-380-8	Sequence 8, Appl
40	69.5	17.2	79	2	US-08-480-478-37	Sequence 37, Appl
41	69.5	17.2	79	2	US-08-486-397-8	Sequence 8, Appl
42	69.5	17.2	79	2	US-08-486-399-8	Sequence 8, Appl
43	69.5	17.2	79	2	US-08-461-965-8	Sequence 8, Appl
44	69.5	17.2	79	2	US-08-326-110A-37	Sequence 37, Appl
45	69.5	17.2	79	2	US-08-634-641-8	Sequence 8, Appl

ALIGNMENTS

```

RESULT 1
US-08-810-572A-6
; Sequence 6, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent-in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-810-572A-6
Query Match 97.0%; Score 393; DB 2; Length 166;
Best Local Similarity 94.4%; Pred. No. 8.7e-35;

```

Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 Qy 1 CPEQYWDPLLTGTCMCKTICNHQSORTCAAFCAFC---CRKEQKGYDHLRLDCISCASIC 56
 Db 34 CPEQYWDPLLTGTCMCKTICNHQSORTCAAFCAFC---CRKEQKGYDHLRLDCISCASIC 93
 Qy 57 GQHPKQCAAYFC 67
 Db 94 GQHPKQCAAYFC 104
 RESULT 2
 US-09-290-333-6
 ; Sequence 6, Application US/09290333
 ; Patent No. 6316222
 ; GENERAL INFORMATION:
 ; APPLICANT: Bram, Richard J.
 ; von Bulow, Gotz
 ; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
 ; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
 ; THEREOF
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David A. Jackson, Esq.
 ; STREET: 411 Hackensack Ave, Continental Plaza, 4th
 ; Floor
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/290,333
 ; FILING DATE: 12-Apr-1999
 ; CLASSIFICATION: <unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-487-5800
 ; TELEFAX: 201-343-1684
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 166 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-09-290-333-6

Query Match 97.0%; Score 393; DB 4; Length 166;
 Best Local Similarity 94.4%; Pred. No. 8.7e-35;
 Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 Qy 1 CPEQYWDPLLTGTCMCKTICNHQSORTCAAFCAFC---CRKEQKGYDHLRLDCISCASIC 56
 Db 34 CPEQYWDPLLTGTCMCKTICNHQSORTCAAFCAFC---CRKEQKGYDHLRLDCISCASIC 93
 Qy 57 GQHPKQCAAYFC 67
 Db 94 GQHPKQCAAYFC 104
 RESULT 3
 US-08-810-572A-2
 ; Sequence 2, Application US/08810572A
 ; Patent No. 5969102
 ; GENERAL INFORMATION:
 ; APPLICANT: Bram, Richard J.
 ; von Bulow, Gotz
 ; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
 ; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
 ; THEREOF
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David A. Jackson, Esq.
 ; STREET: 411 Hackensack Ave, Continental Plaza, 4th
 ; Floor
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/810,572A
 ; FILING DATE: 28-FEB-1997
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 1340-1-007
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-487-5800
 ; TELEFAX: 201-343-1684
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 293 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 166 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-09-290-333-6

Query Match 97.0%; Score 393; DB 4; Length 166;
 Best Local Similarity 94.4%; Pred. No. 8.7e-35;
 Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 Qy 1 CPEQYWDPLLTGTCMCKTICNHQSORTCAAFCAFC---CRKEQKGYDHLRLDCISCASIC 56
 Db 34 CPEQYWDPLLTGTCMCKTICNHQSORTCAAFCAFC---CRKEQKGYDHLRLDCISCASIC 93
 Qy 57 GQHPKQCAAYFC 67
 Db 94 GQHPKQCAAYFC 104

RESULT 3
 US-08-810-572A-2
 ; Sequence 2, Application US/08810572A
 ; Patent No. 5969102
 ; GENERAL INFORMATION:
 ; APPLICANT: Bram, Richard J.
 ; von Bulow, Gotz
 ; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
 ; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
 ; THEREOF
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David A. Jackson, Esq.
 ; STREET: 411 Hackensack Ave, Continental Plaza, 4th
 ; Floor
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/810,572A
 ; FILING DATE: 28-FEB-1997
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 1340-1-007
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-487-5800
 ; TELEFAX: 201-343-1684
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 293 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 166 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-08-810-572A-2
 Query Match 97.0%; Score 393; DB 2; Length 293;
 Best Local Similarity 94.4%; Pred. No. 1.5e-34;
 Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 Qy 1 CPEQYWDPLLTGTCMCKTICNHQSORTCAAFCAFC---CRKEQKGYDHLRLDCISCASIC 56
 Db 34 CPEQYWDPLLTGTCMCKTICNHQSORTCAAFCAFC---CRKEQKGYDHLRLDCISCASIC 93
 Qy 57 GQHPKQCAAYFC 67
 Db 94 GQHPKQCAAYFC 104
 RESULT 4
 US-09-290-333-2
 ; Sequence 2, Application US/09290333
 ; Patent No. 6316222
 ; GENERAL INFORMATION:
 ; APPLICANT: Bram, Richard J.
 ; von Bulow, Gotz
 ; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
 ; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
 ; THEREOF
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/290.333
FILING DATE: 12-Apr-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-343-1684
TELEFAX: 201-487-5800

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEetical: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2

Query Match 97.0%; Score 393; DB 4; Length 293;
Best Local Similarity 94.4%; Pred. No. 1.5e-34;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 CPEQYWDPLGTGMSCKTICNHOSQRTCAFC---CRKEQGFYDHLRDICSCASTC 56
DB 34 CPEQYWDPLGTGMSCKTICNHOSQRTCAFCRSLSCKRQCKFYDHLRDICSCASTC 93
QY 57 GQHPKQCAVFC 67
DB 94 GQHPKQCAVFC 104

RESULT 5
US-08-915-795-3
Sequence 3, Application US/08915795
Patent No. 6235713
GENERAL INFORMATION:
APPLICANT: Marc G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STRACKER
APPLICANT: Kari ALITALO
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NW, Suite 700
CITY: Washington
STATE: DC
COUNTRY: United States of America
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915.795
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/42983
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
TELEX: N/A
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEtical: NO
ORIGINAL SOURCE:
TISSUE TYPE: Human Breast
US-08-915-795-3

Query Match 18.9%; Score 76.5; DB 4; Length 325;
Best Local Similarity 24.8%; Pred. No. 0.57; 22; Indels 57; Gaps 7;
Matches 28; Conservative 6; Mismatches 22;

QY 1 CPEQYWDPLGTGMSCKTICNHOSQRTCAFC---CRKEQGFYDHLRDICSCASTC 56
DB 193 CPEQYWDPLGTGMSCKTICNHOSQRTCAFCRSLSCKRQCKFYDHLRDICSCASTC 93
QY 24 -OSQRTCAFC---CRKEQGFYDHLRDICSCASTC 64
DB 252 LQHPKQCAVFC 104

RESULT 6
US-08-915-795-5
Sequence 5, Application US/08915795
Patent No. 6235713
GENERAL INFORMATION:
APPLICANT: Marc G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STRACKER
APPLICANT: Kari ALITALO
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NW, Suite 700
CITY: Washington
STATE: DC
COUNTRY: United States of America
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915.795
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/42983
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
TELEX: N/A
INFORMATION FOR SEQ ID NO: 5:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 354 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Lung
US-08-915-795-5
Query Match 18.9%; Score 76.5; DB 4; Length 354;
Best Local Similarity 24.8%; Pred. No. 0.62; Indels 57; Gaps 7;
Matches 28; Conservative 6; Mismatches 22; Indels 57; Gaps 7;

QY 1 CPERQYWD-----PLIGT-----CMSGKTCNH- 23
Db 222 CPIDMLWSNKKCVLQENPLAGTDSHLQEPALCGPHMFEDRCECV-CKTPCPKD 280

QY 24 --QSORTCAAF-----CCRKEQGFYDHL--RDCISCAICGQHPKQCA 64
Db 281 LIQHPKNCSCFECKESLETCQK-----HKLFPDPTCSCEDRCDFPHTRPCA 326

RESULT 7
US-08-284-941-2
; Sequence 2, Application US/08284941
; Patent No. 5863756
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J
; APPLICANT: KIEFER, MICHAEL C
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
; TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
; STREET: FIVE PALO ALTO SQUARE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,941
; FILING DATE: 2 August 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: NEELEY PH.D., RICHARD L.
; REGISTRATION NUMBER: 30092
; REFERENCE/DOCKET NUMBER: CHIR-009/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5070
; TELEFAX: (415) 857-0663
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 969 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-284-941-2
Query Match 18.4%; Score 74.5; DB 2; Length 969;
Best Local Similarity 27.8%; Pred. No. 2.6;
Matches 15; Conservative 9; Mismatches 23; Indels 7; Gaps 3;

QY 14 CMSCKT-ICNHQSORTCAAFCCRKEQGFYDHLRLDRCISC---ASICGQHPKQC 63
Db 764 CLSCRRGFYHHQEMNTCVTLCL---PAGFYADESQKNCLKCHPSCKKCVDEPEKC 814

RESULT 9
US-09-236-503-2
; Sequence 2, Application US/09236503
; Patent No. 6277590
; GENERAL INFORMATION:
; APPLICANT: Barr, Philip J
; APPLICANT: Kiefer, Michael C
; TITLE OF INVENTION: Compositions and Methods for PACE 4 and 4.1 Gene and
; TITLE OF INVENTION: Polypeptides in Cells
; FILE REFERENCE: CHIR-009/04US
; CURRENT APPLICATION NUMBER: US/09/236,503
; CURRENT FILING DATE: 1999-01-25
; EARLIER APPLICATION NUMBER: 08/447,642
; EARLIER FILING DATE: 1995-05-23
; EARLIER APPLICATION NUMBER: 08/284,941
; EARLIER FILING DATE: 1994-08-02
; EARLIER APPLICATION NUMBER: 07/848,629

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/ EARLIER FILING DATE: 1992-03-09
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 2
/ LENGTH: 969
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-236-503-2

Query Match
Best Local Similarity 18.4%; Score 74.5; DB 4; Length 969;
Matches 15; Conservative 9; Mismatches 23; Indels 7; Gaps 3;

QY 14 CAGCKT-ICNHSQRTCAFCCKEKGKFDHLRDCISC--ASTCGGHPKQC 63
DB 764 CLSCRGFYHNMTCVTLC--PAGFYADESQKNCKLKCHPSCKKCVDEPERK 814

RESULT 10
PCT-US93-02147A-2
/ Sequence 2, Application PC/TUS9302147A
/ GENERAL INFORMATION:
/ APPLICANT: BARR, PHILIP J
/ APPLICANT: KIEFER, MICHAEL C
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PAGE 4 AND
/ TITLE OF INVENTION: PAGE 4.1 GENE AND POLYPEPTIDES IN CELLS
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
/ STREET: FIVE PALO ALTO SQUARE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94306
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/02147A
/ FILING DATE: 19930309
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/848,629
/ FILING DATE: 09-MAR-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: NEBLEY PH.D., RICHARD L
/ REGISTRATION NUMBER: 30092
/ REFERENCE/DOCKET NUMBER: CHIR-009/0005
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 494-7622
/ TELEFAX: (415) 857-0663
/ TELEX: 380816 COOLEY PA
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 969 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
PCT-US93-02147A-2

Query Match
Best Local Similarity 18.4%; Score 74.5; DB 5; Length 969;
Matches 15; Conservative 9; Mismatches 23; Indels 7; Gaps 3;

QY 14 CAGCKT-ICNHSQRTCAFCCKEKGKFDHLRDCISC--ASTCGGHPKQC 63
DB 764 CLSCRGFYHNMTCVTLC--PAGFYADESQKNCKLKCHPSCKKCVDEPERK 814

RESULT 11
US-09-590-656-2
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/ Sequence 2, Application US/09590656
/ Patent No. 6413932
/ GENERAL INFORMATION:
/ APPLICANT: Cerretti, Douglas P.
/ APPLICANT: Borges, Luis G.
/ APPLICANT: Fanslow, III, William C.
/ TITLE OF INVENTION: 'TEK ANTAGONISTS
/ FILE REFERENCE: 2900-A
/ CURRENT APPLICATION NUMBER: US/09/590,656
/ PRIOR FILING DATE: 2000-06-07
/ PRIOR FILING DATE: 1999-06-07
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 2
/ LENGTH: 704
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-590-656-2

Query Match
Best Local Similarity 17.3%; Score 70; DB 4; Length 704;
Matches 24; Conservative 4; Mismatches 37; Indels 26; Gaps 3;

QY 3 EEOYWDP---LIGTCM-----SCKTICN-HQSRTCAFCCKR 36
DB 212 EAQKMGPECNHLCYACNNNGVCHEDTGEICOPGFMGRTCEKXCELHTFRTCKERSGQ 271
QY 37 EOGKFDHLRDCISCASICGQHPKQCAVFC 67
DB 272 EGCKSYVFCLEPDPYGSCATGWMKGLQCNEAC 302

RESULT 12
US-09-590-656-1
/ Sequence 1, Application US/09590656
/ Patent No. 6413932
/ GENERAL INFORMATION:
/ APPLICANT: Cerretti, Douglas P.
/ APPLICANT: Borges, Luis G.
/ APPLICANT: Fanslow, III, William C.
/ TITLE OF INVENTION: 'TEK ANTAGONISTS
/ FILE REFERENCE: 2900-A
/ CURRENT APPLICATION NUMBER: US/09/590,656
/ PRIOR FILING DATE: 2000-06-07
/ PRIOR FILING DATE: 1999-06-07
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 977
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-590-656-1

Query Match
Best Local Similarity 17.3%; Score 70; DB 4; Length 977;
Matches 24; Conservative 4; Mismatches 37; Indels 26; Gaps 3;

QY 3 EEOYWDP---LIGTCM-----SCKTICN-HQSRTCAFCCKR 36
DB 212 EAQKMGPECNHLCYACNNNGVCHEDTGEICOPGFMGRTCEKXCELHTFRTCKERSGQ 271
QY 37 EOGKFDHLRDCISCASICGQHPKQCAVFC 67
DB 272 EGCKSYVFCLEPDPYGSCATGWMKGLQCNEAC 302

RESULT 13
US-08-323-474-2
/ Sequence 2, Application US/08323474
/ Patent No. 5447860
/ GENERAL INFORMATION:
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; APPLICANT: Ziegler, Steven F.
; TITLE OF INVENTION: NOVEL TYROSINE KINASE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Protein Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/323,474
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/905,600
; FILING DATE: 26-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2609
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-06093-2
;
; Query Match 17.3%; Score 70; DB 1; Length 1124;
; Best Local Similarity 26.4%; Pred. No. 9.1;
; Matches 24; Conservative 4; Mismatches 37; Indels 26; Gaps 3;
;
; QY 3 EQQYDHP-----LLGTCM-----SKTTCN-HOSORTCAAFCCRK 36
; DB 212 EAQKWGPECNHLCTACNMNGVCHDTGECICPPGFMGRTCEKACELHTFGRTCKERCSCG 271
;
; QY 37 EQQFYDHLRLDCISCASICGQHPKQCAVFC 67
; DB 272 EGCKSYVFCPLDPYGCSCATGWKGLQCNEAC 302
;
; RESULT 14
; US-08-465-380-6
; Sequence 2, Application PC/TUS9306093
; GENERAL INFORMATION:
; APPLICANT: Ziegler, Steven F.
; TITLE OF INVENTION: NOVEL TYROSINE KINASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06093
; FILING DATE: 19930625
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; Query Match 17.3%; Score 70; DB 1; Length 1124;
; Best Local Similarity 26.4%; Pred. No. 9.1;
; Matches 24; Conservative 4; Mismatches 37; Indels 26; Gaps 3;
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; QY 3 EQQYDHP-----LLGTCM-----SKTTCN-HOSORTCAAFCCRK 36
; DB 212 EAQKWGPECNHLCTACNMNGVCHDTGECICPPGFMGRTCEKACELHTFGRTCKERCSCG 271
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; QY 37 EQQFYDHLRLDCISCASICGQHPKQCAVFC 67
; DB 272 EGCKSYVFCPLDPYGCSCATGWKGLQCNEAC 302
;
; RESULT 14
; US-08-465-380-6
; Sequence 2, Application PC/TUS9306093
; GENERAL INFORMATION:
; APPLICANT: Ziegler, Steven F.
; TITLE OF INVENTION: NOVEL TYROSINE KINASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06093
; FILING DATE: 19930625
;
; Query Match 17.3%; Score 70; DB 5; Length 1124;
; Best Local Similarity 26.4%; Pred. No. 9.1;
; Matches 24; Conservative 4; Mismatches 37; Indels 26; Gaps 3;
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; QY 3 EQQYDHP-----LLGTCM-----SKTTCN-HOSORTCAAFCCRK 36
; DB 212 EAQKWGPECNHLCTACNMNGVCHDTGECICPPGFMGRTCEKACELHTFGRTCKERCSCG 271
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; QY 37 EQQFYDHLRLDCISCASICGQHPKQCAVFC 67
; DB 272 EGCKSYVFCPLDPYGCSCATGWKGLQCNEAC 302
;
; RESULT 15
; US-08-465-380-6
; Sequence 6, Application US/08465380
; GENERAL INFORMATION:
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
; APPLICANT: Yannick G.J. Ganssemans, Matthew Moyle,
; APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,380
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 213/268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
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TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-08-465-380-6

Query Match 17.2%; Score 69.5; DB 2; Length 75;
Best Local Similarity 27.9%; Pred. No. 0.79; Indels 11; Gaps 4;
Matches 19; Conservative 10; Mismatches 28;
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Qy 52 CASICGQH 59
Db 64 -EEECDOH 70

Search completed: January 7, 2003, 09:42:08
Job time : 9.22807 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 7, 2003, 09:40:20 ; Search time 5.03759 Seconds
(without alignments)
252.055 Million cell updates/sec

Title: US-09-855-158-16

Perfect score: 405

Sequence: 1 CPEEQYMDPLIGTMSCKTI.....DCISGASICGHPKQCAVFC 67

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Gapop 10.0, Gapext 0.5

Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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14: /cgn2_6/ptodata/1/pubpa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	393	97.0	251	9	US-09-779-050A-42
5	393	97.0	253	9	US-10-084-971-2
6	393	97.0	293	10	US-09-879-919-22
7	393	97.0	293	10	US-09-854-864-14
8	393	97.0	293	10	US-09-854-864-12
9	393	97.0	397	10	US-09-854-864-18
10	313	77.3	59	10	US-09-854-864-20
11	304	50.4	38	9	US-09-779-050A-46
12	201	49.6	37	9	US-09-779-050A-45
13	105	25.9	81	10	US-09-854-864-13
14	84.5	20.9	220	10	US-10-042-141-54
15	84.5	20.9	220	10	US-09-726-643-54
16	76.5	18.9	207	9	US-10-077-438-3
17	76.5	18.9	207	9	US-10-077-437-3
18	76.5	18.9	354	10	US-09-956-095-2
19	76.5	18.9	354	10	US-09-219-345A-11

20	76.5	18.9	354	10	US-09-795-006A-119	Sequence 119, App
21	76.5	18.9	362	12	US-10-139-876-4	Sequence 4, Appl1
22	76	18.8	77	10	US-09-840-795-17	Sequence 17, Appl
23	76	18.8	231	10	US-09-840-795-19	Sequence 19, Appl
24	76	18.8	299	9	US-10-119-466-12	Sequence 12, Appl1
25	75	18.5	1497	10	US-09-060-854B-2	Sequence 2, Appl1
26	72	17.8	100	10	US-09-864-761-47388	Sequence 47388, A
27	71	17.5	1617	10	US-09-784-358-16	Sequence 16, Appl
28	71	17.5	1691	10	US-09-784-358-2	Sequence 2, Appl1
29	67.5	16.7	3084	10	US-09-938-275-4	Sequence 4, Appl1
30	66.5	16.4	34	10	US-09-854-864-7	Sequence 7, Appl1
31	66.5	16.4	51	10	US-09-854-864-6	Sequence 6, Appl1
32	66.5	16.4	58	10	US-09-854-864-21	Sequence 21, Appl1
33	66.5	16.4	181	10	US-09-854-864-5	Sequence 5, Appl1
34	66.5	16.4	184	9	US-10-077-438-1	Sequence 1, Appl1
35	66.5	16.4	184	9	US-10-077-438-7	Sequence 7, Appl1
36	66.5	16.4	184	9	US-10-077-137-7	Sequence 7, Appl1
37	66.5	16.4	184	9	US-10-077-137-7	Sequence 7, Appl1
38	66.5	16.4	184	9	US-09-854-864-9	Sequence 9, Appl1
39	66.5	16.4	184	9	US-09-854-864-13	Sequence 13, Appl1
40	65.5	16.2	358	12	US-10-139-876-4	Sequence 12, Appl1
41	65.5	16.2	358	12	US-10-139-876-4	Sequence 12, Appl1
42	65	16.0	292	10	US-09-745-763-166	Sequence 166, App
43	65	16.0	4679	10	US-09-804-898-2	Sequence 2, Appl1
44	64.5	15.9	798	9	US-10-117-295A-1	Sequence 1, Appl1
45	64	15.8	162	10	US-09-798-789-13	Sequence 13, Appl1

ALIGNMENTS

RESULT 1
US-09-854-864-16
; Sequence 16, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/570, BCMA,
; TITLE OF INVENTION: BLS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-16

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Best Local Similarity 100.0%; Pred. No. 2.8e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPEEQYMDPLIGTMSCKTICNHQSORTCAFCCKRKGKGFYHLADDCISGASICGHP 60
DB 1 CPEEQYMDPLIGTMSCKTICNHQSORTCAFCCKRKGKGFYHLADDCISGASICGHP 60
QY 61 KQCAVFC 67
DB 61 KQCAVFC 67
RESULT 2
US-09-854-864-15
; Sequence 15, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:

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; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TAC1
; CURRENT FILING DATE: 2001-02-12
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-854-864-15

Query Match          97.0%; Score 393; DB 10; Length 166;
Best Local Similarity 94.4%; Pred. No. 9e-32; 0; Indels 4; Gaps 1;
Matches 67; Conservative

Qy 1 CPEQYWDPLLGTCMSCKTICNHQSORTCAAF-----CRKEQKGYDHLRLDCISCASIC 56
Db 34 CPEQYWDPLLGTCMSCKTICNHQSORTCAAFCSRSLSCRKEQKGYDHLRLDCISCASIC 93

Qy 57 GQHPKQCAFC 67
Db 94 GQHPKQCAFC 104

RESULT 3
US-09-779-050A-43
; Sequence 43, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-779-050A-43

Query Match          97.0%; Score 393; DB 9; Length 291;
Best Local Similarity 94.4%; Pred. No. 1.5e-31;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 CPEQYWDPLLGTCMSCKTICNHQSORTCAAF-----CRKEQKGYDHLRLDCISCASIC 56
Db 34 CPEQYWDPLLGTCMSCKTICNHQSORTCAAFCSRSLSCRKEQKGYDHLRLDCISCASIC 93

Qy 57 GQHPKQCAFC 67
Db 94 GQHPKQCAFC 104

US-09-779-050A-42
; Sequence 42, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-779-050A-42

Query Match          97.0%; Score 393; DB 9; Length 293;
Best Local Similarity 94.4%; Pred. No. 1.5e-31;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

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Db 34 CPEQYWDPLLGTCMSCKTICNHQSORTCAAFCSRSLSCRKEQKGYDHLRLDCISCASIC 93

Qy 57 GQHPKQCAFC 67
Db 94 GQHPKQCAFC 104

US-09-879-919-22
; Sequence 22, Application US/09879919
; Patent No. US20020064829A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P1
; CURRENT APPLICATION NUMBER: US/09/879,919
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; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-919-22

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Best Local Similarity 94.4%; Pred. No. 1,5e-31;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

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DB 34 CPEQYWDPLGTGCMSCKTCNHOSQRTCAFCRSLSCKREQKGYDHLRDCISCASIC 93
QY 57 GQHPKQCAVFC 67
DB 94 GQHPKQCAVFC 104

RESULT 7
US-09-854-864-14
; Sequence 14, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-14

Query Match          97.0%; Score 393; DB 10; Length 293;
Best Local Similarity 94.4%; Pred. No. 1,5e-31;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

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DB 34 CPEQYWDPLGTGCMSCKTCNHOSQRTCAFCRSLSCKREQKGYDHLRDCISCASIC 93
QY 57 GQHPKQCAVFC 67
DB 94 GQHPKQCAVFC 104
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RESULT 8
US-09-961-376-2
; Sequence 2, Application US/09961376
; Patent No. US20020106736A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR17
; FILE REFERENCE: PFS24P1
; CURRENT APPLICATION NUMBER: US/09/961,376
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/254,874
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/235,991
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/533,822
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/188,208
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-376-2

Query Match          97.0%; Score 393; DB 10; Length 293;
Best Local Similarity 94.4%; Pred. No. 1,5e-31;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

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QY 57 GQHPKQCAVFC 67
DB 94 GQHPKQCAVFC 104

RESULT 9
US-09-854-864-18
; Sequence 18, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 18
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-18

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Best Local Similarity 94.4%; Pred. No. 1,9e-31;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

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DB 34 CPEQYWDPLGTGCMSCKTCNHOSQRTCAFCRSLSCKREQKGYDHLRDCISCASIC 93
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? PRIOR APPLICATION NUMBER: PCT/US00/5187
? PRIOR FILING DATE: 2000-06-02
? PRIOR APPLICATION NUMBER: 60/037,725
? PRIOR FILING DATE: 1999-06-07
? NUMBER OF SEQ ID NOS: 190
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 54
? LENGTH: 220
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: SITE
? LOCATION: (170)
? OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
? US-10-042-141-54

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Gencore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

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543.836 Million cell updates/sec

Title: US-09-855-158-16

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	393	97.0	293	6	US-10-268-951-22
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4	393	97.0	293	6	US-10-293-816-2
5	393	97.0	301	6	US-10-258-368-12
6	393	97.0	324	6	US-10-258-368-8
7	393	97.0	366	6	US-10-258-368-6
8	393	97.0	404	6	US-10-258-368-15
9	393	97.0	34	1	PCT-US02-34376-14
10	204	50.4	34	6	US-10-281-053-14
11	204	49.6	33	6	PCT-US02-34376-13
12	201	49.6	33	6	US-10-281-053-13
13	201	48.9	325	6	US-10-274-953-3
14	18.5	18.9	354	6	US-10-274-953-5
15	18.5	18.5	1548	6	US-10-180-903-2
16	74.5	18.4	685	5	US-09-724-676-81464
17	74.5	18.4	685	5	US-09-724-676A-81464
18	74.5	18.4	687	5	US-09-724-676-81462
19	74.5	18.4	687	5	US-09-724-676A-81462
20	74.5	18.4	700	5	US-09-724-676-81463
21	74.5	18.4	700	5	US-09-724-676A-81463
22	74.5	18.4	700	5	US-09-724-676A-81463
23	74.5	18.4	700	5	US-09-724-676A-81466
24	74.5	18.4	713	5	US-09-724-676-81467
25	74.5	18.4	713	5	US-09-724-676A-81467
26	74.5	18.4	733	5	US-09-724-676-81444

27	74.5	18.4	733	5	US-09-724-676A-81444	Sequence 81444, A
28	74.5	18.4	735	5	US-09-724-676-81442	Sequence 81442, A
29	74.5	18.4	735	5	US-09-724-676A-81442	Sequence 81442, A
30	74.5	18.4	748	5	US-09-724-676-81443	Sequence 81443, A
31	74.5	18.4	748	5	US-09-724-676-81446	Sequence 81446, A
32	74.5	18.4	748	5	US-09-724-676A-81443	Sequence 81443, A
33	74.5	18.4	748	5	US-09-724-676A-81446	Sequence 81446, A
34	74.5	18.4	752	5	US-09-724-676-81457	Sequence 81457, A
35	74.5	18.4	752	5	US-09-724-676A-81457	Sequence 81457, A
36	74.5	18.4	754	5	US-09-724-676-81455	Sequence 81455, A
37	74.5	18.4	754	5	US-09-724-676A-81455	Sequence 81455, A
38	74.5	18.4	760	5	US-09-724-676-81458	Sequence 81458, A
39	74.5	18.4	760	5	US-09-724-676A-81447	Sequence 81447, A
40	74.5	18.4	761	5	US-09-724-676-81447	Sequence 81447, A
41	74.5	18.4	778	5	US-09-724-676A-81453	Sequence 81453, A
42	74.5	18.4	778	5	US-09-724-676-81453	Sequence 81453, A
43	74.5	18.4	780	5	US-09-724-676-81451	Sequence 81451, A
44	74.5	18.4	780	5	US-09-724-676A-81451	Sequence 81451, A
45	74.5	18.4	780	5	US-09-724-676A-81451	Sequence 81451, A

ALIGNMENTS

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RESULT 1
US-10-293-816-6
Sequence 6 Application US/10293816
GENERAL INFORMATION:
APPLICANT: Yon, Richard J.
TITLE OF INVENTION: A LIPROCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CANAL AND METHODS OF USE THEREOF
FILE REFERENCE: 44158/254623
CURRENT APPLICATION NUMBER: US/10/293,816
PRIOR FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 09/782,857
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/290,333
PRIOR FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: US 08/810,572
PRIOR FILING DATE: 1997-03-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-816-6

Query Match          97.0% Score 393; DB 6; Length 166;
Best Local Similarity 94.4%; Pred. No. 1.8e-37;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 CPEBYWDPPLGTCTCMSCCKTICNHSQRTCAFC---CRKQGFYDHLIPDCTSCASIC 56
DB 34 CPEBYWDPPLGTCTCMSCCKTICNHSQRTCAFCRSLCKRQGFYDHLIPDCTSCASIC 93
QY 57 GQHPKOCAYFC 67
DB 94 GQHPKOCAYFC 104

RESULT 2
US-10-268-951-22
Sequence 22 Application US/10268951
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang, et al.
TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
FILE REFERENCE: P253P2
CURRENT APPLICATION NUMBER: US/10/268,951
CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 10/082,260
PRIOR FILING DATE: 2002-02-26
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; PRIOR APPLICATION NUMBER: 09/879,919
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/328,401
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/293,812
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-268-951-22

Query Match          97.0%; Score 393; DB 6; Length 293;
Best Local Similarity 94.4%; Pred. No. 2.7e-37;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 CPEEQYWDPLLGTCMCKTICNHQSORTCAAF-----CRKEQKGFYDHLRLDCISCASIC 56
Db 34 CPEEQYWDPLLGTCMCKTICNHQSORTCAAF-----CRKEQKGFYDHLRLDCISCASIC 93

QY 57 GOHPKQCAAYFC 67
Db 94 GOHPKQCAAYFC 104

RESULT 3
US-10-258-368-1
; Sequence 1, Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; APPLICANT: Rennett, Paul
; TITLE OF INVENTION: Taci As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT APPLICATION NUMBER: US/10/258,368
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: USSN 60/199,946
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-1

Query Match          97.0%; Score 393; DB 6; Length 293;
Best Local Similarity 94.4%; Pred. No. 2.7e-37;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 CPEEQYWDPLLGTCMCKTICNHQSORTCAAF-----CRKEQKGFYDHLRLDCISCASIC 56
Db 34 CPEEQYWDPLLGTCMCKTICNHQSORTCAAF-----CRKEQKGFYDHLRLDCISCASIC 93

QY 57 GOHPKQCAAYFC 67
Db 94 GOHPKQCAAYFC 104
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RESULT 4
US-10-293-816-2
; Sequence 2, Application US/10293816
; GENERAL INFORMATION:
; APPLICANT: Von Bulow, Gotz
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/10/293,816
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-816-2

Query Match          97.0%; Score 393; DB 6; Length 293;
Best Local Similarity 94.4%; Pred. No. 2.7e-37;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 CPEEQYWDPLLGTCMCKTICNHQSORTCAAF-----CRKEQKGFYDHLRLDCISCASIC 56
Db 34 CPEEQYWDPLLGTCMCKTICNHQSORTCAAF-----CRKEQKGFYDHLRLDCISCASIC 93

QY 57 GOHPKQCAAYFC 67
Db 94 GOHPKQCAAYFC 104

RESULT 5
US-10-258-368-12
; Sequence 12, Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; APPLICANT: Rennett, Paul
; TITLE OF INVENTION: Taci As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT APPLICATION NUMBER: US/10/258,368
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: USSN 60/199,946
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 12
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-12

Query Match          97.0%; Score 393; DB 6; Length 301;
Best Local Similarity 94.4%; Pred. No. 2.7e-37;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 CPEEQYWDPLLGTCMCKTICNHQSORTCAAF-----CRKEQKGFYDHLRLDCISCASIC 56
Db 42 CPEEQYWDPLLGTCMCKTICNHQSORTCAAF-----CRKEQKGFYDHLRLDCISCASIC 101

QY 57 GOHPKQCAAYFC 67
Db 102 GOHPKQCAAYFC 112
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RESULT 6
US-10-258-368-8
; Sequence 8 Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; APPLICANT: Renner, Paul
; TITLE OF INVENTION: Tact As As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT APPLICATION NUMBER: US/10/258,368
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: USSN 60/199,946
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-8

Query Match          97.0%; Score 393; DB 6; Length 334;
Best Local Similarity 94.4%; Pred. No. 2,9e-37;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 CPEQYMDPLGTGMSCTTCNHSORTCAFC-----CRKQKGFYDHLRDCISASC 56
Db 25 CPEQYMDPLGTGMSCTTCNHSORTCAFCRSLSCKRQKGFYDHLRDCISASC 84
Qy 57 GQHPKQCAVFC 67
Db 85 GQHPKQCAVFC 95

RESULT 7
US-10-258-368-6
; Sequence 6 Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; APPLICANT: Renner, Paul
; TITLE OF INVENTION: Tact As As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT APPLICATION NUMBER: US/10/258,368
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: USSN 60/199,946
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-6

Query Match          97.0%; Score 393; DB 6; Length 366;
Best Local Similarity 94.4%; Pred. No. 3,2e-37;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 CPEQYMDPLGTGMSCTTCNHSORTCAFC-----CRKQKGFYDHLRDCISASC 56
Db 57 CPEQYMDPLGTGMSCTTCNHSORTCAFCRSLSCKRQKGFYDHLRDCISASC 116
Qy 57 GQHPKQCAVFC 67
Db 117 GQHPKQCAVFC 127

RESULT 8
US-10-258-368-15
; Sequence 15 Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; APPLICANT: Renner, Paul
; TITLE OF INVENTION: Tact As As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT APPLICATION NUMBER: US/10/258,368
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: USSN 60/199,946
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-15

Query Match          97.0%; Score 393; DB 6; Length 404;
Best Local Similarity 94.4%; Pred. No. 3,4e-37;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 CPEQYMDPLGTGMSCTTCNHSORTCAFC-----CRKQKGFYDHLRDCISASC 56
Db 51 CPEQYMDPLGTGMSCTTCNHSORTCAFCRSLSCKRQKGFYDHLRDCISASC 110
Qy 57 GQHPKQCAVFC 67
Db 111 GQHPKQCAVFC 121

RESULT 9
PCT-US02-34376-14
; Sequence 14 Application PC/TUS0234376
; GENERAL INFORMATION:
; APPLICANT: Zhang, Gongyi
; APPLICANT: Shu, Hong-Bing
; APPLICANT: Liu, Yingfang
; APPLICANT: Xu, Liangguo
; TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
; FILE REFERENCE: 2879-86-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/34376
; PRIOR FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,106
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/348,962
; PRIOR FILING DATE: 2002-01-14/354,966
; PRIOR APPLICATION NUMBER: 60/354,966
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/403,364
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-34376-14

Query Match          50.4%; Score 204; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1,5e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 CRKQKGFYDHLRDCISASCICGQHPKQCAVFC 67
Db 1 CRKQKGFYDHLRDCISASCICGQHPKQCAVFC 34

RESULT 10
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;
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Breast
; US-10-274-953-3

Query Match 18.9%; Score 76.5; DB 6; Length 325;
Best Local Similarity 24.8%; Pred. No. 0.23;
Matches 28; Conservative 6; Mismatches 22; Indels 57; Gaps 7;

QY 1 CPEQYWD-----PLIGT-----CMSCRTICNH- 23
DB 193 CPIMLWDSNKKCVLOEENPLAGTETHSHLOEPALCGPHMFDRCBCV-CKTPCPKD 251
QY 24 --QSORTCAAF-----CCRKQGFYDHL--RDCISCASICGHPKQCA 64
DB 252 LIQHPKNCSCFECKESLETCCQK-----HKLPHPTCSCEDRCPPHTRPCA 297

RESULT 14
US-10-274-953-5
; Sequence 5, Application US/10274953
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Karl ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKee, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/274,953
; FILING DATE: 22-oct-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/296,275
; FILING DATE:
; APPLICATION NUMBER: 08/915,795
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354 amino acids

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Lung
; US-10-274-953-5

Query Match 18.9%; Score 76.5; DB 6; Length 354;
Best Local Similarity 24.8%; Pred. No. 0.25;
Matches 28; Conservative 6; Mismatches 22; Indels 57; Gaps 7;

QY 1 CPEQYWD-----PLIGT-----CMSCRTICNH- 23
DB 222 CPIMLWDSNKKCVLOEENPLAGTETHSHLOEPALCGPHMFDRCBCV-CKTPCPKD 280
QY 24 --QSORTCAAF-----CCRKQGFYDHL--RDCISCASICGHPKQCA 64
DB 281 LIQHPKNCSCFECKESLETCCQK-----HKLPHPTCSCEDRCPPHTRPCA 326

RESULT 15
US-10-180-903-2
; Sequence 2, Application US/10180903
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: SPC6 SERINE PROTEASE GENE DISRUPTIONS,
; FILE REFERENCE: R-720
; CURRENT APPLICATION NUMBER: US/10/180,903
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/300,978
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/324,820
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 1548
; TYPE: prt
; ORGANISM: Mus Musculus
; US-10-180-903-2

Query Match 18.5%; Score 75; DB 6; Length 1548;
Best Local Similarity 25.0%; Pred. No. 1.1;
Matches 21; Conservative 5; Mismatches 34; Indels 24; Gaps 3;

QY 1 CPEQYWDPLIGTMSCKTICNHOS-----QRTCAFCCKRQKGFYD 43
DB 1152 CAAYVWDEGSHRCQPCRRKCSRGSPSEDQCYTCPRFTPLNTTCKEC---BEGYHTD 1208
QY 44 HLLRDCISCASIC---GQHPKQC 63
DB 1209 KDSQOCVLCSSCRTEGPHSMQC 1232

Search completed: January 7, 2003, 09:54:19
Job time : 9.73183 secs

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GenCore version 5.1.3
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OM protein - protein seq, using sw model

Run on: January 7, 2003, 09:37:34 ; Search time 112.338 Seconds

(without alignments)
384.527 Million cell updates/sec

Title: US-09-855-158-16

Perfect score: 405

Sequence: 1 CPEEQYMDPLIGTCMSCKTI.....DCISCSICGHPKCAVFC 67

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents: AA Main:*

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27: /cgn2_6/ptodata/1/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	405	100.0	67	22	US-09-854-864-16
2	405	100.0	67	22	US-09-855-158-16
3	393	97.0	166	12	US-08-810-472-6
4	393	97.0	166	21	US-09-789-857-6
5	393	97.0	166	21	US-09-784-857A-6
6	393	97.0	166	22	US-09-854-864-15

7	393	97.0	166	22	US-09-855-158-15	Sequence 15, Appl
8	393	97.0	245	19	US-09-479-855-9	Sequence 9, Appl
9	393	97.0	245	19	US-09-569-245-9	Sequence 9, Appl
10	393	97.0	245	20	US-09-627-205-9	Sequence 9, Appl
11	393	97.0	245	21	US-09-724-341-9	Sequence 9, Appl
12	393	97.0	245	21	US-09-779-050A-43	Sequence 2, Appl
13	393	97.0	245	1	PCT-US00-07966-2	Sequence 2, Appl
14	393	97.0	245	1	PCT-US01-19028-22	Sequence 2, Appl
15	393	97.0	245	1	PCT-US02-16105-46	Sequence 2, Appl
16	393	97.0	245	12	US-08-810-572-2	Sequence 2, Appl
17	393	97.0	245	17	US-09-302-863-2	Sequence 2, Appl
18	393	97.0	245	17	US-09-479-856-6	Sequence 2, Appl
19	393	97.0	245	18	US-09-533-822-2	Sequence 2, Appl
20	393	97.0	245	19	US-09-569-245-6	Sequence 2, Appl
21	393	97.0	245	21	US-09-627-205-6	Sequence 2, Appl
22	393	97.0	245	21	US-09-724-341-2	Sequence 2, Appl
23	393	97.0	245	21	US-09-779-050A-42	Sequence 2, Appl
24	393	97.0	245	21	US-09-782-857-2	Sequence 2, Appl
25	393	97.0	245	21	US-09-782-857A-2	Sequence 2, Appl
26	393	97.0	245	22	US-09-848-295-4	Sequence 2, Appl
27	393	97.0	245	22	US-09-854-864-14	Sequence 14, Appl
28	393	97.0	245	22	US-09-855-158-14	Sequence 14, Appl
29	393	97.0	245	22	US-09-855-564-2	Sequence 2, Appl
30	393	97.0	245	22	US-09-879-912-22	Sequence 2, Appl
31	393	97.0	245	23	US-09-961-316-2	Sequence 2, Appl
32	393	97.0	245	23	US-10-008-065-8	Sequence 8, Appl
33	393	97.0	245	24	US-10-068-725-4	Sequence 8, Appl
34	393	97.0	245	24	US-10-084-971-2	Sequence 2, Appl
35	393	97.0	245	25	US-10-151-882-46	Sequence 2, Appl
36	393	97.0	245	25	US-10-152-363A-2	Sequence 2, Appl
37	393	97.0	245	25	US-10-152-363A-52	Sequence 52, Appl
38	393	97.0	245	25	US-10-152-363A-54	Sequence 54, Appl
39	393	97.0	245	25	US-10-152-363A-56	Sequence 56, Appl
40	393	97.0	245	25	US-10-152-363A-50	Sequence 50, Appl
41	393	97.0	245	25	US-09-854-864-18	Sequence 18, Appl
42	393	97.0	245	22	US-09-855-158-18	Sequence 18, Appl
43	393	97.0	245	22	US-09-854-864-20	Sequence 20, Appl
44	393	97.0	245	22	US-09-855-158-20	Sequence 20, Appl
45	393	97.0	245	22	US-09-855-158-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-09-854-864-16
Sequence 16, Application US/09854864
GENERAL INFORMATION: LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
PRIOR FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-16

Query Match 100.0%; Score 405; DB 22; Length 67;
Best Local Similarity 100.0%; Pred. No. 7e-35; 0; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 0

QY 1 CPEEQYMDPLIGTCMSCKTI CNHOSORTCAFCCKRQGRFYDHLFDICISCSICGHP 60
|||||

Db 1 CPEQYWDPLLTGTCMCKTICNHQSORTCAAFCCRKQKGFYDHLRLDCISCASICQHP 60
QY 61 KQAYFC 67
Db 61 KQAYFC 67

RESULT 2
US-09-855-158-16
; Sequence 16, Application US/09855158
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 16
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-16

Query Match 100.0%; Score 405; DB 22; Length 67;
Best Local Similarity 100.0%; Pred. No. 7e-35;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPEQYWDPLLTGTCMCKTICNHQSORTCAAFCCRKQKGFYDHLRLDCISCASICQHP 60
Db 1 CPEQYWDPLLTGTCMCKTICNHQSORTCAAFCCRKQKGFYDHLRLDCISCASICQHP 60

QY 61 KQAYFC 67
Db 61 KQAYFC 67

RESULT 3
US-08-810-572-6
; Sequence 6, Application US/08810572
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 28-FEB-1997
; APPLICATION NUMBER: US/08/810,572
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742

; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-810-572-6

Query Match 97.0%; Score 393; DB 12; Length 166;
Best Local Similarity 94.4%; Pred. No. 3e-33;
Matches 67; Conservative 0; Mismatches 4; Gaps 1;

QY 1 CPEQYWDPLLTGTCMCKTICNHQSORTCAAFCCRKQKGFYDHLRLDCISCASIC 56
Db 34 CPEQYWDPLLTGTCMCKTICNHQSORTCAAFCCRKQKGFYDHLRLDCISCASIC 93

QY 57 GQHPKQAYFC 67
Db 94 GQHPKQAYFC 104

RESULT 4
US-09-782-857-6
; Sequence 6, Application US/09782857
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 14-FEB-2001
; APPLICATION NUMBER: US/09/782,857
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/810,572
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear


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;
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-782-857-6

Query Match          97.0%; Score 393; DB 21; Length 166;
Best Local Similarity 94.4%; Pred. No. 3e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

OY 1 CPEEQYWDPLGTGCMSCKTCINHSORTCAFC---CRKEQGFYDHLRDCISCASIC 56
DB 34 CPEEQYWDPLGTGCMSCKTCINHSORTCAFCRSLSCKREQGFYDHLRDCISCASIC 93
OY 57 GQHPKOCAYFC 67
DB 94 GQHPKOCAYFC 104

RESULT 5
US-09-782-857A-6
; Sequence 6, Application US/09782857A
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; THEREOF
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
;
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,857A
; FILING DATE: 14-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/810,572
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-782-857A-6

Query Match          97.0%; Score 393; DB 21; Length 166;
Best Local Similarity 94.4%; Pred. No. 3e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

OY 1 CPEEQYWDPLGTGCMSCKTCINHSORTCAFC---CRKEQGFYDHLRDCISCASIC 56
DB 34 CPEEQYWDPLGTGCMSCKTCINHSORTCAFCRSLSCKREQGFYDHLRDCISCASIC 93
OY 57 GQHPKOCAYFC 67
DB 94 GQHPKOCAYFC 104

RESULT 6
US-09-854-864-15
; Sequence 15, Application US/09854864
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-15

Query Match          97.0%; Score 393; DB 22; Length 166;
Best Local Similarity 94.4%; Pred. No. 3e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

OY 1 CPEEQYWDPLGTGCMSCKTCINHSORTCAFC---CRKEQGFYDHLRDCISCASIC 56
DB 34 CPEEQYWDPLGTGCMSCKTCINHSORTCAFCRSLSCKREQGFYDHLRDCISCASIC 93
OY 57 GQHPKOCAYFC 67
DB 94 GQHPKOCAYFC 104

RESULT 7
US-09-855-158-15
; Sequence 15, Application US/09855158
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; YS/AGP-3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-15

Query Match          97.0%; Score 393; DB 22; Length 166;
Best Local Similarity 94.4%; Pred. No. 3e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
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Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 1 CPEEQYWDPLGTCMCKTICNHQSORTCAAF-----CRKEQGFYDHLRLDCISCASIC 56
Db 34 CPEEQYWDPLGTCMCKTICNHQSORTCAAF-----CRKEQGFYDHLRLDCISCASIC 93
QY 57 GQHPKQCAAYFC 67
Db 94 GQHPKQCAAYFC 104

RESULT 8
US-09-479-856-9
; Sequence 9, Application US/09479856
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen
; APPLICANT: Yee, David P.
; TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
; CURRENT APPLICATION NUMBER: US/09/479,856
; EARLIER FILING DATE: 2000-01-07
; EARLIER FILING DATE: 1999-01-07
; EARLIER FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-479-856-9

Query Match 97.0%; Score 393; DB 18; Length 245;
Best Local Similarity 94.4%; Pred. No. 4.3e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 1 CPEEQYWDPLGTCMCKTICNHQSORTCAAF-----CRKEQGFYDHLRLDCISCASIC 56
Db 30 CPEEQYWDPLGTCMCKTICNHQSORTCAAF-----CRKEQGFYDHLRLDCISCASIC 89
QY 57 GQHPKQCAAYFC 67
Db 90 GQHPKQCAAYFC 100

RESULT 9
US-09-569-245-9
; Sequence 9, Application US/09569245
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen
; APPLICANT: Yee, David P.
; TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
; CURRENT APPLICATION NUMBER: US/09/569,245
; CURRENT FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 60/115,068
; PRIOR FILING DATE: 1999-01-07
; PRIOR APPLICATION NUMBER: 60/169,890
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/479,856
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-569-245-9

Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 1 CPEEQYWDPLGTCMCKTICNHQSORTCAAF-----CRKEQGFYDHLRLDCISCASIC 56
Db 30 CPEEQYWDPLGTCMCKTICNHQSORTCAAF-----CRKEQGFYDHLRLDCISCASIC 89
QY 57 GQHPKQCAAYFC 67
Db 90 GQHPKQCAAYFC 100

RESULT 10
US-09-627-206-9
; Sequence 9, Application US/09627206
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen
; APPLICANT: Yee, David P.
; TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
; CURRENT APPLICATION NUMBER: US/09/627,206
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/115,068
; PRIOR FILING DATE: 1999-01-07
; PRIOR APPLICATION NUMBER: 60/169,890
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/479,856
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/569,245
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-627-206-9

Query Match 97.0%; Score 393; DB 20; Length 245;
Best Local Similarity 94.4%; Pred. No. 4.3e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 1 CPEEQYWDPLGTCMCKTICNHQSORTCAAF-----CRKEQGFYDHLRLDCISCASIC 56
Db 30 CPEEQYWDPLGTCMCKTICNHQSORTCAAF-----CRKEQGFYDHLRLDCISCASIC 89
QY 57 GQHPKQCAAYFC 67
Db 90 GQHPKQCAAYFC 100

RESULT 11
US-09-724-341-9
; Sequence 9, Application US/09724341
; GENERAL INFORMATION:
; APPLICANT: AVI J. ASHKENAZI
; APPLICANT: KELLY H. DODGE
; APPLICANT: IOBAL GREWAL
; APPLICANT: KYUNG JIN KIM
; APPLICANT: SCOT A. MARSTERS
; APPLICANT: ROBERT M. PITTI
; APPLICANT: MINHONG YAN
; TITLE OF INVENTION: USES OF AGONISTS AND ANTAGONISTS TO MODULATE ACTIVITY
; FILE REFERENCE: P1805R1
; CURRENT APPLICATION NUMBER: US/09/724,341
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/182,938
; PRIOR FILING DATE: 2000-02-16
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Query Match 97.0%; Score 393; DB 19; Length 245;
Best Local Similarity 94.4%; Pred. No. 4.3e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 1 CPEEQYWDPLGTCMCKTICNHQSORTCAAF-----CRKEQGFYDHLRLDCISCASIC 56
Db 30 CPEEQYWDPLGTCMCKTICNHQSORTCAAF-----CRKEQGFYDHLRLDCISCASIC 89
QY 57 GQHPKQCAAYFC 67
Db 90 GQHPKQCAAYFC 100
```

```
RESULT 10
US-09-627-206-9
; Sequence 9, Application US/09627206
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen
; APPLICANT: Yee, David P.
; TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
; CURRENT APPLICATION NUMBER: US/09/627,206
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/115,068
; PRIOR FILING DATE: 1999-01-07
; PRIOR APPLICATION NUMBER: 60/169,890
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/479,856
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/569,245
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-627-206-9
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Query Match 97.0%; Score 393; DB 20; Length 245;
Best Local Similarity 94.4%; Pred. No. 4.3e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 1 CPEEQYWDPLGTCMCKTICNHQSORTCAAF-----CRKEQGFYDHLRLDCISCASIC 56
Db 30 CPEEQYWDPLGTCMCKTICNHQSORTCAAF-----CRKEQGFYDHLRLDCISCASIC 89
QY 57 GQHPKQCAAYFC 67
Db 90 GQHPKQCAAYFC 100
```

```
RESULT 11
US-09-724-341-9
; Sequence 9, Application US/09724341
; GENERAL INFORMATION:
; APPLICANT: AVI J. ASHKENAZI
; APPLICANT: KELLY H. DODGE
; APPLICANT: IOBAL GREWAL
; APPLICANT: KYUNG JIN KIM
; APPLICANT: SCOT A. MARSTERS
; APPLICANT: ROBERT M. PITTI
; APPLICANT: MINHONG YAN
; TITLE OF INVENTION: USES OF AGONISTS AND ANTAGONISTS TO MODULATE ACTIVITY
; FILE REFERENCE: P1805R1
; CURRENT APPLICATION NUMBER: US/09/724,341
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/182,938
; PRIOR FILING DATE: 2000-02-16
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; PRIOR APPLICATION NUMBER: US 60/226,986
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 9
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-341-9

Query Match
Best Local Similarity 97.0%; Score 393; DB 21; Length 265;
Best Local Similarity 94.4%; Pred. No. 4.7e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 CPEQYWDPLGTGCTMCKTICNHOSORTCAFC---CRKEQGFYDHLRDCISCASIC 56
Db 34 CPEQYWDPLGTGCTMCKTICNHOSORTCAFCRSLSCKRKGKFDHLRDCISCASIC 93
Qy 57 GQHPKQCAAYFC 67
Db 94 GQHPKQCAAYFC 104

RESULT 12
US-09-779-050A-43
; Sequence 43, Application US/09779050A
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-43

Query Match
Best Local Similarity 97.0%; Score 393; DB 21; Length 291;
Best Local Similarity 94.4%; Pred. No. 5.1e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 CPEQYWDPLGTGCTMCKTICNHOSORTCAFC---CRKEQGFYDHLRDCISCASIC 56
Db 34 CPEQYWDPLGTGCTMCKTICNHOSORTCAFCRSLSCKRKGKFDHLRDCISCASIC 93
Qy 57 GQHPKQCAAYFC 67
Db 94 GQHPKQCAAYFC 104

RESULT 13
PCT-US00-07966-2
; Sequence 2, Application PC/TUS0007966
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Neutrophin-alpha Binding Proteins and Methods Based Thereon
; FILE REFERENCE: PF54PCT
; CURRENT APPLICATION NUMBER: PCT/US00/07966
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,599
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/188,208
; EARLIER FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT

; ORGANISM: Homo sapiens
PCT-US00-07966-2

Query Match
Best Local Similarity 97.0%; Score 393; DB 1; Length 293;
Best Local Similarity 94.4%; Pred. No. 5.1e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 CPEQYWDPLGTGCTMCKTICNHOSORTCAFC---CRKEQGFYDHLRDCISCASIC 56
Db 34 CPEQYWDPLGTGCTMCKTICNHOSORTCAFCRSLSCKRKGKFDHLRDCISCASIC 93
Qy 57 GQHPKQCAAYFC 67
Db 94 GQHPKQCAAYFC 104

RESULT 14
PCT-US01-19026-22
; Sequence 22, Application PC/TUS0119026
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc., et al
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PR253PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19026
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19026-22

Query Match
Best Local Similarity 97.0%; Score 393; DB 1; Length 293;
Best Local Similarity 94.4%; Pred. No. 5.1e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

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Db 34 CPEQYWDPLGTGCTMCKTICNHOSORTCAFCRSLSCKRKGKFDHLRDCISCASIC 93
Qy 57 GQHPKQCAAYFC 67
Db 94 GQHPKQCAAYFC 104

RESULT 15
PCT-US02-16106-46
; Sequence 46, Application PC/TUS0216106
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF54PCT
; CURRENT APPLICATION NUMBER: PCT/US02/16106
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 293
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; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-16106-46

Query Match 97.0%; Score 393; DB 1; Length 293;
Best Local Similarity 94.4%; Pred. No. 5.1e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 CPEEQYWDPLLGTCMSCKTICNHOSQRTCAAF-----CRKEQKGYDHLRLDCISCASIC 56
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Db 34 CPEEQYWDPLLGTCMSCKTICNHOSQRTCAAFCRSLSCRKEQKGYDHLRLDCISCASIC 93
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QY 57 GQHPKQCAAYFC 67
|||
Db 94 GQHPKQCAAYFC 104
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Search completed: January 7, 2003, 09:53:21
Job time : 113.338 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:37:34 ; Search time 135.812 Seconds

(without alignments)
384.527 Million cell updates/sec

Title: US-09-855-158-13

Sequence: 1 CSQNEYFDSLHACIPCOLR.....SEYFDSLHACFPATCPYC 81

Scoring table:

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Searched: 4569144 seqs, 64473110 residues

4569144

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	498	100.0	81	22	US-09-854-864-13
2	498	100.0	81	22	US-09-855-158-13
3	230.5	46.3	207	24	US-10-077-137-3
4	230.5	46.3	207	24	US-10-077-438-3
5	205	41.2	302	25	US-10-115-192-12
6	205	41.2	302	27	US-60-215-688-12

7	201.5	40.5	283	22	US-09-854-864-9	Sequence 9, Appl
8	201.5	40.5	283	22	US-09-855-158-9	Sequence 9, Appl
9	201	40.4	34	22	US-09-854-864-7	Sequence 7, Appl
10	201	40.4	34	22	US-09-855-158-7	Sequence 7, Appl
11	201	40.4	51	22	US-09-854-864-6	Sequence 6, Appl
12	201	40.4	51	22	US-09-855-158-6	Sequence 6, Appl
13	201	40.4	58	22	US-09-854-864-21	Sequence 21, Appl
14	201	40.4	58	22	US-09-855-158-21	Sequence 21, Appl
15	201	40.4	181	22	US-09-854-864-5	Sequence 5, Appl
16	201	40.4	181	22	US-09-855-158-5	Sequence 5, Appl
17	201	40.4	184	1	PCT-US00-04625-1	Sequence 1, Appl
18	201	40.4	184	1	PCT-US00-04925-1	Sequence 1, Appl
19	201	40.4	184	18	PCT-US02-16106-47	Sequence 47, Appl
20	201	40.4	184	18	US-09-479-856-8	Sequence 8, Appl
21	201	40.4	184	19	US-09-565-423-11	Sequence 11, Appl
22	201	40.4	184	19	US-09-565-245-8	Sequence 8, Appl
23	201	40.4	184	20	US-09-627-206-8	Sequence 8, Appl
24	201	40.4	184	21	US-09-724-341-4	Sequence 4, Appl
25	201	40.4	184	23	US-09-914-119A-1	Sequence 1, Appl
26	201	40.4	184	24	US-10-008-063-7	Sequence 7, Appl
27	201	40.4	184	24	US-10-068-725-2	Sequence 2, Appl
28	201	40.4	184	24	US-10-077-137-1	Sequence 1, Appl
29	201	40.4	184	24	US-10-077-137-7	Sequence 1, Appl
30	201	40.4	184	24	US-10-077-438-1	Sequence 1, Appl
31	201	40.4	184	24	US-10-077-438-7	Sequence 7, Appl
32	201	40.4	184	25	US-10-115-192-8	Sequence 8, Appl
33	201	40.4	184	25	US-10-115-182-47	Sequence 47, Appl
34	201	40.4	184	25	US-10-152-363A-27	Sequence 27, Appl
35	201	40.4	184	27	US-60-215-688-8	Sequence 8, Appl
36	201	40.4	192	21	US-09-758-471-5100	Sequence 5100, Ap
37	201	40.4	192	26	US-10-235-953-5100	Sequence 5100, Ap
38	201	40.4	288	1	PCT-US02-06518-120	Sequence 120, Ap
39	153	30.7	117	22	US-09-854-864-12	Sequence 12, Appl
40	153	30.7	117	22	US-09-855-158-12	Sequence 12, Appl
41	139.5	28.0	281	22	US-09-854-864-10	Sequence 10, Appl
42	139.5	28.0	281	22	US-09-855-158-10	Sequence 10, Appl
43	136	27.3	185	1	PCT-US00-04665-2	Sequence 2, Appl
44	136	27.3	185	1	PCT-US00-04925-2	Sequence 2, Appl
45	136	27.3	185	19	US-09-565-423-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-854-864-13
; Sequence 13, Application US/09854864
; GENERAL INFORMATION:
; APPLICANT: THEIL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854, 864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204, 039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214, 591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13

Query Match 100.0%; Score 498; DB 22; Length 81;
Best Local Similarity 100.0%; Pred No. 3.2e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CSQNEYFDSLHACIPCOLRCSNTPLTORYCEYFDSLHACIPCOLRCSPTCYCCP 60
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Db 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCCYFDSLHACPCRLCSPPTCQYCCF 60
QY 61 HSEYFDSLHACPPATCPYC 81
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Db 61 HSEYFDSLHACPPATCPYC 81
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RESULT 2
US-09-855-158-13
; Sequence 13, Application US/09855158
; GENERAL INFORMATION:
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCWA, BI
; FILE REFERENCE: A-686A
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US/09/855,158
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-855-158-13

Query Match 100.0%; Score 498; DB 22; Length 81;
Best Local Similarity 100.0%; Pred. No. 3.2e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCCYFDSLHACPCRLCSPPTCQYCCF 60
Db 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCCYFDSLHACPCRLCSPPTCQYCCF 60

QY 61 HSEYFDSLHACPPATCPYC 81
Db 61 HSEYFDSLHACPPATCPYC 81

RESULT 3
US-10-077-137-3
; Sequence 3, Application US/10077137
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCWA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-3
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Query Match 46.3%; Score 230.5; DB 24; Length 207;
Best Local Similarity 57.8%; Pred. No. 2.5e-12;
Matches 48; Conservative 0; Mismatches 4; Indels 31; Gaps 4;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCCYFDSLHAC-PC-LRCSPTCQYC 58
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Db 46 CSQNEYFDSLHACIPQCLRCSSNTPPLTC-----LHACIPQCLRCSSNT- 90
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QY 59 CFHSEYFDSLHACPPATCPYC 81
Db 91 -----PPLTCQRYC 99
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RESULT 4
US-10-077-438-3
; Sequence 3, Application US/10077438
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCWA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-3
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Query Match 46.3%; Score 230.5; DB 24; Length 207;
Best Local Similarity 57.8%; Pred. No. 2.5e-12;
Matches 48; Conservative 0; Mismatches 4; Indels 31; Gaps 4;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCCYFDSLHAC-PC-LRCSPTCQYC 58
    |||||
Db 46 CSQNEYFDSLHACIPQCLRCSSNTPPLTC-----LHACIPQCLRCSSNT- 90
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QY 59 CFHSEYFDSLHACPPATCPYC 81
Db 91 -----PPLTCQRYC 99
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RESULT 5
US-10-115-192-12
; Sequence 12, Application US/10115192
; GENERAL INFORMATION:
; APPLICANT: Apotech R & D S.A.
; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: April Receptor (BCWA) and Uses Thereof
; FILE REFERENCE: A083PCT
; CURRENT APPLICATION NUMBER: US/10/115,192
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
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;; PRIOR FILING DATE: 1999-10-06
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 12
;; LENGTH: 302
;; TYPE: PRT
;; ORGANISM: homo sapiens
US-10-115-192-12

Query Match 41.2%; Score 205; DB 25; Length 302;
Best Local Similarity 67.8%; Pred. No. 6.1e-10;
Matches 40; Conservative 2; Mismatches 9; Indels 8; Gaps 3;

QY 1 CSONEYFDSLHACIPQCLRCSSNTPLTCORYC-CEYFDSL-----LHACPLRCSP 53
DB 31 CSONEYFDSLHACIPQCLRCSSNTPLTCORYCNCASVTNSVKGVDKHTCP--PCPAP 87

RESULT 6
US-60-215-688-12
;; Sequence 12, Application US/60215688
;; GENERAL INFORMATION:
;; APPLICANT: BIOGEN, INC.
;; TITLE OF INVENTION: APRIL RECEPTOR AND USES THEREOF
;; FILE REFERENCE: A083 P3
;; CURRENT APPLICATION NUMBER: US/60/215,688
;; PRIOR FILING DATE: 2000-06-30
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 12
;; LENGTH: 302
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-60-215-688-12

Query Match 41.2%; Score 205; DB 27; Length 302;
Best Local Similarity 67.8%; Pred. No. 6.1e-10;
Matches 40; Conservative 2; Mismatches 9; Indels 8; Gaps 3;

QY 1 CSONEYFDSLHACIPQCLRCSSNTPLTCORYC-CEYFDSL-----LHACPLRCSP 53
DB 31 CSONEYFDSLHACIPQCLRCSSNTPLTCORYCNCASVTNSVKGVDKHTCP--PCPAP 87

RESULT 7
US-09-854-864-9
;; Sequence 9, Application US/09854864
;; GENERAL INFORMATION:
;; APPLICANT: THEILL, LARS EYDE
;; APPLICANT: YU, GANG
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
;; FILE REFERENCE: A-686B
;; CURRENT APPLICATION NUMBER: US/09/854,864
;; PRIOR FILING DATE: 2001-09-11
;; PRIOR APPLICATION NUMBER: US 60/204,039
;; PRIOR FILING DATE: 2000-05-12
;; PRIOR APPLICATION NUMBER: US 60/214,591
;; PRIOR FILING DATE: 2000-06-27
;; NUMBER OF SEQ ID NOS: 31
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 9
;; LENGTH: 283
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-854-864-9

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Best Local Similarity 60.6%; Pred. No. 1.2e-09;
Matches 40; Conservative 2; Mismatches 9; Indels 15; Gaps 3;
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DB 5 CSONEYFDSLHACIPQCLRCSSNTPLTCORYCNCASVTNSVKGVDKHTCP--PCPAP 63
QY 48 LRCSP 53
DB 64 -PCPAP 68

RESULT 8
US-09-855-158-9
;; Sequence 9, Application US/09855158
;; GENERAL INFORMATION:
;; APPLICANT: THEILL, LARS EYDE
;; APPLICANT: YU, GANG
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
;; FILE REFERENCE: A-686A
;; CURRENT APPLICATION NUMBER: US/09/855,158
;; PRIOR FILING DATE: 2001-09-11
;; PRIOR APPLICATION NUMBER: US 60/214,591
;; PRIOR FILING DATE: 2000-06-27
;; PRIOR APPLICATION NUMBER: US 60/204,039
;; PRIOR FILING DATE: 2000-05-12
;; NUMBER OF SEQ ID NOS: 30
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 9
;; LENGTH: 283
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-855-158-9

Query Match 40.5%; Score 201.5; DB 22; Length 283;
Best Local Similarity 60.6%; Pred. No. 1.2e-09;
Matches 40; Conservative 2; Mismatches 9; Indels 15; Gaps 3;

QY 1 CSONEYFDSLHACIPQCLRCSSNTPLTCORYC-CEYFDSL-----LHACPC 47
DB 5 CSONEYFDSLHACIPQCLRCSSNTPLTCORYCNCASVTNSVKGVDKHTCP--PCPAP 63

QY 48 LRCSP 53
DB 64 -PCPAP 68

RESULT 9
US-09-854-864-7
;; Sequence 7, Application US/09854864
;; GENERAL INFORMATION:
;; APPLICANT: THEILL, LARS EYDE
;; APPLICANT: YU, GANG
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
;; FILE REFERENCE: A-686B
;; CURRENT APPLICATION NUMBER: US/09/854,864
;; PRIOR FILING DATE: 2001-09-11
;; PRIOR APPLICATION NUMBER: US 60/204,039
;; PRIOR FILING DATE: 2000-05-12
;; PRIOR APPLICATION NUMBER: US 60/214,591
;; PRIOR FILING DATE: 2000-06-27
;; NUMBER OF SEQ ID NOS: 31
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 7
;; LENGTH: 34
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-854-864-7

Query Match 40.4%; Score 201; DB 22; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSONEYFDSLHACIPQCLRCSSNTPLTCORYC 34
DB 1 CSONEYFDSLHACIPQCLRCSSNTPLTCORYC 34

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; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-6

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Best Local Similarity 100.0%; Pred. No. 3.2e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34

RESULT 10
US-09-855-158-7
; Sequence 6, Application US/09855158
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCWA, BI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-7

Query Match          40.4%; Score 201; DB 22; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34

RESULT 11
US-09-854-864-6
; Sequence 6, Application US/09854864
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCWA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-6

Query Match          40.4%; Score 201; DB 22; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 5 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 38

RESULT 12
US-09-855-158-6
; Sequence 6, Application US/09855158
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCWA, BI
```

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; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-6

Query Match          40.4%; Score 201; DB 22; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
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QY 1 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 5 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 38

RESULT 13
US-09-854-864-21
; Sequence 21, Application US/09854864
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCWA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-21

Query Match          40.4%; Score 201; DB 22; Length 58;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 1 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34

RESULT 14
US-09-855-158-21
; Sequence 21, Application US/09855158
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCWA, BI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
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SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-21

Query Match 40.4%; Score 201; DB 22; Length 58;
Best Local Similarity 100.0%; Pred. No. 3.Se-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CSQNEYFDSLHACIPQCRCSNTPPLTCQRYC 34

RESULT 15
US-09-854-864-5
; Sequence 5, Application US/09854864
; GENERAL INFORMATION:
; APPLICANT: THEILL, IARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5

Query Match 40.4%; Score 201; DB 22; Length 181;
Best Local Similarity 100.0%; Pred. No. 9e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCRCSNTPPLTCQRYC 34
Db 5 CSQNEYFDSLHACIPQCRCSNTPPLTCQRYC 38

Search completed: January 7, 2003, 09:53:19
Job time : 136.812 secs

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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:37:34 ; Search time 57.0075 Seconds
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Title: US-09-855-158-7

Sequence: 1 CSONEYFDLHACIPCOLRCSNTPPLTCORYC 34

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Total number of hits satisfying chosen parameters: 4569144

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	201	100.0	34	22	US-09-855-158-7
3	201	100.0	51	22	US-09-854-864-6
4	201	100.0	51	22	US-09-855-158-6
5	201	100.0	58	22	US-09-854-864-21
6	201	100.0	58	22	US-09-855-158-21

7	201	100.0	81	22	US-09-854-864-13	Sequence 13, Appl
8	201	100.0	81	22	US-09-855-158-13	Sequence 13, Appl
9	201	100.0	181	22	US-09-854-864-5	Sequence 5, Appl
10	201	100.0	181	22	US-09-855-158-5	Sequence 5, Appl
11	201	100.0	184	1	PCT-US00-04665-1	Sequence 1, Appl
12	201	100.0	184	1	PCT-US00-04665-1	Sequence 1, Appl
13	201	100.0	184	1	PCT-US02-16106-47	Sequence 47, Appl
14	201	100.0	184	18	US-09-479-856-8	Sequence 8, Appl
15	201	100.0	184	19	US-09-565-423-11	Sequence 11, Appl
16	201	100.0	184	19	US-09-569-245-8	Sequence 8, Appl
17	201	100.0	184	20	US-09-627-206-8	Sequence 8, Appl
18	201	100.0	184	21	US-09-724-341-4	Sequence 1, Appl
19	201	100.0	184	23	US-09-914-119A-1	Sequence 1, Appl
20	201	100.0	184	24	US-10-008-063-7	Sequence 2, Appl
21	201	100.0	184	24	US-10-068-725-2	Sequence 2, Appl
22	201	100.0	184	24	US-10-077-137-1	Sequence 7, Appl
23	201	100.0	184	24	US-10-077-137-7	Sequence 7, Appl
24	201	100.0	184	24	US-10-077-438-1	Sequence 7, Appl
25	201	100.0	184	24	US-10-077-438-7	Sequence 7, Appl
26	201	100.0	184	25	US-10-115-192-8	Sequence 8, Appl
27	201	100.0	184	25	US-10-151-883-47	Sequence 27, Appl
28	201	100.0	184	25	US-10-152-363A-27	Sequence 27, Appl
29	201	100.0	184	27	US-09-758-471-5100	Sequence 5100, Ap
30	201	100.0	182	21	US-09-758-471-5100	Sequence 5100, Ap
31	201	100.0	182	26	US-10-235-953-5100	Sequence 5100, Ap
32	201	100.0	283	22	US-09-854-864-9	Sequence 9, Appl
33	201	100.0	283	22	US-09-855-158-9	Sequence 9, Appl
34	201	100.0	288	1	PCT-US02-06518-120	Sequence 120, Appl
35	201	100.0	302	25	US-10-115-192-12	Sequence 12, Appl
36	201	100.0	302	27	US-10-215-688-12	Sequence 12, Appl
37	201	100.0	207	24	US-10-077-137-3	Sequence 3, Appl
38	181	90.0	207	24	US-10-077-438-3	Sequence 3, Appl
39	136	67.7	185	1	PCT-US00-04665-2	Sequence 2, Appl
40	136	67.7	185	19	US-09-565-423-17	Sequence 17, Appl
41	136	67.7	185	22	US-09-854-864-11	Sequence 11, Appl
42	136	67.7	185	22	US-09-855-158-11	Sequence 11, Appl
43	136	67.7	185	23	US-09-914-119A-2	Sequence 2, Appl
44	136	67.7	185	23	US-09-914-119A-2	Sequence 2, Appl
45	136	67.7	281	22	US-09-854-864-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-854-864-7
Sequence 7, Application US/09854864
GENERAL INFORMATION: LARS EYDE
APPLICANT: TUL GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
FILE REFERENCE: A-686B
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US/09/854,864
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 34
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-7
Query Match 100.0%; Score 201; DB 22;
Best local similarity 100.0%; Pred. No. 8, 1e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 CSONEYFDLHACIPCOLRCSNTPPLTCORYC 34
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NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 21
LENGTH: 58
TYPE: PRT
ORGANISM: Homo sapiens
US-09-855-158-21

Query Match 100.0%; Score 201; DB 22; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPCOLRCSSNTPLTCORYC 34
Db 1 CSONEYFDSLHACIPCOLRCSSNTPLTCORYC 34

RESULT 7
US-09-854-864-13

Sequence 13, Application US/09854864
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 81
TYPE: PRT
ORGANISM: Consensus
US-09-854-864-13

Query Match 100.0%; Score 201; DB 22; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.8e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CSONEYFDSLHACIPCOLRCSSNTPLTCORYC 34

RESULT 8
US-09-855-158-13

Sequence 13, Application US/09855158
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BI
FILE REFERENCE: A-686A
CURRENT APPLICATION NUMBER: US/09/855,158
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 81
TYPE: PRT
ORGANISM: Consensus
US-09-855-158-13

Query Match 100.0%; Score 201; DB 22; Length 81;

Best Local Similarity 100.0%; Pred. No. 1.8e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPCOLRCSSNTPLTCORYC 34
Db 1 CSONEYFDSLHACIPCOLRCSSNTPLTCORYC 34

RESULT 9
US-09-854-864-5

Sequence 5, Application US/09854864
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 181
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-5

Query Match 100.0%; Score 201; DB 22; Length 181;
Best Local Similarity 100.0%; Pred. No. 3.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPCOLRCSSNTPLTCORYC 34
Db 5 CSONEYFDSLHACIPCOLRCSSNTPLTCORYC 38

RESULT 10
US-09-855-158-5

Sequence 5, Application US/09855158
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BI
FILE REFERENCE: A-686A
CURRENT APPLICATION NUMBER: US/09/855,158
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 181
TYPE: PRT
ORGANISM: Homo sapiens
US-09-855-158-5

Query Match 100.0%; Score 201; DB 22; Length 181;
Best Local Similarity 100.0%; Pred. No. 3.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPCOLRCSSNTPLTCORYC 34
Db 5 CSONEYFDSLHACIPCOLRCSSNTPLTCORYC 38

RESULT 11

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PCT-US00-04665-1
; Sequence 1, Application PC/TUS00004665
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: METHOD FOR CLONING SIGNAL TRANSDUCTION
; FILE REFERENCE: 00786/371WO2
; CURRENT APPLICATION NUMBER: PCT/US00/04665
; CURRENT FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: 60/121,485
; EARLIER FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-04665-1

Query Match      100.0%; Score 201; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 12
PCT-US00-04925-1
; Sequence 1, Application PC/TUS00004925
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: METHOD FOR CLONING SIGNAL TRANSDUCTION
; FILE REFERENCE: 00786/371WO2
; CURRENT APPLICATION NUMBER: PCT/US00/04925
; CURRENT FILING DATE: 2000-02-25
; EARLIER APPLICATION NUMBER: 60/121,485
; EARLIER FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-04925-1

Query Match      100.0%; Score 201; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

PCT-US00-04665-1
; Sequence 1, Application PC/TUS00004665
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: METHOD FOR CLONING SIGNAL TRANSDUCTION
; FILE REFERENCE: 00786/371WO2
; CURRENT APPLICATION NUMBER: PCT/US00/04665
; CURRENT FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: 60/121,485
; EARLIER FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-04665-1

Query Match      100.0%; Score 201; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

PCT-US00-04925-1
; Sequence 1, Application PC/TUS00004925
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: METHOD FOR CLONING SIGNAL TRANSDUCTION
; FILE REFERENCE: 00786/371WO2
; CURRENT APPLICATION NUMBER: PCT/US00/04925
; CURRENT FILING DATE: 2000-02-25
; EARLIER APPLICATION NUMBER: 60/121,485
; EARLIER FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-04925-1

Query Match      100.0%; Score 201; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

PCT-US02-16106-47
; Sequence 47, Application PC/TUS0216106
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554PCT
; CURRENT APPLICATION NUMBER: PCT/US02/16106
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 184
; TYPE: PRT
PCT-US02-16106-47

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Best Local Similarity 100.0%; Pred. No. 3.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

PCT-US02-16106-47
; Sequence 11, Application US/09565423
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-423-11

Query Match      100.0%; Score 201; DB 19; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

PCT-US02-16106-47
; Sequence 11, Application US/09565423
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-423-11

Query Match      100.0%; Score 201; DB 19; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.7e-16;
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Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41
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Tue Jan 7 10:36:58 2003

us-09-855-158-7.rapm

Page 5

Db 8 CSQNEFYDLSLHACTPCQJRCSSNTPPLTCQRYC 41

Search completed: January 7, 2003, 09:53:18
Job time : 57.0075 secs

This Page Blank (uspto)

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:37:34 ; Search time 85.513 Seconds

(without alignments)
384,527 Million cell updates/sec

Title: US-09-855-158-6

Perfect score: 284

Sequence: 1 MAGGCSQNEYFDLSILHACIP.....LTGCRYCNASVTNSVKGTNA 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents - AA Main:*

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27: /cgn2_6/ptodata/1/paa/US111_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	284	100.0	51	22	US-09-855-158-6
3	284	100.0	181	22	US-09-854-864-5
4	284	100.0	181	22	US-09-855-158-5
5	284	100.0	184	1	PCT-US00-04665-1
6	284	100.0	184	1	PCT-US00-04925-1

7	284	100.0	184	1	PCT-US02-16106-47	Sequence 47, Appl
8	284	100.0	184	18	US-09-479-855-8	Sequence 8, Appl
9	284	100.0	184	19	US-09-565-423-11	Sequence 11, Appl
10	284	100.0	184	19	US-09-569-245-8	Sequence 8, Appl
11	284	100.0	184	20	US-09-627-206-8	Sequence 8, Appl
12	284	100.0	184	21	US-09-724-341-4	Sequence 4, Appl
13	284	100.0	184	23	US-10-09-014-119A-1	Sequence 1, Appl
14	284	100.0	184	24	US-10-068-725-2	Sequence 1, Appl
15	284	100.0	184	24	US-10-077-137-1	Sequence 1, Appl
16	284	100.0	184	24	US-10-077-137-7	Sequence 1, Appl
17	284	100.0	184	24	US-10-077-438-1	Sequence 1, Appl
18	284	100.0	184	24	US-10-077-438-7	Sequence 1, Appl
19	284	100.0	184	25	US-10-115-192-8	Sequence 8, Appl
20	284	100.0	184	25	US-10-115-192-8	Sequence 8, Appl
21	284	100.0	184	25	US-10-152-363A-27	Sequence 27, Appl
22	284	100.0	184	27	US-09-758-471-5100	Sequence 8, Appl
23	284	100.0	184	27	US-09-758-471-5100	Sequence 8, Appl
24	284	100.0	184	27	US-09-758-471-5100	Sequence 8, Appl
25	284	100.0	184	27	US-09-758-471-5100	Sequence 8, Appl
26	284	100.0	184	27	US-09-758-471-5100	Sequence 8, Appl
27	284	100.0	184	27	US-09-758-471-5100	Sequence 8, Appl
28	284	100.0	184	27	US-09-758-471-5100	Sequence 8, Appl
29	284	100.0	184	27	US-09-758-471-5100	Sequence 8, Appl
30	284	100.0	184	27	US-09-758-471-5100	Sequence 8, Appl
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35	284	100.0	184	27	US-09-758-471-5100	Sequence 8, Appl
36	284	100.0	184	27	US-09-758-471-5100	Sequence 8, Appl
37	284	100.0	184	27	US-09-758-471-5100	Sequence 8, Appl
38	284	100.0	184	27	US-09-758-471-5100	Sequence 8, Appl
39	284	100.0	184	27	US-09-758-471-5100	Sequence 8, Appl
40	284	100.0	184	27	US-09-758-471-5100	Sequence 8, Appl
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45	284	100.0	184	27	US-09-758-471-5100	Sequence 8, Appl

ALIGNMENTS

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RESULT 1
US-09-854-864-6
; Sequence 6, Application US/09854864
; GENERAL INFORMATION:
; APPLICANT: THELL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-854-864-6
Query Match 100.0%; Score 284; DB 22; Length 51;
Best local similarity 100.0%; Pred. No. 2.3e-25; Index 0; Gaps 0;
Matches 51; Conservative 0; Mismatches 0;
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Db 1 MAGQCSQNEYFDSLHACIPCOLRCSNTPLTTCORYCNASVTNSVKGTNA 51

RESULT 2

US-09-855-158-6

; Sequence 6, Application US/09855158

; GENERAL INFORMATION:

; APPLICANT: THEILL, LARS EYDE

; APPLICANT: YU, GANG

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCWA, BI

; FILE REFERENCE: A-686A

; CURRENT APPLICATION NUMBER: US/09/855,158

; PRIOR FILING DATE: 2001-09-11

; PRIOR APPLICATION NUMBER: US 60/214,591

; PRIOR FILING DATE: 2000-06-27

; PRIOR APPLICATION NUMBER: US 60/204,039

; PRIOR FILING DATE: 2000-05-12

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6

; LENGTH: 51

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-855-158-6

Query Match 100.0%; Score 284; DB 22; Length 51;

Best Local Similarity 100.0%; Pred. No. 2.3e-25;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAGQCSQNEYFDSLHACIPCOLRCSNTPLTTCORYCNASVTNSVKGTNA 51

RESULT 3

US-09-854-864-5

; Sequence 5, Application US/09854864

; GENERAL INFORMATION:

; APPLICANT: THEILL, LARS EYDE

; APPLICANT: YU, GANG

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCWA,

; FILE REFERENCE: A-686B

; CURRENT APPLICATION NUMBER: US/09/854,864

; PRIOR FILING DATE: 2001-09-11

; PRIOR APPLICATION NUMBER: US 60/204,039

; PRIOR FILING DATE: 2000-05-12

; PRIOR APPLICATION NUMBER: US 60/214,591

; PRIOR FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 181

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-854-864-5

Query Match 100.0%; Score 284; DB 22; Length 181;

Best Local Similarity 100.0%; Pred. No. 7.5e-25;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGQCSQNEYFDSLHACIPCOLRCSNTPLTTCORYCNASVTNSVKGTNA 51

Db 1 MAGQCSQNEYFDSLHACIPCOLRCSNTPLTTCORYCNASVTNSVKGTNA 51

RESULT 4

US-09-855-158-5

; Sequence 5, Application US/09855158

; GENERAL INFORMATION:

; APPLICANT: THEILL, LARS EYDE

; APPLICANT: YU, GANG

Db 1 MAGQCSQNEYFDSLHACIPCOLRCSNTPLTTCORYCNASVTNSVKGTNA 51

RESULT 2

US-09-855-158-6

; Sequence 6, Application US/09855158

; GENERAL INFORMATION:

; APPLICANT: THEILL, LARS EYDE

; APPLICANT: YU, GANG

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCWA, BI

; FILE REFERENCE: A-686A

; CURRENT APPLICATION NUMBER: US/09/855,158

; PRIOR FILING DATE: 2001-09-11

; PRIOR APPLICATION NUMBER: US 60/214,591

; PRIOR FILING DATE: 2000-06-27

; PRIOR APPLICATION NUMBER: US 60/204,039

; PRIOR FILING DATE: 2000-05-12

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6

; LENGTH: 51

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-855-158-6

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Best Local Similarity 100.0%; Pred. No. 2.3e-25;

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RESULT 3

US-09-854-864-5

; Sequence 5, Application US/09854864

; GENERAL INFORMATION:

; APPLICANT: THEILL, LARS EYDE

; APPLICANT: YU, GANG

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCWA,

; FILE REFERENCE: A-686B

; CURRENT APPLICATION NUMBER: US/09/854,864

; PRIOR FILING DATE: 2001-09-11

; PRIOR APPLICATION NUMBER: US 60/204,039

; PRIOR FILING DATE: 2000-05-12

; PRIOR APPLICATION NUMBER: US 60/214,591

; PRIOR FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 181

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-854-864-5

Query Match 100.0%; Score 284; DB 22; Length 181;

Best Local Similarity 100.0%; Pred. No. 7.5e-25;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4

US-09-855-158-5

; Sequence 5, Application US/09855158

; GENERAL INFORMATION:

; APPLICANT: THEILL, LARS EYDE

; APPLICANT: YU, GANG

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCWA, BI

; FILE REFERENCE: A-686A

; CURRENT APPLICATION NUMBER: US/09/855,158

; PRIOR FILING DATE: 2001-09-11

; PRIOR APPLICATION NUMBER: US 60/214,591

; PRIOR FILING DATE: 2000-06-27

; PRIOR APPLICATION NUMBER: US 60/204,039

; PRIOR FILING DATE: 2000-05-12

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 181

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-855-158-5

Query Match 100.0%; Score 284; DB 22; Length 181;

Best Local Similarity 100.0%; Pred. No. 7.5e-25;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGQCSQNEYFDSLHACIPCOLRCSNTPLTTCORYCNASVTNSVKGTNA 51

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RESULT 5

PCT-US00-04665-1

; Sequence 1, Application PC/TUS0004665

; GENERAL INFORMATION:

; APPLICANT: The General Hospital Corporation

; TITLE OF INVENTION: METHOD FOR CLONING SIGNAL TRANSDUCTION

; FILE REFERENCE: INTERMEDIATES

; CURRENT APPLICATION NUMBER: PCT/US00/04665

; CURRENT FILING DATE: 2000-02-24

; EARLIER APPLICATION NUMBER: 60/121,485

; EARLIER FILING DATE: 1999-02-24

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 184

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US00-04665-1

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Best Local Similarity 100.0%; Pred. No. 7.6e-25;

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Db 4 MAGQCSQNEYFDSLHACIPCOLRCSNTPLTTCORYCNASVTNSVKGTNA 54

RESULT 6

PCT-US00-04925-1

; Sequence 1, Application PC/TUS0004925

; GENERAL INFORMATION:

; APPLICANT: The General Hospital Corporation

; TITLE OF INVENTION: METHOD FOR CLONING SIGNAL TRANSDUCTION

; FILE REFERENCE: INTERMEDIATES

; CURRENT APPLICATION NUMBER: PCT/US00/04925

; CURRENT FILING DATE: 2000-02-25

; EARLIER APPLICATION NUMBER: 60/121,485

; EARLIER FILING DATE: 1999-02-24

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 184

; TYPE: PRT

; ORGANISM: Homo sapiens

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RESULT 7
PCT-US02-16106-47
; Sequence 47, Application PC/TUS0216106
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554PCT
; CURRENT APPLICATION NUMBER: PCT/US02/16106
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Version 3.0
; SEQ ID NO 47
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-16106-47

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RESULT 8
US-09-479-856-8
; Sequence 8, Application US/09479856
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen
; APPLICANT: Yee, David P.
; TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
; FILE REFERENCE: 98-75
; CURRENT APPLICATION NUMBER: US/09/479,856
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,068
; EARLIER FILING DATE: 1999-01-07
; EARLIER APPLICATION NUMBER: 60/169,890
; EARLIER FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-479-856-8

Query Match      100.0%; Score 284; DB 18; Length 184;
Best Local Similarity 100.0%; Pred. No. 7,6e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGCCSONEYFDSLHACIPCOLRCSNTPTLCORYCNASVTNSVKGTNA 51
DB 4 MAGCCSONEYFDSLHACIPCOLRCSNTPTLCORYCNASVTNSVKGTNA 54

RESULT 9
US-09-565-423-11
; Sequence 11, Application US/09565423
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TAIL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-423-11

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Best Local Similarity 100.0%; Pred. No. 7,6e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 4 MAGCCSONEYFDSLHACIPCOLRCSNTPTLCORYCNASVTNSVKGTNA 54

RESULT 10
US-09-569-245-8
; Sequence 8, Application US/09569245
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen
; APPLICANT: Yee, David P.
; TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
; FILE REFERENCE: 98-75
; CURRENT APPLICATION NUMBER: US/09/569,245
; CURRENT FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 60/115,068
; PRIOR FILING DATE: 1999-01-07
; PRIOR APPLICATION NUMBER: 60/169,890
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/479,856
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-569-245-8

Query Match      100.0%; Score 284; DB 19; Length 184;
Best Local Similarity 100.0%; Pred. No. 7,6e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGCCSONEYFDSLHACIPCOLRCSNTPTLCORYCNASVTNSVKGTNA 51
DB 4 MAGCCSONEYFDSLHACIPCOLRCSNTPTLCORYCNASVTNSVKGTNA 54

RESULT 11
US-09-627-206-8
; Sequence 8, Application US/09627206
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen
; APPLICANT: Yee, David P.
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; TITLE OF INVENTION: SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING
; FILE REFERENCE: 98-75C2
; CURRENT APPLICATION NUMBER: US/09/627,206
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/115,068
; PRIOR FILING DATE: 1999-01-07
; PRIOR APPLICATION NUMBER: 60/169,890
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/479,856
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/569,245
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-627-206-8

Query Match      100.0%; Score 284; DB 20; Length 184;
Best Local Similarity 100.0%; Pred. No. 7.6e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4 MAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTSVKGTNA 54

RESULT 12
US-09-724-341-4
; Sequence 4, Application US/09724341
; GENERAL INFORMATION:
; APPLICANT: AVI J. ASHKENAZI
; APPLICANT: KELLY H. DODGE
; APPLICANT: IOBAL GREWAL
; APPLICANT: KYUNG JIN KIM
; APPLICANT: SCOT A. MARSTERS
; APPLICANT: ROBERT M. PITTI
; APPLICANT: MINHONG YAN
; TITLE OF INVENTION: USES OF AGONISTS AND ANTAGONISTS TO MODULATE ACTIVITY
; FILE REFERENCE: P180581
; CURRENT APPLICATION NUMBER: US/09/724,341
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/182,938
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: US 60/226,986
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 4
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-341-4

Query Match      100.0%; Score 284; DB 21; Length 184;
Best Local Similarity 100.0%; Pred. No. 7.6e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTSVKGTNA 51
Db 4 MAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTSVKGTNA 54

RESULT 13
US-09-914-119A-1
; Sequence 1, Application US/09914119A
; GENERAL INFORMATION:
; APPLICANT: Seed, Brian
; APPLICANT: Tsiang, Adrian
; TITLE OF INVENTION: METHOD FOR CLONING SIGNAL TRANSDUCTION
; INTERMEDIATES
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; FILE REFERENCE: 00786/371002
; CURRENT APPLICATION NUMBER: US/09/914,119A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/04925
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/121,485
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-914-119A-1

Query Match      100.0%; Score 284; DB 23; Length 184;
Best Local Similarity 100.0%; Pred. No. 7.6e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTSVKGTNA 51
Db 4 MAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTSVKGTNA 54

RESULT 14
US-10-008-063-7
; Sequence 7, Application US/10008063
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Henne, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-008-063-7

Query Match      100.0%; Score 284; DB 24; Length 184;
Best Local Similarity 100.0%; Pred. No. 7.6e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTSVKGTNA 51
Db 4 MAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTSVKGTNA 54

RESULT 15
US-10-068-725-2
; Sequence 2, Application US/10068725
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
; TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI
; FILE REFERENCE: 01-04
; CURRENT APPLICATION NUMBER: US/10/068,725
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/270,274
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/283,447
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-725-2
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Tue Jan 7 10:36:56 2003

us-09-855-158-6.rapm

Page 5

Query Match 100.0%; Score 284; DB 24; Length 184;
Best Local Similarity 100.0%; Pred. No. 7.6e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 4 MAGCCSQQNEYPDSLHACIPQQLRCSSNTPPLTCORYCNASYTNSVKGTNA 54
Search completed: January 7, 2003, 09:53:18
Job time : 86.513 secs

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GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: January 7, 2003, 09:35:14 ; Search time 6.26316 Seconds
(without alignment)
239.587 Million cell updates/sec

Title: US-09-855-158-6

Perfect score: 284
Sequence: 1 MAGCCSQNEVFDLSLHACIP.....LTCRCYNASVTNSVKGSTNA 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	67.5	23.8	166	2	US-08-810-572A-6 Sequence 6, Appli
2	67.5	23.8	166	4	US-09-290-333-6 Sequence 6, Appli
3	67.5	23.8	293	2	US-08-810-572A-2 Sequence 2, Appli
4	67.5	23.8	293	4	US-09-290-333-2 Sequence 2, Appli
5	56	19.7	2476	2	US-08-276-967-2 Sequence 2, Appli
6	55.5	19.5	5405	4	US-08-718-388-9 Sequence 2, Appli
7	54.5	19.2	350	2	US-08-999-811-4 Sequence 4, Appli
8	54.5	19.2	350	2	US-08-824-996-2 Sequence 4, Appli
9	54.5	19.2	350	3	US-09-042-105-4 Sequence 4, Appli
10	54.5	19.2	350	4	US-08-510-133A-3 Sequence 3, Appli
11	54.5	19.2	350	4	US-08-585-895-33 Sequence 3, Appli
12	54.5	19.2	419	2	US-08-999-811-2 Sequence 2, Appli
13	54.5	19.2	419	3	US-09-042-105-2 Sequence 2, Appli
14	54.5	19.2	419	3	US-09-042-105-18 Sequence 18, Appli
15	54.5	19.2	419	4	US-08-795-430-8 Sequence 8, Appli
16	54.5	19.2	419	4	US-08-510-133A-35 Sequence 35, Appli
17	54.5	19.2	419	4	US-09-325-730-8 Sequence 35, Appli
18	54.5	19.2	419	4	US-08-325-730-8 Sequence 35, Appli
19	54.5	19.2	419	4	US-08-501-133-33 Sequence 33, Appli
20	54.5	19.2	419	4	US-08-501-133-33 Sequence 33, Appli
21	54.5	19.2	419	4	US-08-501-133-33 Sequence 33, Appli
22	54.5	19.2	419	4	US-08-501-133-33 Sequence 33, Appli
23	54.5	19.2	419	4	US-08-501-133-33 Sequence 33, Appli
24	54.5	19.2	419	4	US-08-501-133-33 Sequence 33, Appli
25	54.5	19.2	419	4	US-08-501-133-33 Sequence 33, Appli
26	54.5	19.2	419	4	US-08-501-133-33 Sequence 33, Appli
27	54.5	19.2	419	4	US-08-501-133-33 Sequence 33, Appli

28	53.5	18.8	77	2	US-08-486-397-40 Sequence 40, Appli
29	53.5	18.8	77	2	US-08-486-399-4 Sequence 4, Appli
30	53.5	18.8	77	2	US-08-486-399-40 Sequence 40, Appli
31	53.5	18.8	77	2	US-08-461-965-4 Sequence 4, Appli
32	53.5	18.8	77	2	US-08-461-965-40 Sequence 40, Appli
33	53.5	18.8	77	2	US-08-326-110A-33 Sequence 33, Appli
34	53.5	18.8	77	2	US-08-634-641-4 Sequence 4, Appli
35	53.5	18.8	77	2	US-08-634-641-40 Sequence 40, Appli
36	53.5	18.8	77	3	US-09-249-471-40 Sequence 40, Appli
37	53.5	18.8	77	3	US-09-249-471-40 Sequence 40, Appli
38	53.5	18.8	77	3	US-09-249-472-40 Sequence 40, Appli
39	53.5	18.8	77	3	US-09-249-472-40 Sequence 40, Appli
40	53.5	18.8	77	3	US-09-249-451-40 Sequence 40, Appli
41	53.5	18.8	77	3	US-09-249-451-40 Sequence 40, Appli
42	53.5	18.8	77	3	US-08-809-455-4 Sequence 4, Appli
43	53.5	18.8	77	3	US-08-809-455-40 Sequence 40, Appli
44	53.5	18.8	77	3	US-09-249-461-40 Sequence 40, Appli
45	53.5	18.8	77	3	US-09-249-461-40 Sequence 40, Appli

ALIGNMENTS

RESULT 1
US-08-810-572A-6
Sequence 6, Application US/08810572A
Patent No. 5969102
GENERAL INFORMATION:
APPLICANT: Biam, Richard J.
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,572A
FILING DATE: 28-FEB-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-343-1684
TELEFAX: 201-487-5800
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYDROTHERMAL: N-terminal
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE: Homo sapiens
US-08-810-572A-6
Query Match 23.8%; Score 67.5; DB 2; Length 166;
Best Local Similarity 30.6%; Pred. No. 0.64;


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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/290,333
/ FILING DATE: 12-Apr-1999
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Jackson Esq., David A.
/ REGISTRATION NUMBER: 26,742
/ REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201-487-5800
/ TELEFAX: 201-343-1684
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 293 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ FRAGMENT TYPE: N-terminal
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
/ SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2
Query Match 23.8%; Score 67.5; DB 4; Length 293;
Best Local Similarity 30.6%; Pred. No. 1.2;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

OY 5 CSQNEYFDSLHACIPCOLRGSSNTPPLTCQRYCNA 40
DB 34 CPBEQYWDPLGTGCMCKTICNMG-QRTCAFCRS 68

RESULT 5
US-08-276-967-2
/ Sequence 2, Application US/08276967
/ Patent No. 5851817
/ GENERAL INFORMATION:
/ APPLICANT: Hardy, Daniel M.
/ TITLE OF INVENTION: Specific-Egg-Binding Proteins of
/ TITLE OF INVENTION: Sperm
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Arnold, White & Durkee
/ STREET: P. O. Box 4433
/ CITY: Houston
/ STATE: Texas
/ COUNTRY: USA
/ ZIP: 77210-4433
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/276,967
/ FILING DATE: Submitted Herewith
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kitchell, Barbara S.
/ REGISTRATION NUMBER: 33,928
/ REFERENCE/DOCKET NUMBER: UTSD:418\KIT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 713-787-1400
/ TELEFAX: 713-789-2679
/ TELEX: 79-0924
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2476 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
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/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-276-967-2
Query Match 19.7%; Score 56; DB 2; Length 2476;
Best Local Similarity 31.6%; Pred. No. 2.6e+02;
Matches 12; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

OY 5 CSQNEYFDSLHACIP-CO---LRCSNTPPLTCQRYC 38
DB 1851 CSAHSVITSCVPSCLPSCDPEGQCTGAGAPSTCEGC 1888

RESULT 6
US-08-718-388-9
/ Sequence 9, Application US/08718388
/ Patent No. 6271362
/ GENERAL INFORMATION:
/ APPLICANT: MORIKAWA, MINORU
/ TITLE OF INVENTION: GENE ENCODING I9G FC REGION-BINDING
/ TITLE OF INVENTION: PROTEIN
/ NUMBER OF SEQUENCES: 29
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
/ STREET: PO BOX 747
/ CITY: FALLS CHURCH
/ STATE: VA
/ COUNTRY: USA
/ ZIP: 22040-0747
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/718,388
/ FILING DATE:
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MURPHY JR, GERALD M
/ REGISTRATION NUMBER: 28,977
/ REFERENCE/DOCKET NUMBER: 0230-111
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 205-8000
/ TELEFAX: (703) 205-8050
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5405 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-718-388-9
Query Match 19.5%; Score 55.5; DB 4; Length 5405;
Best Local Similarity 33.3%; Pred. No. 6.8e+02;
Matches 12; Conservative 6; Mismatches 13; Indels 5; Gaps 2;

OY 4 QCSQNEYFDSLHACI-PCQLRGSSNTPPLTCQRYC 38
DB 3933 ECPDMSHTE---LCADTCSTLGCALSAPIQCPCDGC 3964

RESULT 7
US-08-999-811-4
/ Sequence 4, Application US/08999811
/ Patent No. 5932540
/ GENERAL INFORMATION:
/ APPLICANT: HU, JING-SHAN
/ APPLICANT: ROSEN, CRAIG A.
/ APPLICANT: CAO, LIANG
/ TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
/ NUMBER OF SEQUENCES: 15
```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
;; STREET: 1100 NEW YORK AVENUE
;; CITY: WASHINGTON
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/999,811
;; FILING DATE: HEREWITH
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/207,550
;; FILING DATE: 8-MAR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/465,968
;; FILING DATE: 06-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MARKOWICZ, KAREN R.
;; REGISTRATION NUMBER: 36,351
;; REFERENCE/DOCKET NUMBER: 1488.1000004
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)371-2600
;; TELEFAX: (202)371-2540
;; INFORMATION FOR SEQ ID NO: 4:
;; LENGTH: 350 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
US-08-999-811-4

Query Match 19.2%; Score 54.5; DB 2; Length 350;
Best Local Similarity 35.0%; Pred. No. 48;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 4 QCSONEYFDSLHACIPCOLRCSNTP--PLTCORYCNAS 41
DB 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 296

RESULT 8
US-824-996-2
;; Sequence 2, Application US/0824996B
;; Patent No. 5935820
;; GENERAL INFORMATION:
;; APPLICANT: Hu, Jing-Shan
;; APPLICANT: Rosen, Craig A.
;; APPLICANT: Cao, Liang
;; TITLE OF INVENTION: Polynucleotides Encoding Vascular Endothelial Growth
;; TITLE OF INVENTION: Factor 2
;; FILE REFERENCE: PF112D1
;; CURRENT APPLICATION NUMBER: US/08/824,996B
;; CURRENT FILING DATE: 1997-03-27
;; EARLIER APPLICATION NUMBER: 08/207,550
;; EARLIER FILING DATE: 1994-03-08
;; NUMBER OF SEQ ID NOS: 9
;; SOFTWARE: Patent In Ver. 2.0
;; SEQ ID NO 2
;; LENGTH: 350
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;;
US-08-824-996-2

Query Match 19.2%; Score 54.5; DB 2; Length 350;
Best Local Similarity 35.0%; Pred. No. 48;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 4 QCSONEYFDSLHACIPCOLRCSNTP--PLTCORYCNAS 41
DB 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 296
RESULT 9
US-09-042-105-4
;; Sequence 4, Application US/09042105
;; Patent No. 6040157
;; GENERAL INFORMATION:
;; APPLICANT: HU, JING-SHAN
;; APPLICANT: ROSEN, CRAIG A.
;; APPLICANT: CAO, LIANG
;; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
;; NUMBER OF SEQUENCES: 35
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
;; STREET: 1100 NEW YORK AVENUE
;; CITY: WASHINGTON
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/042,105
;; FILING DATE: HEREWITH
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/207,550
;; FILING DATE: 8-MAR-1994
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/465,968
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: TO BE ASSIGNED
;; FILING DATE: 24-DEC-1997
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: ERIC K. STEFFE
;; REGISTRATION NUMBER: 36,688
;; REFERENCE/DOCKET NUMBER: 1488.1000003/EKS
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)371-2600
;; TELEFAX: (202)371-2540
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 350 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
US-09-042-105-4

Query Match 19.2%; Score 54.5; DB 3; Length 350;
Best Local Similarity 35.0%; Pred. No. 48;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 4 QCSONEYFDSLHACIPCOLRCSNTP--PLTCORYCNAS 41
DB 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 296

RESULT 10
US-08-510-133A-33
;; Sequence 33, Application US/08510133A
;; Patent No. 6221839
;; GENERAL INFORMATION:
;; APPLICANT: Alitalo, Kari

Joukov, Vladimir
TITLE OF INVENTION: Receptor Ligand
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/510,133A
FILING DATE: 01-Aug-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Gaas, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28113/32863
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-08-510-133A-33

Query Match 19.2%; Score 54.5; DB 4; Length 350;
Best Local Similarity 35.0%; Pred. No. 48;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy 4 QCSONEYFDSLHACIPQQLRCSSNTP--PLTCQRYCNAS 41
Db 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCAECCTES 296

RESULT 11
US-08-585-895-33
Sequence 33, Application US/08585895
Patent No. 6245530
GENERAL INFORMATION:
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Receptor Ligand
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/585,895
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gaas, David A.
REGISTRATION NUMBER: 38,153

REFERENCE/DOCKET NUMBER: 28113/33072
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-585-895-33

Query Match 19.2%; Score 54.5; DB 4; Length 350;
Best Local Similarity 35.0%; Pred. No. 48;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy 4 QCSONEYFDSLHACIPQQLRCSSNTP--PLTCQRYCNAS 41
Db 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCAECCTES 296

RESULT 12
US-08-999-811-2
Sequence 2, Application US/08999811
Patent No. 5932540
GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/999,811
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MARKOWICZ, KAREN R.
REGISTRATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 1488.1000004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2540
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-999-811-2

Query Match 19.2%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 59;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 4 QCSONEYFDSLHACIPQLRCSNTP--PLTCORYCNAS 41
Db 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 365

RESULT 13
US-09-042-105-2
; Sequence 2, Application US/09042105
; Patent No. 6040157
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: CAO, LIANG
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,105
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,550
; FILING DATE: 8-MAR-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,968
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TO BE ASSIGNED
; FILING DATE: 24-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ERIC K. STEFFE
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1000003/EKS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2540
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-042-105-2

Query Match 19.2%; Score 54.5; DB 3; Length 419;
Best Local Similarity 35.0%; Pred. No. 59;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 4 QCSONEYFDSLHACIPQLRCSNTP--PLTCORYCNAS 41
Db 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 365

RESULT 14
US-09-042-105-18
; Sequence 18, Application US/09042105
; Patent No. 6040157
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN

; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: CAO, LIANG
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,105
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,550
; FILING DATE: 8-MAR-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,968
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TO BE ASSIGNED
; FILING DATE: 24-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ERIC K. STEFFE
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1000003/EKS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-042-105-18

Query Match 19.2%; Score 54.5; DB 3; Length 419;
Best Local Similarity 35.0%; Pred. No. 59;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 4 QCSONEYFDSLHACIPQLRCSNTP--PLTCORYCNAS 41
Db 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 365

RESULT 15
US-08-795-430-8
; Sequence 8, Application US/08795430
; Patent No. 6130071
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Joukov, Vladimir
; TITLE OF INVENTION: Vascular
; TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall,
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America

ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,430
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/F196/00427
FILING DATE: 01-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/571,573
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/601,132
FILING DATE: 14-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,895
FILING DATE: 12-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28967/33691
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-430-8

Query Match 19.2%; Score 54.5; DB 4; Length 419;
Best Local Similarity 35.0%; Pred. No. 59;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 4 QCSQNEYFDSLHACIPQILRCSSTNP--PLTCQRYCNAS 41
DB 327 QCGANREFDENTQCV-CKXTCPRNQPLNPGKXCAECTES 365

Search completed: January 7, 2003, 09:42:02
Job time : 8.26316 secs

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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:34:29 ; Search time 14.4436 Seconds
(without alignments)
727.547 Million cell updates/sec

Title: US-09-855-158-6

Perfect score: 284
Sequence: 1 MAGCOSQNEVFDLSLHACIP.....LTCORICMAVTSNKKVGNNA 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MBC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTERATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74.5	26.2	966	5	Q22378
2	72.5	25.5	499	11	O88714
3	71	25.0	532	5	O17496
4	71	25.0	718	5	O98107
5	69.5	24.5	5374	11	O99ND0
6	67	23.6	62	5	O77419
7	66	23.2	330	5	O18118
8	65.5	23.1	1299	5	O26485
9	65.5	23.1	2551	4	O88W08
10	65	22.9	175	11	O84498
11	63	22.2	341	11	O9D351
12	63	22.0	999	5	O17969
13	62.5	22.0	1513	5	O17970
14	61.5	21.7	353	5	O9VW81
15	61.5	21.7	353	5	O8S258

17	61.5	21.7	483	5	Q22423	Q22423 caenorhabdi
18	61	21.5	263	15	Q9WEJ8	Q9WEJ8 human immun
19	60.5	21.3	1574	11	O88281	O88281 rattus norv
20	60.5	21.3	3034	11	O35161	O35161 mus musculu
21	60	21.1	250	12	Q9DW27	Q9DW27 spodoptera
22	60	21.1	262	15	Q9WDX2	Q9WDX2 human immun
23	60	21.1	369	5	Q9VW90	Q9VW90 drosophila
24	60	21.1	387	13	Q9VVD4	Q9VVD4 xenopus lae
25	60	21.1	5146	6	O8SPM4	O8SPM4 bos taurus
26	59.5	21.0	856	10	Q94SR4	Q94SR4 hordeum vul
27	59	20.8	263	15	Q9WDU5	Q9WDU5 human immun
28	59	20.8	263	15	Q9WDU8	Q9WDU8 human immun
29	59	20.8	263	15	Q9WDV0	Q9WDV0 human immun
30	59	20.8	263	15	Q9WDV6	Q9WDV6 human immun
31	59	20.8	263	15	Q9WDV8	Q9WDV8 human immun
32	59	20.8	263	15	Q9WDW7	Q9WDW7 human immun
33	59	20.8	263	15	Q9WDW8	Q9WDW8 human immun
34	59	20.8	263	15	Q9WDW9	Q9WDW9 human immun
35	59	20.8	263	15	Q9WDX0	Q9WDX0 human immun
36	59	20.8	263	15	Q9WDX6	Q9WDX6 human immun
37	59	20.8	263	15	Q9WE18	Q9WE18 human immun
38	59	20.8	263	15	Q9WE19	Q9WE19 human immun
39	59	20.8	263	15	Q9WEJ0	Q9WEJ0 human immun
40	59	20.8	263	15	Q9WEJ1	Q9WEJ1 human immun
41	59	20.8	263	15	Q9WEJ2	Q9WEJ2 human immun
42	59	20.8	263	15	Q9WEJ4	Q9WEJ4 human immun
43	59	20.8	263	15	Q9WEJ5	Q9WEJ5 human immun
44	59	20.8	263	15	Q9WEJ7	Q9WEJ7 human immun
45	59	20.8	263	15	Q9WEJ9	Q9WEJ9 human immun

ALIGNMENTS

RESULT 1

Q22378 PRELIMINARY; PRT; 966 AA.
ID Q22378
AC Q22378;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 102.5 kDa protein.
GN T10E10.4
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloiderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RT Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Geisel C.;
RT "The sequence of C. elegans cosmid T10E10."
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission";
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; U39644; AAA80360.2; -.
DR HSSP; P10969; IMGT.
DR InterPro; IPR002557; Chitin_bind_PeRA.
DR InterPro; IPR000794; Ketoacyl-Synt.
DR InterPro; IPR003571; Snake_toxin.
DR InterPro; IPR002899; WRI/EB.

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DR Pfam; PF01607; CBM_14; 2.
DR SMART; SM00289; WRI; 12.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
DR PROSITE; PS00272; SNAKE_TOXIN; UNKNOWN_1.
DR PROSITE; PS00272; SNAKE_TOXIN; UNKNOWN_1.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 966 AA; 102460 MW; B565A3CDD25216D9 CRC64;

Query Match
Best Local Similarity 26.2%; Score 74.5; DB 5; Length 966;
Matches 18; Conservative 11; Mismatches 15; Indels 5; Gaps 3;

QY 4 QCSQNEYFDSLHACIPQLR--CSSNTPPLTCQRYCNASVTSVKGTN 50
Db 215 QCSQSTVFNSDLNVCVPLAIGNSCDSSTQPPVCS--C-SQVSSSCPQTS 260

RESULT 2
O88714 PRELIMINARY; PRT; 499 AA.
AC O88714;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE Gastric mucin-like protein (Fragment).
DE GASTRIC MUCIN-LIKE.
GN Mus musculus (Mouse).
OS Mus musculus; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=STOMACH;
RA Tomasetto C., Masson R., Wendling C., Lefebvre O., Chenard M.P.,
RA Rio M.C.;
RT "Identification of interactions between trefoil peptides and members
RT of the mucin protein family using the yeast two-hybrid system.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ010752; CAA09343.1;
DR HSP; P56682; ICCV
DR InterPro; IPR002919; TIL_Cysrich.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF01826; TIL; 1.
DR Pfam; PF00094; Vwd; 1.
DR SMART; SM00216; VWD; 1.
DR NON_TER 499
FT SEQUENCE 499 AA; 54190 MW; 04F89EF4F23EB61E CRC64;

Query Match
Best Local Similarity 25.5%; Score 72.5; DB 11; Length 499;
Matches 14; Conservative 1; Mismatches 7; Indels 7; Gaps 1;

QY 5 CSQNEYFDSLHACIPQLRCSNTPPLT 33
Db 430 CSQNEYFDHSEGTGVCPC-----APPTT 451

RESULT 3
O17496 PRELIMINARY; PRT; 532 AA.
AC O17496;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 09, Last sequence update)
DE Serotonin receptor.
DE Serotonin receptor.
OS Ascaris suum (pig roundworm) (Ascaris lumbricoide),
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99339391; PubMed=10413046;
RX Huang X., Duran E., Diaz F., Xiao H., Messer W.S. Jr., Komuniecki R.;

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RT "Alternative-splicing of serotonin receptor isoforms in the pharynx
RT and muscle of the parasitic nematode, Ascaris suum.";
RL Mol. Biochem. Parasitol. 101:95-106(1999).
DR EMBL; AF005486; AAC78396.1;
DR InterPro; IPR00276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_2; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 532 AA; 60140 MW; 4D795D1C249D55F6 CRC64;

Query Match
Best Local Similarity 25.0%; Score 71; DB 5; Length 532;
Matches 16; Conservative 14; Mismatches 16; Indels 20; Gaps 2;

QY 1 MAGQCSQNEYFDSLHACIPQ-----LRCSNTPPLTCQRYCNASVTS 45
Db 435 MGVCKVFGYNSN-----VCSRNEFVLTDRQLDNVTYSERPLLCGKHCSSGNS 489

QY 46 VKGTNA 51
Db 490 LQNNSA 495

RESULT 4
Q9BI07 PRELIMINARY; PRT; 718 AA.
AC Q9BI07;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Putative cysteine surface protein (Fragment).
DE Putative cysteine surface protein (Fragment).
GN CSP.
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HMI; IMSS;
EX MEDLINE=21428166; PubMed=11545438;
RA Willhoeft U., Campos-Gongora E., Fouzni S., Bruchhaus I., Tannich E.;
RT "Introns of Entamoeba histolytica and Entamoeba dispar.";
RL Proctist 152:149-156(2001).
DR EMBL; AJ409106; CAC34072.1;
DR InterPro; IPR002174; Furin-like.
DR SMART; SM00261; FU; 7.
DR NON_TER 718
FT SEQUENCE 718 AA; 80231 MW; FFF6362A49F2827A CRC64;

Query Match
Best Local Similarity 25.0%; Score 71; DB 5; Length 718;
Matches 13; Conservative 6; Mismatches 29; Indels 0; Gaps 0;

QY 1 MAGQCSQNEYFDSLHACIPQLRCSNTPPLTCQRYCNASVTSVKG 48
Db 137 LCGRCNDGSGYFDSRTTRTCQKCFNCELCTSTNCFKCSNKTLTLESNG 184

RESULT 5
Q99ND0 PRELIMINARY; PRT; 5374 AA.
AC Q99ND0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE ZAN (Zonadhesin).
DE ZAN (Zonadhesin).
GN ZAN
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=21138439; PubMed=11239002;
RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
RA Miller W., Koop B.F.;
RT "Comparative analysis of the gene-dense ACHIE/TFR2 region on human
RT chromosome 7q22 with the orthologous region on mouse chromosome 5.";
RL Nucleic Acids Res. 29:1352-1365 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RA Cheung T.L., Wilson M.D., Koop B.F., Hardy D.M.;
RT "Genomic Basis of Inter- and Intra-species Variation in Zonadhesin
RT Domain Structure.";
RT Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 3 MAM DOMAINS.
DR EMBL, AF312033, AAK28824.1; -.
DR EMBL, AF046036, AAL0416.1; -.
DR MGD, MGI:106566; Zm.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR003645; FOLN.
DR InterPro; IPR000998; MAM_domain.
DR InterPro; IPR003328; TIL_Cyrich.
DR InterPro; IPR002919; VWF_C.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF00629; MAM; 3.
DR Pfam; PF01826; TIL; 25.
DR Pfam; PF02345; TIL; 25.
DR Pfam; PF00094; vwd; 4.
DR SMART; SM00001; EGF_like; 1.
DR SMART; SM00274; FOLN; 21.
DR SMART; SM00214; WVC; 25.
DR SMART; SM00216; VWD; 4.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 18.
DR PROSITE; PS00060; MAM_2; 3.
DR EGF-like domain; Glycoprotein.
KM EGF-like domain; 5374 AA; 579536 MW; 90D2D8CF5B24EB CRC64;
SQ SEQUENCE 5374 AA; 579536 MW; 90D2D8CF5B24EB CRC64;

Query Match 24.5%; Score 69.5; DB 11; Length 5374;
Best Local Similarity 36.8%; Pred. No. 1.4;
Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

Qy 4 QCSQNEYPDSLHACIP-CQLRCSSNTP--PLTCQRYC 38
Db 3297 QCPNISOFTDCLPSCVPSCSNRCVTSFVSFCRGCG 3334

RESULT 6
O77419 PRELIMINARY; PRT; 62 AA.
ID O77419;
AC 077419;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Chymotrypsin/elastase inhibitor-1 (Fragment).
GN ASC/-1
OS Ascaris suum (pig roundworm) (Ascaris lumbricoideae).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_Taxid=6253;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98297373; PubMed=9635450;
RA Lu C.C., Nguyen T., Morris S., Hill D., Sakanari J.A.;
RA "Antialexin complex: mutational bursts in the reactive site centers of
RT serine protease inhibitors from an ascarid nematode.";
RL Exp. Parasitol. 89:257-261 (1998).
DR EMBL; U94499; AAC61300.1; -.
DR HSSP; P07851; IEAI.
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DR InterPro; IPR002919; TIL_Cyrich.
DR Pfam; PF01826; TIL; 1.
FT NON_TER 1
FT NON_TER 62
SQ SEQUENCE 62 AA; 6794 MW; 154CE25A375E0B2C CRC64;

Query Match 23.6%; Score 67; DB 5; Length 62;
Best Local Similarity 33.3%; Pred. No. 0.037;
Matches 17; Conservative 8; Mismatches 18; Indels 8; Gaps 4;

Qy 4 QCSQNEYPDSLHACIPQQLRCS--SNTPLTCQRYCNASVTNSVKGTN 50
Db 4 RCGNEVWTE---CTGCEMKCGDPENTPCPLMCRPRRPSCESPGRWRRTN 50

RESULT 7
O18118 PRELIMINARY; PRT; 330 AA.
ID O18118;
AC O18118;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JUN-1998 (TREMblrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE T23FL.6 protein.
GN T23FL.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilkinson J.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018 (1998).
DR EMBL; Z81129; CAB03405.1; -.
DR InterPro; IPR003341; DUF139.
DR Pfam; PF02363; DUF139; 7.
SQ SEQUENCE 330 AA; 36605 MW; F043B1A90DJA8FE9 CRC64;

Query Match 23.2%; Score 66; DB 5; Length 330;
Best Local Similarity 28.3%; Pred. No. 0.27;
Matches 15; Conservative 8; Mismatches 22; Indels 8; Gaps 2;

Qy 5 CSQNEYPDSLHACIP-----CQLRCSSNTPPL--TCQRYCNASVTNSVKGT 49
Db 59 CASSQYQLQRTSCMPACQSCSQCCSSNTNTQCQPTCQSCQRTSCNPMTST 111

RESULT 8
O9GQ45 PRELIMINARY; PRT; 548 AA.
ID O9GQ45;
AC O9GQ45;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Variant-specific surface protein M21-1 (Fragment).
GN M21-1.
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
OX NCBI_Taxid=5741;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AD-1;
RA Mansouri M., By P.L.;
RA "A segment of a vsp12-like gene homolog from a type A-I (group 1)
RT Giardia intestinalis isolate.";
RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF298862; AAG37862.1; -.
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DR HSP; P00136; 2CY3.
DR InterPro; IPR000564; 2Fe2S_ferredoxin.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002174; Furin-like.
DR InterPro; IPR002350; kazal.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00001; EGF-like; 1.
DR SMART; SM00261; FU; 5.
DR PROSITE; PS00197; 2FE2S_FERREDOXIN; UNKNOWN_1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
DR PROSITE; PS00282; KAZAL; UNKNOWN_1.
DR NON_TER 1
FT NON_TER 548
SQ SEQUENCE 548 AA; 56557 MW; 578FE4FDA0A2CF0E CRC64;

Query Match 23.1%; Score 65.5; DB 5; Length 548;
Best Local Similarity 33.3%; Pred. No. 0.54;
Matches 19; Conservative 3; Mismatches 26; Indels 9; Gaps 3;

QY 2 AGCQNEYFDSLHACIPCOL----RCSSN---TPP--LTCQRYCNASVTSVKGT 49
DB 209 AGCQDQGYADFTTGCKPCGTCATCEYNATISQPCQKCTCTSSNWKVTAADGI 265

RESULT 9
ID Q26489 PRELIMINARY; PRT; 1299 AA.
AC Q26489;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Endoprotease furin.
GN FURIN.
OS Spodoptera frugiperda (Fall armyworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Noctuidae; Noctuidae; Amphipyridae; Spodoptera.
OX NCBI_TaxID=7108;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SF9;
RA Clepik M.; Klenk H.;
RT "Cloning and functional characterization of FURIN from Spodoptera
RL frugiperda (SF9) cells."
RL Submitted (JAN1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z68886; CAA93116.1; -.
DR HSP; Q99405; IMPI.
DR InterPro; IPR002174; Furin-like.
DR InterPro; IPR000209; Peptidase_S8.
DR InterPro; IPR002884; P_domain.
DR Pfam; PF01483; P; 1.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR ProDom; PD000717; P_domain; 1.
DR SMART; SM00261; FU; 10.
DR PROSITE; PS00136; SUBTILASE ASP; 1.
DR PROSITE; PS00137; SUBTILASE HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Protease.
SQ SEQUENCE 1299 AA; 142020 MW; 4C3799C7BBC572AB CRC64;

Query Match 23.1%; Score 65.5; DB 5; Length 1299;
Best Local Similarity 34.0%; Pred. No. 1.3;
Matches 18; Conservative 8; Mismatches 14; Indels 13; Gaps 4;

QY 5 CSQNEYFDSLHACIPCOLRCS-----SNTPTLTCQRYCNAS-----VTNSVKG 48
DB 1150 CSRPLRLDRLNQCVCPC---CSRGVNTSPTPTDC-CHCNPENGEINSSVAG 1198

RESULT 10
Q8WQ8

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ID Q8WQ8 PRELIMINARY; PRT; 2551 AA.
Q8WQ8;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Stabilin-2.
GN STAB2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Politz O.; Gratchev A.; McCourt P.A.G.; Schledzewski K.; Guillot P.;
RA Johansson S.; Birk R.; Hakiy N.; Franke P.; Kodelja V.; Kannicht C.;
RA Orfanos C.E.; Johansson S.; Goerdt S.;
RT "Stabilin-1 and stabilin-2 constitute a novel family of fasciclin-
RT domain-containing adhesion molecules associated with endothelial-
RT macrophage differentiation and angiogenic processes."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ295695; CAC82105.1; -.
DR InterPro; IPR000782; BgH3_fasciclin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR000538; Link.
DR Pfam; PF00008; EGF; 20.
DR Pfam; PF02469; Fasciclin; 5.
DR Pfam; PF00193; Xlink; 1.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00181; EGF; 24.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS00022; EGF 1; UNKNOWN 7.
DR PROSITE; PS01186; EGF 2; UNKNOWN 16.
DR PROSITE; PS01248; LAMININ TYPE EGF; UNKNOWN 2.
SQ SEQUENCE 2551 AA; 276952 MW; 60A44651CC2BB569 CRC64;

Query Match 22.9%; Score 65; DB 4; Length 2551;
Best Local Similarity 30.0%; Pred. No. 3;
Matches 15; Conservative 4; Mismatches 9; Indels 22; Gaps 2;

QY 15 LHACIPCOL---RCSSNTPPLT-----CORYCNASV 42
DB 674 LGTCVCSLVYWSRCFANSEPTALFTRCVYSGRFGSLKSGCARYCNAIV 723

RESULT 11
Q8R4W8 PRELIMINARY; PRT; 175 AA.
ID Q8R4W8
AC Q8R4W8;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE TRAF3 binding protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno K.; Irie S.; Sato T.-A.;
RT "Identification of novel TRAF3 binding protein, T3BP, which increases
RT cellular p-actin content."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF350257; AAL63914.1; -.
SQ SEQUENCE 175 AA; 18846 MW; B64EFP4B52EE93B1 CRC64;

Query Match 22.2%; Score 63; DB 11; Length 175;
Best Local Similarity 30.0%; Pred. No. 0.39;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 QCSQNEYFDSLHACIPCOL 23
DB 21 QCNQTECFDPLVRNCVSCSEL 40

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RESULT 12
ID Q9D351 PRELIMINARY; PRT; 341 AA.
AC Q9D351;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE 7420700M05RIK protein.
GN 7420700M05RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=IN VITRO FERTILIZED EGGS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kankawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsumoto Y., Niki K., Pesole G., Quackenbush J.,
RA Schmitt L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
RA Lyons P., Marchionni L., Maehama J., Mazzarelli J., Mombauer P.,
RA Norone P., Rang B., Ringwald M., Rostiguer I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyokawa K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsaki S.,
RA Hasehizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL AK018361; BDB31177.1; -
DR HSSP; P08047; ISPL 7420700M05RIK.
DR InterPro; IPR000822; Znf_C2H2.
DR Pfam; PF00096; Zf-C2H2; 3.
DR ProDom; PD000003; Znf_C2H2; 1.
DR SMART; SM00355; Znf_C2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 3.
DR DNA-binding; Metal-binding; Zinc-finger.
KW SEQUENCE 341 AA; 38094 MW; A332D87FE231AFPC CRC64;
SQ
Query Match 22.2%; Score 63; DB 11; Length 341;
Best Local Similarity 28.2%; Pred. No. 0.76; Mismatches 19; Indels 0; Gaps 0;
Matches 11; Conservative
OY 4 QGSONEYFDSLHACIPCOLRGSSNTPPLTCORYCNASV 42-
DB 59 RCNEREMESQLIRSLPEHGVRCPSQLAPIPFQNYCORSI 97

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RESULT 13
ID Q17969 PRELIMINARY; PRT; 999 AA.
AC Q17969; Q19998;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE F34D10.2 protein.
GN F34D10.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nemata; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peleoiderinae; Caenorhabditis.
OX NCBI_TaxId=6239;

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RN [1]
RP SEQUENCE FROM N.A.
RL Harris B.;
RA Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z37139; CA85494.1; -
DR EMBL; Z34799; CA85494.1; JOINED.
DR EMBL; Z34799; CA84320.1; -
DR EMBL; Z37139; CA84320.1; JOINED.
DR InterPro; IPR003874; CDC45_1like.
DR Pfam; PF02724; CDC45; 1.
SQ SEQUENCE 999 AA; 114887 MW; 8B46A4EB375357C9 CRC64;
Query Match 22.0%; Score 62.5; DB 5; Length 999;
Best Local Similarity 42.5%; Pred. No. 2.6; Mismatches 20; Indels 1; Gaps 1;
Matches 17; Conservative
OY 10 YFDSLHACIPCOL-RGSSNTPPLTCORYCNASVTVK 48
DB 516 YFDSLHACIPCOL-RGSSNTPPLTCORYCNASVTVK 555

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RESULT 14
ID Q17970 PRELIMINARY; PRT; 1513 AA.
AC Q17970;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE M02G9.1 protein.
GN M02G9.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nemata; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peleoiderinae; Caenorhabditis.
OX NCBI_TaxId=6239;
[1]
RP SEQUENCE FROM N.A.
RA Matthews L.;
RT Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT Investigating Biology;
RL Science 282:2012-2018(1998).
DR EMBL; Z81573; CAB04625.1; -
DR InterPro; IPR003341; DUF139.
DR Pfam; PF02363; DUF139; 32.
SQ SEQUENCE 1513 AA; 161580 MW; 10BCB4287BA28285 CRC64;
Query Match 22.0%; Score 62.5; DB 5; Length 1513;
Best Local Similarity 35.8%; Pred. No. 4; Mismatches 18; Indels 13; Gaps 3;
Matches 19; Conservative
OY 12 DSLHAC-IPQLRC-SSNTPPLTCORYCNASV-----TNSVKGTNA 51
DB 141 DSCQNVCCNVCGAGCAGVSONSPAVCCQOTCRSCQFCGATNEQLPTTSTSTNA 193

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RESULT 15
ID Q9YW81 PRELIMINARY; PRT; 353 AA.
AC Q9YW81;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CG7348 protein.
GN CG7348.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;

```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:31:59 ; Search time 3.8459 Seconds
(without alignments)
551.635 Million cell updates/sec

Title: US-09-855-158-6

Perfect score: 284
Sequence: 1 MAGCCQNEYPDSLHACIP.....LTCORCNASVTSVKGTNA 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	284	100.0	184	1	Q02223 homo sapien
2	186	65.5	185	1	TR17_HUMAN
3	71.5	25.2	249	1	Q9E335 mus musculu
4	70.5	24.8	1877	1	PKCK_MOUSE
5	69.5	24.5	5376	1	ZAN_MOUSE
6	67.5	23.8	293	1	TI3X_HUMAN
7	66	23.2	63	1	ICEL_ASCSU
8	63	22.2	175	1	TI3C_MOUSE
9	62	21.8	1592	1	SORL_CHICK
10	61.5	21.7	99	1	GAS3_ARATH
11	60.5	21.3	3034	1	CLRI_MOUSE
12	60	21.1	1867	1	SSPO_BOVIN
13	60	20.4	1816	1	LM4_MOUSE
14	58	20.1	1816	1	LM4_HUMAN
15	57.5	20.2	1680	1	FUR2_DROME
16	57	20.1	708	1	YB40_HUMAN
17	56.5	19.9	701	1	YAB5_SCHPO
18	56	19.7	2476	1	ZAN_PIG
19	55.5	19.5	339	1	CATE_RAT
20	55.5	19.5	3695	1	LM4E_HUMAN
21	55	19.4	3695	1	CATE_MOUSE
22	55	19.4	687	1	VS41_GALPA
23	55	19.4	760	1	YJ06_YEAST
24	55	19.4	760	1	EZ_DROME
25	54.5	19.2	419	1	VEGC_HUMAN
26	54.5	19.2	532	1	TNR8_RAT
27	54.5	19.2	532	1	KPCZ_MOUSE
28	54	19.0	1980	1	MY9B_RAT
29	54	19.0	2114	1	MY9B_MOUSE
30	53.5	18.8	2158	1	MY9B_HUMAN
31	53.5	18.8	3323	1	TNR8_BOVIN
32	53.5	18.8	3325	1	VT2_SFVKA
33	53.5	18.8	381	1	P53_CANPA

34	53.5	18.8	1576	1	YLK3_CAEEL	P41951 caenorhabdi
35	53	18.7	131	1	ALX1_MOUSE	P97430 mus musculu
36	53	18.7	455	1	TR1A_HUMAN	P19438 homo sapien
37	53	18.7	591	1	KPCZ_RABIT	O19111 oryctolagus
38	53	18.7	712	1	ENV_HV22	P32536 human immun
39	53	18.7	859	1	ENV_HV22	P20872 human immun
40	53	18.7	3075	1	LM41_HUMAN	P25391 homo sapien
41	52.5	18.5	495	1	TNR8_MOUSE	O60846 mus musculu
42	52.5	18.5	847	1	Y083_NPVAC	O06570 autocographa
43	52.5	18.5	971	1	RECK_MOUSE	O92011 mus musculu
44	52.5	18.5	3718	1	LM45_MOUSE	O61001 mus musculu
45	52	18.3	56	1	ITR4_RADMA	P16344 radiataneus

ALIGNMENTS

RESULT 1
ID TR17_HUMAN STANDARD; PRT; 184 AA.
AC Q02223;
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 17 (B-cell maturation protein).
GN TNFRSF17 OR BCM4 OR BCM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_Taxid=9606;
[1]
RP SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION.
RC TISSUE=Peripheral blood leukocytes, and lymph node;
RX MEDLINE=93010984; PubMed=1396583;
RA Laabi Y., Gras M.P., Carbonnel F., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;
RT "A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)(q25;p13) translocation in a malignant T cell lymphoma.";
RL EMO J. 11:3897-3904(1992).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94218235; PubMed=8165126;
RA Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;
RT "The BCM gene, preferentially expressed during B lymphoid maturation, is bidirectionally transcribed.";
RL Nucleic Acids Res. 22:1147-1154(1994).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=9425270; PubMed=10493829;
RA Lotfus B.J., Kim U.-J., Shedd V.P., Kalush F., Brandon R., Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L., Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S., Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
RT "Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";
RL Genomics 60:295-308(1999).
[4]
RP SEQUENCE FROM N.A., AND VARIANT THR-153.
RX MEDLINE=21419161; PubMed=11528522;
RA Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;
RT "presence of four major haplotypes in human BCM4 gene: lack of association with systemic lupus erythematosus and rheumatoid arthritis.";
RL Genes Immun. 2:276-279(2001).
[5]
RP FUNCTION.
RX MEDLINE=20363816; PubMed=10903733;
RA Hatzoglou A., Rousset J., Bourgaud M.-F., Rogier E., Madry C., Inoue J., Devygne O., Tsapis A.;
RT "TNF receptor family member BCM4 (B cell maturation) associates with TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38

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DR EMBL; AF061505; AAC23799.1; -
 DR EMBL; AK020247; BAB32038.1; -
 DR MGI; MGI:1343050; TnfRsf17.
 KM Receptor; Immune response; Signal-anchor; Transmembrane;
 KM Alternative splicing.
 FT DOMAIN 1
 FT TRANSMEM 50 70
 FT REPEAT 71 185
 FT REPEAT 4 36
 FT DISULFID 5 18
 FT DISULFID 21 32
 FT DISULFID 25 36
 FT VARSPLIC 87 91
 FT SEQUENCE 185 AA; 20442 MW; 8806352BAFD28A8E CRC64;

Query Match
 Best Local Similarity 71.4%; Score 186; DB 1; Length 185;
 Matches 35; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 1 MAQCSEYFDSLHACTPQLRGSSNTPPLTCORYCNASTNSVYGT 49
 Db 1 MAQCSEYFDSLHACTPQLRGSSNTPPLTCORYCNASTNSVYGT 47

RESULT 3
 ID T13X MOUSE STANDARD; PRT; 249 AA.
 AC Q9ERT5; Q9DB23;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane activator and CAMD interactor).
 GN TNFRSF13B OR TRAF1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxId=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=espleen;
 RX MEDLINE=21177254; PubMed=10881172;
 RA Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A., Dixit V.M.;
 RT "Identification of a receptor for BLyS demonstrates a crucial role in humoral immunity";
 RL Nat. Immunol. 1:37-41 (2000).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai T., Hara A., Fukunishi Y., Konno H., Adachi Y., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi Y., Yamada S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamano R., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadono K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischer M.W., Gaasterland T., Gissi C., King B., Kochava H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staudt R., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Olego I., Furuno M., Aono H., Balakrishnan R., Barsh G., Blake U., Bollella R.P., Bojunga N., Carninci F., de Bonaldo M., Brownstein M.J., Bulc C., Fletcher C., Fujita N., Gariboldi M., Gustinich S., Hill D., Holman W., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli U., Kombergs P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,

RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 RL [3]
 RP FUNCTION.
 RX MEDLINE=20341628; PubMed=10880535;
 RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M., Thall L.E., Colombero A., Solovay I., Lee F., McCabe S., Elliott R., Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J., Meng S.-Y., Boyle W.J., Hsu H.;
 RT "TRAF1 is a TRAF-interacting receptor for TALL-1, a tumor necrosis factor family member involved in B cell regulation";
 RL J. Exp. Med. 192:137-143 (2000).
 RL [4]
 RP FUNCTION.
 RX MEDLINE=21322748; PubMed=11429548;
 RA Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.;
 RT "TRAF1 and TRAF2 interact with NF-kappaB and are required for T cell activation and collagen-induced arthritis in mice";
 RL Nat. Immunol. 2:632-637 (2001).
 CC -1- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS that binds both ligands with similar high affinity. Mediates cell-neurin-dependent activation of NF-kappaB, as well as activation of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-cell function and the regulation of humoral immunity (By similarity).
 CC -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal domain of CAMLG with its C-terminus (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
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DR EMBL; AF257673; AA000081.1; -
 DR EMBL; AK004668; BAB23457.1; -
 DR MGI; MGI:188941; TnfRsf13b.
 DR PROSITE; PS00652; TNFR_NGFR_2; 1.
 DR PROSITE; PS00050; TNFR_NGFR_2; 2.
 KM Receptor; Immune response; Signal-anchor; Transmembrane; Repeat.
 FT DOMAIN 1 128
 FT TRANSMEM 129 149
 FT REPEAT 150 249
 FT REPEAT 5 38
 FT DISULFID 6 14
 FT DISULFID 22 34
 FT DISULFID 26 38
 FT DISULFID 43 58
 FT DISULFID 61 72
 FT DISULFID 65 76
 FT CONFLICT 137 137
 FT SEQUENCE 249 AA; 26947 MW; CB2F2D61C2931D81 CRC64;

Query Match
 Best Local Similarity 25.2%; Score 71.5; DB 1; Length 249;
 Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

Qy 5 CSQNEYPDSLHACTPQLRGSSNTPPLTCORYC 38
 Db 6 CPKQDQWMSRKSCVSCALTRSCQS-ORCTDFC 38

RESULT 4
 ID PKCS MOUSE STANDARD; PRT; 1877 AA.

AC Q04592; Q62040;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Proprotein convertase subtilisin/kexin type 5 precursor (BC 3.4.21.-)
 DE (Proprotein convertase PCS) (Subtilisin/kexin-like protease PCS)
 DE (Convertase PCS) (PC6) (Subtilisin-like proprotein convertase 6)
 DE (SPC6).
 DE PCS5.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1] SEQUENCE OF 330-1877 FROM N.A. (ISOFORM PCSB).
 RP STRAIN=ICR; TISSUE=Intestine;
 RC MEDLINE=9337934; PubMed=8335106;
 RA Nakagawa T., Murakami K., Nakayama K.;
 RT "Identification of an isoform with an extremely large Cys-rich region
 of PC6, a Kex2-like processing endoprotease.";
 RL FEBS Lett. 327:165-171(1993).
 [2]
 RN SEQUENCE FROM N.A. (ISOFORM PCSA).
 RP TISSUE=Brain, and Intestine;
 RC MEDLINE=93224489; PubMed=8468318;
 RA Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,
 RA Nakayama K.;
 RT "Identification and functional expression of a new member of the
 mammalian Kex2-like processing endoprotease family: its striking
 structural similarity to PACE4.";
 RL J. Biochem. 113:132-135(1993).
 [3]
 RN SEQUENCE FROM N.A. (ISOFORM PCSA).
 RP TISSUE=Adrenal cortex.
 RC MEDLINE=93342056; PubMed=8341687;
 RA Lussan J., Vieau D., Hamelin J., Day R., Chretien M., Seidah N.G.;
 RT "cDNA structure of the mouse and rat subtilisin/kexin-like PCS: a
 candidate proprotein convertase expressed in endocrine and
 nonendocrine cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
 [4]
 RN PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.
 RP MEDLINE=97103178; PubMed=8947550;
 RA De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,
 RA Bendayan M., Seidah N.G.;
 RT "The isoforms of proprotein convertase PC5 are sorted to different
 subcellular compartments.";
 RL J. Cell Biol. 135:1261-1275(1996).
 [5]
 RN DEVELOPMENTAL EXPRESSION.
 RP MEDLINE=96293359; PubMed=8698813;
 RA Constam D.B., Calfon M., Robertson E.J.;
 RT "SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone
 morphogenetic proteins at distinct sites during embryogenesis.";
 RL J. Cell Biol. 134:181-191(1996).
 [6]
 RN DEVELOPMENTAL EXPRESSION.
 RP MEDLINE=97436919; PubMed=9291583;
 RA Rancourt S.L., Rancourt D.E.;
 RT "Murine subtilisin-like proteinase SPC6 is expressed during embryonic
 implantation, somitogenesis, and skeletal formation.";
 RL Dev. Genet. 21:75-81(1997).
 CC -1- FUNCTION LIKELY TO REPRESENT A WIDESPREAD ENDOPEPTASE ACTIVITY
 WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY CAPABLE
 OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF. MAY BE RESPONSIBLE
 FOR THE MATURATION OF GASTROINTESTINAL PEPTIDES. MAY BE INVOLVED
 IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA THE ACTIVATION
 OF GROWTH FACTORS.
 CC -1- CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
 PROPEPTINS BY CLEAVAGE OF ARG-XAA-YAA-ARG-|-ZAA BONDS, WHERE XAA
 CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
 CC -1- SUBCELLULAR LOCATION: PCSA IS SECRETED THROUGH THE REGULATED
 SECRETORY PATHWAY. PCSB IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO

CC A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH
 CC EARLY ENDOSOMES.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; PCSB/LONG (SHOWN HERE)
 CC AND PCSA/SHORT; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: PCSA IS EXPRESSED IN MOST TISSUES BUT IS MOST
 CC ABUNDANT IN THE INTESINE AND ADRENALS. PCSB IS EXPRESSED IN THE
 CC INTESINE, ADRENALS AND LUNG BUT NOT IN THE BRAIN.
 CC -1- DEVELOPMENTAL STAGE: WEAKLY EXPRESSED THROUGHOUT THE EMBRYO,
 CC EXCEPT IN THE STAGEING NERVOUS SYSTEM, THE RIBS AND THE LIVER,
 CC BUT MARKEDLY UPREGULATED AT DISCRETE SITES DURING DEVELOPMENT. AT
 CC E6.5, PROMINENT EXPRESSION OBSERVED IN DIFFERENTIATED DECIDUA. AT
 CC E7.5, INTENSE EXPRESSION IN EXTRAEMBRYONIC ENDODERM, AMNION AND
 CC NASCENT MESODERM. AT 8.5, ABUNDANT EXPRESSION IN SOMITES AND YOLK
 CC SAC FOLLOWED BY A CONFINATION TO DERMATOTOME COMPARTMENT. BETWEEN
 CC E9.5 AND E11.5, ABUNDANT EXPRESSION IN AER (THICKENED ECTODERMAL
 CC CELLS OF LIMB BUDS). AT E12.5, EXPRESSION IN THE LIMBS IS CONFINED
 CC TO THE CONDENSING MESENCHYM SURROUNDING THE CARTILAGE. AT THIS
 CC STAGE, STRONG EXPRESSION ALSO DETECTED IN VERTEBRAL AND FACIAL
 CC CARTILAGE PRIMORDIA AND IN THE MUSCLE OF THE TONGUE. AT E16.5,
 CC ABUNDANT EXPRESSION IN EPITHELIAL CELLS OF THE INTESTINAL VILLI.
 CC ISOFORM A IS MOST ABUNDANT AT ALL STAGES BUT SIGNIFICANT LEVELS OF
 CC ISOFORM B OCCUR AT E12.5.
 CC -1- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
 CC ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC
 CC RETICULUM.
 CC -1- DOMAIN: AC 1 AND AC 2 (CLUSTERS OF ACIDIC AMINO ACIDS) CONTAIN
 CC SORTING INFORMATION. AC 1 DIRECTS TGN LOCALIZATION AND INTERACTS
 CC WITH THE TGN SORTING PROTEIN PACS-1.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
 CC -1- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
 CC -----
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 CC -----
 CC EMBL; D17593; BAA04507.1; -;
 CC EMBL; D12619; BAA02143.1; -;
 CC EMBL; U14932; AAA74636.1; -;
 CC FIR; JX0248; JX0248.
 CC FIR; A48225; A48225.
 CC HSP; Q99405; IMPT.
 CC MEROPS; S08.076; -;
 CC MGD; MGI:97515; Pcsk5.
 CC InterPro; IPR000561; EGF-like.
 CC InterPro; IPR002174; Furin-like.
 CC InterPro; IPR002884; P domain.
 CC InterPro; IPR000209; Peptidase S8.
 CC Pfam; PF00082; Peptidase_S8; 1.
 CC Pfam; PF01483; P; PARTIAL.
 CC PRINTS; PR00723; SUBTILISIN.
 CC ProDom; PD000717; P domain; 1.
 CC SMART; SM00181; EGF_3.
 CC SMART; SM00001; EGF-like; 2.
 CC SMART; SM00261; FU_22.
 CC PROSITE; PS00136; SUBTILASE ASP; 1.
 CC PROSITE; PS00137; SUBTILASE_HIS; 1.
 CC PROSITE; PS00138; SUBTILASE_SER; 1.
 CC Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;
 CC Cleavage on pair of basic residues; Repeat; Alternative splicing;
 CC Transmembrane. 1 34
 CC SIGNAL 35 116
 CC PROPEP 117 1877
 CC CHAIN 117 1877
 CC PROPROTEIN CONVERTASE SUBTILISIN/KEXIN
 CC TYPE 5.
 CC DOMAIN 117 1768 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 1769 1789 POTENTIAL.
 CC DOMAIN 1790 1877 CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 117 452 CATALYTIC.
 CC DOMAIN 464 602 HOMO B.


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FT DOMAIN 638 1753 CYS-RICH MOTIF (CRM) REGION.
FT DOMAIN 1825 1844 AC 1.
FT DOMAIN 1856 1877 AC 2.
FT SITE 116 117 CLEAVAGE (AUTO-) (BY SIMILARITY).
FT SITE 521 523 CELL ATTACHMENT SITE (POTENTIAL).
FT ACT SITE 173 173 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 214 214 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 388 388 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 227 227 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 383 383 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 667 667 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 754 754 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 804 804 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 854 854 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 951 951 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1016 1016 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1220 1220 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1317 1317 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1523 1523 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1711 1711 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1733 1733 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 878 915 GEYIDQGHCHTCFCEASCAKCMWPTQEDCISCPTFVLD
  (IN ISOFORM PCSA).
FT VARSPLIC 916 1877 ATEESWAEGFMCVLVKNNLCQKXVLDLCKCTFPG
  (IN ISOFORM PCSA).
FT VARSPLIC 1877 AA; 209287 MW; BC850E2DF20EA1C3 CRC64;
  MISSING (IN ISOFORM PCSA).
SQ SEQUENCE 1877 AA; 209287 MW; BC850E2DF20EA1C3 CRC64;

Query Match 24.8%; Score 70.5; DB 1; Length 1877;
Best Local Similarity 34.7%; Pred. No. 0.96;
Matches 17; Conservative 5; Mismatches 22; Indels 5; Gaps 1;

OY 4 OCSQNYFDSLHACIPCOLRGCSNTPP-----LTCORXCNAVTSYVK 47
DB 1480 ECAAVVEYWDGSHRCQPCCHKKSCRGSPEDQCYTCRPREPLFNTTVCVK 1528

RESULT 5
ID_ZAN_MOUSE STANDARD; PRT; 5376 AA.
AC 088799; 008647; Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Zonadhesin precursor.
GN ZAN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Testis;
RX MEDLINE=98123114; PubMed=9452463;
RA Gao Z.; Garbers D.L.;
RT "Species diversity in the structure of zonadhesin, a sperm-specific
RT membrane protein containing multiple cell adhesion molecule-like
RT domains."
RL J. Biol. Chem. 273:3415-3421 (1998).
RN [2]
RP SEQUENCE OF 4864-5376 FROM N.A.
RC TISSUE-Testis; PubMed=9126492;
RX MEDLINE=97271566; PubMed=9126492;
RA Gao Z.; Harumi T.; Garbers D.L.;
RT "Chromosome localization of the mouse zonadhesin gene and the human
RT zonadhesin gene (ZAN)."
RL Genomics 41:119-122 (1997).
CC -1- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA
CC OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR
CC SIGNALING.
CC -1- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE
CC APICAL REGION OF THE SPERM HEAD.
CC -1- TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPLOID SPERMATIDS.

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CC -1- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATES SPERM ADHESION TO THE
CC ZONA PELLUCIDA.
CC -1- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS,
CC THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF
CC SPERMATOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS.
CC -1- DOMAIN: THE VWFD DOMAIN 2 MAY MEDIATE COVALENT
CC OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).
CC -1- SIMILARITY: CONTAINS 3 MAM DOMAINS.
CC -1- SIMILARITY: CONTAINS 25 VWFD DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U97068; AAC26680.1; -;
CC EMBL; U83190; AAC53125.1; -;
CC MGD; MGI:106656; Zan.
CC InterPro; IPR000561; EGF-like.
CC InterPro; IPR003645; FOLN.
CC InterPro; IPR000998; MAM domain.
CC InterPro; IPR002919; TIL_Cysrich.
CC InterPro; IPR003328; TIL_Cysrich.
CC InterPro; IPR001007; VWF_C.
CC InterPro; IPR001846; VWF_D.
CC Pfam; PF00094; vwd; 4.
CC Pfam; PF00629; MAM; 3.
CC Pfam; PF01826; TIL; 25.
CC Pfam; PF02345; TIL; 25.
CC SMART; SM00181; EGF; 2.
CC SMART; SM00274; FOLN; 11.
CC SMART; SM00137; MAM; 2.
CC SMART; SM00214; vwd; 17.
CC SMART; SM00216; vwd; 4.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS01186; EGF_2; 18.
CC PROSITE; PS00740; MAM_1; FALSE_NEG.
CC PROSITE; PS50060; MAM_2; 3.
CC Signal; Glycoprotein; Transmembrane; EGF-like domain; Cell adhesion;
CC Repeat.
CC FT SIGNAL 1 17
CC FT CHAIN 18 5376
CC FT DOMAIN 18 5310
CC FT TRANSMEM 5311 5337
CC FT DOMAIN 5338 5376
CC FT DOMAIN 45 210
CC FT DOMAIN 215 374
CC FT DOMAIN 377 542
CC FT DOMAIN 547 1170
CC FT DOMAIN 1171 1280
CC FT DOMAIN 1281 1669
CC FT DOMAIN 1670 2056
CC FT DOMAIN 2057 2459
CC FT DOMAIN 2460 2579
CC FT DOMAIN 2580 2699
CC FT DOMAIN 2700 2819
CC FT DOMAIN 2820 2939
CC FT DOMAIN 2940 3059
CC FT DOMAIN 3060 3179
CC FT DOMAIN 3180 3299
CC FT DOMAIN 3300 3416
CC FT DOMAIN 3417 3536
CC FT DOMAIN 3537 3656
CC FT DOMAIN 3657 3776
CC FT DOMAIN 3777 3892
CC FT DOMAIN 3893 4928
CC FT DOMAIN 4029 4148
CC FT DOMAIN 4149 4263

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FT DOMAIN 4264 4283 VFWD 20 (PARTIAL).
FT DOMAIN 4384 4503 VFWD 21 (PARTIAL).
FT DOMAIN 4504 4623 VFWD 22 (PARTIAL).
FT DOMAIN 4624 4743 VFWD 23 (PARTIAL).
FT DOMAIN 4744 4863 VFWD 24 (PARTIAL).
FT DOMAIN 4864 5295 VFWD 25.
FT DOMAIN 5259 5295 EGF-LIKE.
FT DISULFID 5263 5274 BY SIMILARITY.
FT DISULFID 5268 5283 BY SIMILARITY.
FT DISULFID 5285 5294 BY SIMILARITY.
FT CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 499 499 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1216 1216 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1239 1239 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1314 1314 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1814 1814 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1908 1908 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1933 1933 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2028 2028 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2111 2111 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2142 2142 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2332 2332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2533 2533 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2575 2575 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2692 2692 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2812 2812 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3052 3052 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3065 3065 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3144 3144 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3172 3172 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3288 3288 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3292 3292 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3782 3782 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4005 4005 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4136 4136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4243 4243 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4254 4254 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4335 4335 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4376 4376 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4586 4586 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 5136 5136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 5252 5252 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 5376 AA; 57998 MW; 0E44DB77DF2A2620 CRC64;

Query Match 24.5%; Score 69.5; DB 1; Length 5376;
Best Local Similarity 36.8%; Pred. No. 3.4;
Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

QY 4 QCSONEYFDSLHACIP-CQLRCSSNTP--PLTCQRYC 38
Db 3299 QCPTNSQFTDCLPSCVPCSCNRCEVTSFVSPVSSCREGC 3336

RESULT 6
ID T13X HUMAN STANDARD; PRT; 293 AA.
AC O14836.
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE tumor necrosis factor receptor superfamily member 13B (Transmembrane
DE activator and CAML receptor).
GN TNFRSF13B OR TACI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA MEDLINE=97458245; PubMed=9311921;
RA von Buelow G.-U.; Bram R.J.;
"NF-AT activation induced by a CAML-interacting member of the tumor

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RT necrosis factor receptor superfamily.";
RL Science 278:138-141(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP FUNCTION.
RX MEDLINE=20519647; PubMed=10956646;
RA Wu Y., Bressette D., Carroll J.A., Kaufman T., Feng P., Taylor K.,
RA Gan Y., Cho Y.H., Garcia A.D., Gollatz B., Dinko D., Lalleur D.,
RA Misone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J.,
RA Olsen H.S., Kanakaraj P., Moore P.A., Baker K.P.,
RT "Tumor necrosis factor (TNF) receptor superfamily member TACI is a
RT high affinity receptor for TNF family members APRIL and BLYS.";
RL J. Biol. Chem. 275:35478-35485 (2000).
RN [4]
RP FUNCTION.
RX MEDLINE=21170294; PubMed=10973284;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.B.;
RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
RT humoral immunity.";
RL Nat. Immunol. 1:252-256(2000).
CC -!- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAPF/BLYS
CC that binds both ligands with similar high affinity. Mediates
CC calcineurin-dependent activation of NF-AT, as well as activation
CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
CC cell function and the regulation of humoral immunity.
CC -!- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
CC domain of CAMLG with its C-terminus.
CC -!- SUBCELLULAR LOCATION: Type III membrane protein.
CC interesting and peripheral blood leukocytes. Expressed in resting B-
CC cells and activated T-cells, but not in resting T-cells.
CC -!- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC -!- CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.
CC
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CC -----
CC EMBL; AF023614; AAC51790.1; -
CC EMBL; BC028072; AAH28072.1; -
CC Genew; HGNC:18153; TNFRSF13B.
CC MIM; 604907; -
CC InterPro; IPR001368; TNFR_C6.
CC PROSITE; PS00652; TNFR_NGFR_1; 1.
CC PROSITE; PS00500; TNFR_NGFR_2; FALSE NEG.
CC Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;
CC Repeat.
CC DOMAIN 1 165 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 166 186 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
CC
CC DOMAIN 187 293 CYTOPLASMIC (POTENTIAL).
CC REPEAT 33 67 TNFR-CYS 1.
CC REPEAT 70 104 TNFR-CYS 2.
CC DISULFID 34 47 BY SIMILARITY.
CC DISULFID 50 62 BY SIMILARITY.
CC DISULFID 54 66 BY SIMILARITY.
CC DISULFID 71 86 BY SIMILARITY.
CC DISULFID 89 100 BY SIMILARITY.
CC DISULFID 93 104 BY SIMILARITY.
CC CARBOHYD 128 128 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CONFLICT 251 251 P -> L (IN REF. 2).
CC SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;

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Query Match      23.8%; Score 67.5; DB 1; Length 293;
Best Local Similarity 30.6%; Pred. No. 0.38;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

OY 5 CSQNEFYDSLHACIPQCRSSNTPLPTLCORYCNA 40
   34 CPEQYWDPLGLGCMCKKTCIKNHQS-QRTCAAFCHS 68

RESULT 7
ID ICE1_ASCSU STANDARD; PRT; 63 AA.
AC P07851;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last annotation update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Chymotrypsin/elastase isoinhibitor 1 (C/E-1 inhibitor).
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoidea).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_Taxid=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=84255715; PubMed=6564898;
RA Babin D.R., Peanasky R.J., Goos S.M.;
RT "The isoinhibitors of chymotrypsin/elastase from Ascaris
RT lumbricoidea: the primary structure."
RL Arch. Biochem. Biophys. 232:143-161(1984).
RN [2]
RX X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH ELASTASE.
RP MEDLINE=95060335; PubMed=7922044;
RA Huang K., Strynadka N.C., Bernard V.D., Peanasky R.J., James M.N.;
RT "The molecular structure of the complex of Ascaris
RT chymotrypsin/elastase inhibitor with porcine elastase."
RL Structure 2:679-689(1994).
CC -1- FUNCTION: BELONGS TO THE ASCARIS TRYPSIN INHIBITOR FAMILY.
CC -1- SIMILARITY: BELONGS TO THE ASCARIS TRYPSIN INHIBITOR FAMILY.
DR PIR: S07127; S07127.
DR InterPro: IPR002919; TIL_Cysrich.
DR Pfam: PF01826; TIL_1.
KW Serine protease inhibitor; 3d-structure.
FT DISULFID 5 38
FT DISULFID 14 33
FT DISULFID 17 29
FT DISULFID 21 60
FT DISULFID 40 54
FT ACT SITE 31 32
SQ SEQUENCE 63 AA; 6862 MW; 5DC10DE75B375F16 CRC64;

Query Match      23.2%; Score 66; DB 1; Length 63;
Best Local Similarity 34.0%; Pred. No. 0.14;
Matches 17; Conservative 7; Mismatches 18; Indels 8; Gaps 4;

OY 5 CSQNEFYDSLHACIPQCRSSNTPLPTLCORYCNA 50
   5 CGNEVWTE---CTGCEMKKCGPDENTPCPLMCRPRSCSPGRGMRRTN 50

RESULT 8
ID T13C_MOUSE STANDARD; PRT; 175 AA.
AC Q9P8D0;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13C (B cell-
DE activating factor receptor) (BAFF receptor) (BAFF-R) (Blys receptor
DE 3) (B-cell maturation defect).
GN TNFRSF13C OR BAFFR OR BCMD OR BR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1 AND 2).
RC STRAIN=BALB/C; TISSUE=B-cell lymphoma;
RX MEDLINE=21442025; PubMed=11509692;
RA Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
RA Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C.,
RA Strauch K., Zafari M., Benjamin C.D., Teschop J., Browning J.L.,
RA Ambrose C.;
RT "BAFF-R, a newly identified TNF receptor that specifically interacts
RT with BAFF."
RL Science 293:2108-2111(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND DISEASE.
RC STRAIN=A/J;
RX MEDLINE=21475520; PubMed=11591325;
RA Yan M., Brady T.R., Chan B., Lee W.P., Hsu B., Harless S.M.,
RA Cacero M.P., Grewal I.S., Dixie V.M.;
RT "Identification of a novel receptor for B lymphocyte stimulator that
RT is mutated in a mouse strain with severe B cell deficiency."
RL Curr. Biol. 11:1547-1552(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamada I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsumoto H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schirral L.M., Scambli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Blake K., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shiota Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,
RA Wyman-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [4]
RP FUNCTION.
RX MEDLINE=21614654; PubMed=11747827;
RA Harless S.M., Lentz V.M., Sah A.P., Heu B.L., Clise-Dwyer K.,
RA Hilbert D.M., Hayes C.E., Cancro M.P.;
RT "Competition for Blys-mediated signaling through Bemd/BR3 regulates
RT peripheral B lymphocyte numbers."
RL Curr. Biol. 11:1986-1989(2001).
CC -1- FUNCTION: B-cell receptor specific for TNFRSF13B/TNFR1/BAFF/Blys.
CC Promotes the survival of mature B-cells and the B-cell response.
CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: Highly expressed in spleen and testis;
CC detected at lower levels in lung and thymus.
CC -1- DISEASE: Defects in TNFRSF13C are a cause of severe B-cell
CC deficiency. B-cell deficient strain A/WySnJ has a 4.7 kb insertion
CC in the BAFF gene leading to an altered C-terminus. The mutant RNA
CC is not detectable. B-cell lymphoproliferation is normal, but the life
CC span of peripheral B-cells is much reduced.
CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
CC -----
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FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 581 581 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 725 725 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 778 778 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 975 975 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 1098 1098 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 1152 1152 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 1366 1366 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 1454 1454 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 1514 1514 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT NON TER 1592 1592 N-LINKED (GLCNAC. . .) (POTENTIAL)
SO SEQUENCE 1592 AA; 178409 MW; 24EDPA5BA231B203 CRC64;

Query Match 21.8%; Score 62; DB 1; Length 1592;
Best Local Similarity 33.3%; Pred. No. 8.6;
Matches 15; Conservative 6; Mismatches 18; Indels 6; Gaps 2;

Cy 3 GGCSONEYFDSLHACIP---COLF-CSSNTPPLTCGRYCNAS 41
Db 1376 GRCSTRFECQQLHKCIPMWKRCDCGRDCDGTDRSCPTHSLS 1420

RESULT 10
GAS3_ARATH STANDARD; PRT; 99 AA.
ID GAS3_ARATH STANDARD; PRT; 99 AA.
AC P46687;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gibberellin-regulated protein 3 precursor.
GN GAS3 OR AT4G09600 OR T25P22.40.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Ericaceae; Ericales; Brassicaceae; Arabidopsids.
OK NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia; TISSUE=Seed;
RX MEDLINE=95244835; PubMed=7727751;
RA Herzog M., Dorn A.-M., Grellet F.;
RT "GAS3, a gibberellin-regulated gene family from Arabidopsis thaliana
RT related to the tomato GASTI gene."
RL Plant Mol. Biol. 27:743-752(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Scheller C., Wandt R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Ertter K.-D., Terryn N.,
RA Harris B., Anstorge W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA Kreis M., Delany M., Puidgomech P., Watson M., Schmidheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hohenseil J., Zimmermann W., Medler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bligh M., Robben J., Vandenbusche F.,
RA van der Schueren U., Grymonprez B., Chuang I.-O., Vandenbusche F.,
RA Breken W., Melchers I., Voet M., Baetians I., Aert K., Defoor E.,
RA Weitzemesser I., Botne G., Kampeger U., Hilbert H., Braun W.,
RA Holzner B., Brandt A., Peters S., van Staveren M., Dittze W.,
RA Moosman P., Klein Lankhorst R., Rose M., Hauf J., Koeller P.,
RA Bernieris S., Hempel S., Feldpausch M., Lambers S., Van den Daele H.,
RA de Keyser A., Buysaert C., Gielen J., Villarroel R., Van der Clier R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McKay K., Mayes R.,
RA Perletti A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fatmann B., Grandenath K., Danner D., Herzl A.,
RA Neumann S., Argitrou A., Vitale D., Ligouri R., Pitravadi E.,

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RA Massenet O., Outgley F., Clabaud G., Muendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chefor F., Cooke R., Berger C., Monfort A., Caesaberta E.,
RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
RA Perez-Perez A., Punelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bialke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Lattelle P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer U., Fulton L., Mardis E., Dante M., Pepin K., Hiller L.,
RA Nelson U., Spiech U., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali U., Bergholt A., Jones K., Drome K., Cotton W., Joshi C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C.,
RA Ma P., Zhong J., Preston R., Vill D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
RA Granat S., Shohdy N., Hasegawa A., Hamed A., Loch M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana."
RT Nature 402:769-777(1999).
RL Mature 402:769-777(1999).
CC -1- FUNCTION: INVOLVED IN LATE STAGES OF SEED MATURATION, OR IN EARLY
CC STEPS OF GERMINATION.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: SILIQUES AND DRY SEEDS.
CC -1- PTM: SIX DISULFIDE BONDS MAY BE PRESENT.
CC -1- SIMILARITY: BELONGS TO THE GASTI FAMILY.
CC -----
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CC -----
DR EMBL; U11764; AAB06308.1; -
DR EMBL; AL161515; CAB78083.1; -
DR EMBL; AL161831; CAB82127.1; -
DR InterPro; IPR003854; GASA.
DR Pfam; PF02704; GASA; 1.
KW Multigene family; Signal.
FT SIGNAL 1 18
FT CHAIN 19 99
FT SEQUENCE 99 AA; 10704 MW; 84549B74B08A47FA CRC64;
SO SEQUENCE FROM N.A.

Query Match 21.7%; Score 61.5; DB 1; Length 99;
Best Local Similarity 35.6%; Pred. No. 0.72;
Matches 16; Conservative 7; Mismatches 17; Indels 5; Gaps 2;

Cy 3 GGCSONEYFDSLHACIPCOLRCSSNTPPLTCGRY---CNASVT 43
Db 47 GRCSSSRPMLCRLACNSCCRCNC-VFPTAGNHHLCPYASIT 90

RESULT 11
CRL_MOUSE STANDARD; PRT; 3034 AA.
ID CRL_MOUSE STANDARD; PRT; 3034 AA.
AC 03516;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cadherin EGF LAG seven-pass G-type receptor 1 precursor.
GN CERS1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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FT DISULFID 1668 1679 BY SIMILARITY.
FT DISULFID 1673 1688 BY SIMILARITY.
FT DISULFID 1690 1699 BY SIMILARITY.
FT DISULFID 1891 1902 BY SIMILARITY.
FT DISULFID 1896 1911 BY SIMILARITY.
FT DISULFID 1913 1922 BY SIMILARITY.
FT DISULFID 1926 1937 BY SIMILARITY.
FT DISULFID 1931 1949 BY SIMILARITY.
FT DISULFID 1951 1960 BY SIMILARITY.
FT DISULFID 1960 1978 BY SIMILARITY.
FT DISULFID 1968 1983 BY SIMILARITY.
FT DISULFID 2000 2015 BY SIMILARITY.
FT DISULFID 2020 2036 BY SIMILARITY.
FT DISULFID 2030 2050 BY SIMILARITY.
FT MOD_RES 1681 1681 BY SIMILARITY.
FT MOD_RES 1904 1904 HYDROXYLATION (POTENTIAL).
FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 561 561 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 649 649 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 793 793 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1129 1129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1154 1154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1228 1228 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1264 1264 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1274 1274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1302 1302 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1591 1591 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1638 1638 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1655 1655 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1994 1994 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2118 2118 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2137 2137 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2144 2144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2155 2155 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2160 2160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2272 2272 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2430 2430 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2452 2452 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2538 2538 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 3034 AA; 330477 MW; 8FF38180AF5BD8A8 CRC64;

Query Match 21.3%; Score 60.5; DB 1; Length 3034;
Best Local Similarity 28.3%; Pred. No. 24;
Matches 17; Conservative 5; Mismatches 19; Indels 19; Gaps 3;

QY 4 QCSQNEFYFLHACIPCOL-----RCSNTPLPTQ-----RYCN-----ASYTN 44
DB 2001 QCSQNEFYFLHACIPCOL-----RCSNTPLPTQ-----RYCN-----ASYTN 44

RESULT 12
SSPO BOVIN STANDARD; PRT; 867 AA.
AC P98167;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE SCO-spondin (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Kuminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=ependymocyte;
RX MEDLINE=96318614; PubMed=8743952;
RA Gobron S., Monnerie H., Meinzel R., Creveaux I., Lehmann W.,
RA Lamalle D., Dastugue B., Meinzel A.;
RT "SCO-spondin: a new member of the thymospondin family secreted by
RT the subcommissural organ is a candidate in the modulation of neuronal
RT aggregation.";
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RL J. Cell Sci. 109:1053-1061(1996).
CC -1- FUNCTION: INVOLVED IN THE MODULATION OF NEURONAL AGGREGATION.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: SUBCOMMISSURAL ORGAN.
CC -1- DEVELOPMENTAL STAGE: EMBRYO.
CC -1- SIMILARITY: BELONGS TO THE THYMOSPONDIN FAMILY.
CC -1- SIMILARITY: CONTAINS AT LEAST 4 TSP TYPE-1 DOMAINS.
CC -1- SIMILARITY: CONTAINS AT LEAST 2 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS AT LEAST 1 FS/8 TYPE C DOMAIN.
CC -1- SIMILARITY: CONTAINS AT LEAST 3 LDL-RECEPTOR CLASS A DOMAINS.
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DR EMBL; X93922; CAA63815.1; -.
DR HSPB; P01130; IAUJ.
DR InterPro; IPR000421; FA58_C.
DR InterPro; IPR002172; LDL_recept_A.
DR InterPro; IPR002919; TIL_Cysrich.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR01007; VWF_C.
DR Pfam; PF00057; ldl_recept_a; 3.
DR Pfam; PF00090; tsp_1; 4.
DR Pfam; PF00093; vwc_1.
DR Pfam; PF00754; F5_P8_type_C; 1.
DR Pfam; PF01826; TIL; 1.
DR SMART; SM00192; LDCA; 3.
DR SMART; SM00231; FA58C; 1.
DR SMART; SM00192; TSP1; 4.
DR SMART; SM00204; TSP1; 4.
DR PROSITE; PS01285; FA58C_1; 1.
DR PROSITE; PS01208; LDCA_1; 1.
DR PROSITE; PS01208; LDCA_2; 3.
DR PROSITE; PS50068; LDCA_2; 3.
DR PROSITE; PS50068; TSP1; 4.
KM Glycoprotein; Cell adhesion; Calcium-binding; Repeat; EGF-like domain.
FT NON_TER 1 1
FT DOMAIN 26 81 TSP TYPE-1.1.
FT DOMAIN 103 142 EGF-LIKE 1.
FT DOMAIN 143 180 EGF-LIKE 2.
FT DOMAIN 185 243 TSP TYPE-1.2.
FT DOMAIN 344 502 FS/8 TYPE C.
FT DOMAIN 506 544 LDL-RECEPTOR CLASS A 1.
FT DOMAIN 663 701 LDL-RECEPTOR CLASS A 2.
FT DOMAIN 723 761 LDL-RECEPTOR CLASS A 3.
FT DOMAIN 762 813 TSP TYPE-1.3.
FT DOMAIN 814 867 TSP TYPE-1.4.
FT DISULFID 107 122 BY SIMILARITY.
FT DISULFID 116 127 BY SIMILARITY.
FT DISULFID 129 141 BY SIMILARITY.
FT DISULFID 147 166 BY SIMILARITY.
FT DISULFID 149 169 BY SIMILARITY.
FT DISULFID 171 179 BY SIMILARITY.
FT DISULFID 344 502 BY SIMILARITY.
FT DISULFID 506 520 BY SIMILARITY.
FT DISULFID 515 533 BY SIMILARITY.
FT DISULFID 527 542 BY SIMILARITY.
FT DISULFID 665 677 BY SIMILARITY.
FT DISULFID 672 690 BY SIMILARITY.
FT DISULFID 684 699 BY SIMILARITY.
FT DISULFID 725 737 BY SIMILARITY.
FT DISULFID 732 750 BY SIMILARITY.
FT DISULFID 744 759 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 409 409 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 867 867
SQ SEQUENCE 867 AA; 91817 MW; 9538F2108E787B49 CRC64;
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FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 550 550 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 571 571 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 574 574 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 631 631 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 639 639 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 753 753 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 754 754 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 751 751 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 780 780 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 803 803 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 1088 1088 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 1283 1283 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 1361 1361 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CONFLICT 8 8 C -> S (IN REF. 2)
FT CONFLICT 18 18 C -> Y (IN REF. 2)
FT CONFLICT 248 248 C -> R (IN REF. 3)
FT CONFLICT 297 297 G -> A (IN REF. 3)
FT CONFLICT 431 431 THR -> HPS (IN REF. 2)
FT CONFLICT 679 679 S -> C (IN REF. 3)
FT CONFLICT 703 703 D -> G (IN REF. 2)
FT CONFLICT 706 706 N -> H (IN REF. 2)
FT CONFLICT 728 728 K -> R (IN REF. 2)
FT CONFLICT 730 730 F -> I (IN REF. 2)
FT CONFLICT 779 779 R -> G (IN REF. 1; AA SEQUENCE)
FT CONFLICT 810 810 R -> S (IN REF. 3)
FT CONFLICT 865 865 ASP -> QT (IN REF. 2)
FT CONFLICT 936 936 K -> E (IN REF. 3)
FT CONFLICT 970 970 L -> V (IN REF. 3)
FT CONFLICT 1132 1132 H -> R (IN REF. 2)
FT CONFLICT 1200 1200 F -> I (IN REF. 2)
FT CONFLICT 1382 1382 D -> A (IN REF. 2)
FT CONFLICT 1413 1414 NS -> EF (IN REF. 1)
FT CONFLICT 1489 1489 A -> S (IN REF. 2)
SQ SEQUENCE 1816 AA; 201818 MW; B49C45F3A4599D8 CRC64;

Query Match 21.1%; Score 60; DB 1; Length 1816;
Best local Similarity 23.8%; Pred. No. 17;
Matches 15; Conservative 10; Mismatches 22; Indels 16; Gaps 2;

QY 2 AGCCGNEVYDLSLHACIPQ-----LRCSNTPPLTCQRYCNASTNSV 46
DB 64 AERCDAG-FRRTUSGBCAPCDGNGSHCLDSSGFCFLHCORNTGHCERKCLDGYIGDSI 122
QY 47 KGT 49
DB 123 RGT 125

RESULT 14
LMA4_HUMAN STANDARD; PRT; 1816 AA.
ID LMA4_HUMAN Q16353; Q14735; Q9UE18; Q9UUN9;
AC Q16353; Q15335; Q14735; Q9UE18; Q9UUN9;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Laminin alpha-4 chain precursor.
OS LAMA4.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBL_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=95300971; PubMed=7781776;
RA Iivanainen A., Salnio K., Sariola H., Tryggvason K.;
RT "Primary structure and expression of a novel human laminin alpha 4
chain."
RL FEBS Lett. 365:183-188(1995).

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RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=97454279; PubMed=9310354;
RA Richards A.J., Lucchini C., Pope F.M.;
RT "The structural organisation of LAMA4, the gene encoding laminin
alpha4."
RL Eur. J. Biochem. 248:15-23(1997).
RN [3]
RP SEQUENCE OF 236-1816 FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=9504381; PubMed=7959779;
RA Richards A.J., Al-Imara L., Carter N.P., Lloyd J.C., Leversha M.A.,
RA Pope F.M.;
RT "Localization of the gene (LAMA4) to chromosome 6q21 and isolation of
a partial cDNA encoding a variant laminin A chain."
RL Genomics 22:237-239(1994).
RN [4]
RP SEQUENCE OF 66-1816 FROM N.A.
RA Tubbey B.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
is thought to mediate the attachment, migration, and organization
of cells into tissues during embryonic development by interacting
with other extracellular matrix components.
CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
different polypeptide chains (alpha, beta, gamma), which are bound
to each other by disulfide bonds into a cross-shaped molecule
comprising one long and three short arms with globules at each
end.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
MEMBRANES (MAJOR COMPONENT).
CC -1- TISSUE SPECIFICITY: IN ADULT, STRONG EXPRESSION IN HEART, LUNG,
OVARY SMALL, AND LARGE INTESTINES, PLACENTA, LIVER; WEAK OR NO
EXPRESSION IN SKELETAL MUSCLE, KIDNEY, PANCREAS, TESTIS, PROSTATE,
BRAIN. HIGH EXPRESSION IN FETAL LUNG AND KIDNEY. EXPRESSION IN
FETAL AND NEWBORN TISSUES IS OBSERVED IN CERTAIN MESENCHYMAL CELLS
IN TISSUES SUCH AS SMOOTH MUSCLE AND DERMIS.
CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS 1 AND 11 ARE THOUGHT TO INTERACT
WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -1- DOMAIN: DOMAIN G IS GLOBULAR.
CC -1- SIMILARITY: CONTAINS 3.5 LAMININ BGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
CC -1- CAUTION: GENE LAMA4 WAS FORMERLY CALLED LAMA3.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S78569; AAB34635.1; -
DR EMBL; X91171; CA62596.1; -
DR EMBL; Y14240; CA474636.1; -
DR EMBL; X76939; CA454258.1; -
DR EMBL; Z99289; CAB16553.1; -
DR HSSP; P02468; IKLO.
DR Genew; HGNC:6484; LAMA4.
DR MIM; 600133; -
DR InterPro; IPR000561; BGF-like.
DR InterPro; IPR002045; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR Pfam; PF000053; Laminin_BGF; 6.
DR Pfam; PF000054; Laminin_G; 6.
DR SMART; SM00180; EGF_Lam; 5.
DR SMART; SM00282; LamG; 5.
DR PROSITE; PS00022; EGF_1; UNKNOWN 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 3.
DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
DR GlycoProtein; Basement membrane; Extracellular matrix; Coiled coil;
Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
KW

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FT SIGNAL 1 24
CHAIN 25 1816
FT CHAIN 82 131
FT DOMAIN 132 186
FT DOMAIN 187 240
FT DOMAIN 241 255
FT DOMAIN 256 825
FT DOMAIN 826 1028
FT DOMAIN 1040 1220
FT DOMAIN 1227 1395
FT DOMAIN 1462 1633
FT DOMAIN 1640 1813
FT DOMAIN 313 396
FT DOMAIN 466 521
FT DOMAIN 574 607
FT DOMAIN 655 717
FT DOMAIN 770 799
FT SITE 717 91
FT DISULFID 82 91
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FT CARBOHYD 1086 1086
FT CARBOHYD 1281 1281
FT CARBOHYD 1359 1359
FT CARBOHYD 1411 1411
FT CONFLICT 143 143
FT CONFLICT 178 178
FT CONFLICT 265 265
FT CONFLICT 276 276
FT CONFLICT 491 491
FT CONFLICT 1057 1057
FT CONFLICT 1110 1112
SQ SEQUENCE 1816 AA; 201908 MW; 04E9AF379A0F4A4D CRC64;

Query Match
Best Local Similarity 20.4%; Score 58; DB 1; Length 1816;
Matches 13; Conservative 13; Mismatches 20; Indels 16; Gaps 2;
QY 2 AGCCSQNEYFDSLHACIPCO-----LRCSSNTPLTCORYCNASVNSV 46
Db 64 AEKCNAG-FFHTLSGECVPCDCNGNSNECLDGGCYCHVCQRTTGECHCKLGGYIGDSI 122
QY 47 KG 48
Db 123 RG 124

RESULT 15
FUR2_DROME
ID FUR2_DROME STANDARD; PRT; 1680 AA.
AC P30432;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Furin-like protease 2 precursor (EC 3.4.21.75) (Furin 2).
GN FUR2.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
RX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92381036; PubMed=1512259;
RA Roebroek A.J.M., Creemers J.W.M., Pauli I.G.L., Kurzik-Dumke U.,
RA Rentrop M., Gateff E.A.F., Leunissen J.A.M., van de Ven W.J.;
RT "Cloning and functional expression of Dürin2, a subtilisin-like
RT preprotein processing enzyme" of Drosophila melanogaster with multiple
RT repeats of a cysteine motif.;
RL J. Biol. Chem. 267:17208-17215 (1992).
CC -!- FUNCTION: FURIN IS LIKELY TO REPRESENT THE UBIQUITOUS ENDOPEPTIDASE
CC ACTIVITY WITHIN CONSTITUTIVE SECRETORY PATHWAYS AND CAPABLE OF
CC CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Release of mature proteins from their
CC propeptides by cleavage of Arg-Xaa-Yaa-Arg|-Zaa bonds, where Xaa
CC can be any amino acid and Yaa is Arg or Lys. Releases albumin,
CC complement component C3 and von Willebrand factor from their
CC respective precursors.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8. FURIN SUBFAMILY.
CC
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CC EMBL: M94375; AAA28551.1;
CC PIR: A43434; A43434.
CC HSP: Q99405; 1MPT.
CC MEROPS: S08.049;
CC FlyBase: FBgn004598; Fur2.
CC InterPro: IPR000561; Egrf-like.
CC InterPro: IPR002174; Furin-like.
CC InterPro: IPR002884; P_domain.
CC InterPro: IPR000209; Peptidase_S8.
CC Pfam: PF00082; Peptidase_S8; 1.
CC Pfam: PF01483; P; PARTIAL.
CC PRINTS: PR00723; SUBTILISIN.
CC ProDom: PD000717; P_domain; 1.
CC SMART: SM00181; EGF; 1.
CC SMART: SM00261; FU; 10.
CC PROSITE: PS00136; SUBTILASE ASP; 1.
CC PROSITE: PS00137; SUBTILASE_HIS; 1.
CC PROSITE: PS00138; SUBTILASE_SER; 1.
CC Hydrolase; Serine protease; Glycoprotein; Signal; Transmembrane;
KW Multigene family; Zymogen; Repeat.
FT SIGNAL 1 ?
FT PROPEP 1 319
FT CHAIN 320 1680
FT ACT_SITE 418 418
FT ACT_SITE 457 457
FT ACT_SITE 638 638
FT DOMAIN 962 1444
FT REPEAT 962 1007
FT REPEAT 1008 1057
FT REPEAT 1058 1104
FT REPEAT 1105 1153
FT REPEAT 1154 1205

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FT REPEAT 1206 1254 6.  
FT REPEAT 1255 1299 7.  
FT REPEAT 1300 1346 8.  
FT REPEAT 1347 1393 9.  
FT REPEAT 1394 1444 10.  
FT TRANSMEM 1508 1532 POTENTIAL.  
FT DOMAIN 1533 1680 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 130 130 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 203 203 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 928 928 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1061 1061 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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FT CARBOHYD 1440 1440 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 1680 AA; 183599 MW; 0A99CE8770A8E293 CR64;
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Query Match Best Local Similarity 20.2%; Score 57.5; DB 1; Length 1680;

Matches 12; Conservative 5; Mismatches 17; Indels 1; Gaps 1;

Qy 5 CSQNEYFDSLHACIPQOLRCSS-NTPEPTCORYC 38

Db 1199 CSESEFYSGVEGQCRPHASGSGNGPADTSCCTSC 1233

Search completed: January 7, 2003, 09:38:03
Job time : 5.83459 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:40:20 : Search time 3.81459 Seconds
(without alignments)
252.055 Million cell updates/sec

Title: US-09-855-158-6

Perfect score: 284

Sequence: 1 MAGCSONEYFDSLHACIP.....LTCORYCNASVYKGTNA 51

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB_PEP:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_PEP:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB_PEP:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB_PEP:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB_PEP:*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB_PEP:*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB_PEP:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB_PEP:*
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- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB_PEP:*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB_PEP:*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB_PEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	284	100.0	51	10	US-09-854-864-6
2	284	100.0	181	10	US-09-854-864-5
3	284	100.0	184	9	US-10-077-438-1
4	284	100.0	184	9	US-10-077-438-7
5	284	100.0	184	9	US-10-077-137-1
6	284	100.0	184	9	US-10-077-137-7
7	284	100.0	283	10	US-09-854-864-9
8	284	93.0	58	10	US-09-854-864-21
9	249	87.7	207	9	US-10-077-438-3
10	249	87.7	207	9	US-10-077-137-3
11	201	70.8	34	10	US-09-854-864-7
12	201	70.8	34	10	US-09-854-864-13
13	186	65.5	85	10	US-09-854-864-11
14	182	64.1	117	10	US-09-854-864-10
15	109	38.4	117	10	US-09-854-864-12
16	67.5	23.8	37	9	US-09-779-050A-45
17	67.5	23.8	59	10	US-09-854-864-20
18	67.5	23.8	166	10	US-09-854-864-15
19	67.5	23.8	291	9	US-09-779-050A-43

20	67.5	23.8	293	9	US-09-779-050A-42	Sequence 42, Appl
21	67.5	23.8	293	9	US-10-084-971-2	Sequence 2, Appl
22	67.5	23.8	293	10	US-09-879-919-22	Sequence 22, Appl
23	67.5	23.8	293	10	US-09-854-864-14	Sequence 14, Appl
24	67.5	23.8	293	10	US-09-961-376-2	Sequence 2, Appl
25	67.5	23.8	397	10	US-09-854-864-18	Sequence 18, Appl
26	66.5	23.4	67	10	US-09-854-864-16	Sequence 16, Appl
27	65.5	23.1	798	12	US-10-078-928-102	Sequence 197, App
28	64.5	22.7	418	9	US-09-886-429-2	Sequence 2, Appl
29	64.5	22.7	735	10	US-09-898-570-12	Sequence 10, Appl
30	64.5	22.7	845	10	US-09-898-570-12	Sequence 12, Appl
31	64.5	22.7	974	10	US-09-898-570-14	Sequence 14, Appl
32	64.5	22.7	1009	10	US-09-898-570-16	Sequence 16, Appl
33	61.5	21.7	99	9	US-09-950-933A-82	Sequence 82, Appl
34	60.5	21.3	3034	10	US-09-737-149-30	Sequence 25, Appl
35	60.5	21.3	3034	10	US-09-737-149-30	Sequence 30, Appl
36	59	20.8	38	9	US-09-779-050A-46	Sequence 46, Appl
37	58	20.4	162	10	US-09-798-789-10	Sequence 10, Appl
38	55.5	19.5	132	10	US-09-840-795-15	Sequence 15, Appl
39	55.5	19.5	870	12	US-10-078-928-188	Sequence 188, App
40	55.5	19.5	5405	9	US-10-025-380-1116	Sequence 1116, Ap
41	55.5	19.5	5405	10	US-09-922-217-1116	Sequence 359, Ap
42	55	19.4	524	9	US-10-108-605-359	Sequence 3, Appl
43	54.5	19.2	350	9	US-10-060-523-2	Sequence 2, Appl
44	54.5	19.2	419	9	US-10-044-622-3	Sequence 3, Appl
45	54.5	19.2	419	9	US-09-852-209A-12	Sequence 12, Appl

ALIGNMENTS

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RESULT 1
US-09-854-864-6
Sequence 6, Application US/09854864
Patent No. US20020081296A1
GENERAL INFORMATION: LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLVS/ACP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854, 864
PRIOR FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 51
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-6

Query Match      100.0% Score 284; DB 10; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7e-24;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MAGCSONEYFDSLHACIPQLRCSSNTPTLTCORYCNASVYKGTNA 51
Db 1 MAGCSONEYFDSLHACIPQLRCSSNTPTLTCORYCNASVYKGTNA 51

RESULT 2
US-09-854-864-5
Sequence 5, Application US/09854864
Patent No. US20020081296A1
GENERAL INFORMATION: LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLVS/ACP-3, AND TACI

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; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5

Query Match      100.0%; Score 284; DB 10; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGNTA 51
|
Db 1 MAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGNTA 51
|

RESULT 3
US-10-077-438-1
; Sequence 1, Application US/10077438
; Patent No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-1

Query Match      100.0%; Score 284; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGNTA 51
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Db 4 MAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGNTA 54
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RESULT 4
US-10-077-438-7
; Sequence 7, Application US/10077438
; Patent No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
```

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; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-7
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Query Match      100.0%; Score 284; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGNTA 51
|
Db 4 MAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGNTA 54
|
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RESULT 5
US-10-077-137-1
; Sequence 1, Application US/10077137
; Patent No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-1
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Query Match      100.0%; Score 284; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGNTA 51
|
Db 4 MAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGNTA 54
|
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RESULT 6
US-10-077-137-7
; Sequence 7, Application US/10077137
; Patent No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Schnepf, Jurgen
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; PRIOR FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-7

Query Match          100.0%; Score 284; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1,3e-23;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGCCSONEYFDSLHACIPCOLRCSSTPPLTCORYCNASVTNSVKGTNA 51
DB 4 MAGCCSONEYFDSLHACIPCOLRCSSTPPLTCORYCNASVTNSVKGTNA 54

RESULT 7
US-09-854-864-9
; Sequence 9, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-9

Query Match          100.0%; Score 284; DB 10; Length 283;
Best Local Similarity 100.0%; Pred. No. 1,9e-23;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGCCSONEYFDSLHACIPCOLRCSSTPPLTCORYCNASVTNSVKGTNA 51
DB 1 MAGCCSONEYFDSLHACIPCOLRCSSTPPLTCORYCNASVTNSVKGTNA 51
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RESULT 8
US-09-854-864-21
; Sequence 21, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-21

Query Match          93.0%; Score 264; DB 10; Length 58;
Best Local Similarity 100.0%; Pred. No. 5,6e-22;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CSONEYFDSLHACIPCOLRCSSTPPLTCORYCNASVTNSVKGTNA 51
DB 1 CSONEYFDSLHACIPCOLRCSSTPPLTCORYCNASVTNSVKGTNA 47

RESULT 9
US-10-077-438-3
; Sequence 3, Application US/10077438
; Patent No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Schnepf, Jurgen
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc. S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; PRIOR FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-3

Query Match          87.7%; Score 249; DB 9; Length 207;
Best Local Similarity 70.6%; Pred. No. 7,4e-20;
Matches 48; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

QY 1 MAGCCSONEYFDSLHACIPCOLRCSSTPPLTCORYCNASVTNSVKGTNA 40
DB 1 MAGCCSONEYFDSLHACIPCOLRCSSTPPLTCORYCNASVTNSVKGTNA 40
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Db 42 MAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCLHACIPQLRCSSNTPPLTCORYCNA 101

Qy 41 SVTNSVRG 48

Db 102 SVTNSVRG 109

RESULT 10

US-10-077-137-3
; Sequence 3, Application US/10077137
; Patent No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Teschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-3

Query Match 87.7%; Score 249; DB 9; Length 207;

Best Local Similarity 70.6%; Pred. No. 7.4e-20; Indels 20; Gaps 1;

Matches 48; Conservative 0; Mismatches 0;

Qy 1 MAGQCSQNEYFDSL-----LHACIPQLRCSSNTPPLTCLHACIPQLRCSSNTPPLTCORYCNA 40

Db 42 MAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCLHACIPQLRCSSNTPPLTCORYCNA 101

Qy 41 SVTNSVRG 48

Db 102 SVTNSVRG 109

RESULT 11

US-09-854-864-7
; Sequence 7, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-854-864-7

Query Match 70.8%; Score 201; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CSQNEYFDSLHACIPQLRCSSNTPPLTCORYC 38

Db 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCORYC 34

RESULT 12

US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13

Query Match 70.8%; Score 201; DB 10; Length 81;

Best Local Similarity 100.0%; Pred. No. 3.8e-15; Indels 0; Gaps 0;

Matches 34; Conservative 0; Mismatches 0;

Qy 5 CSQNEYFDSLHACIPQLRCSSNTPPLTCORYC 38

Db 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCORYC 34

RESULT 13

US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11

Query Match 65.5%; Score 186; DB 10; Length 185;
Best Local Similarity 71.4%; Pred. No. 3.3e-13;
Matches 35; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 1 MAGCCSONEYFDSLHACIPQLRCCSNTPLTCORYCNASVTSVKGT 49
DB 1 MAQCCFSEYFDSLHACKCHLRCSN--PPATCQPCDPSVTSVKGT 47

RESULT 14

US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10

Query Match 64.1%; Score 182; DB 10; Length 281;

Best Local Similarity 69.4%; Pred. No. 1.3e-12; Mismatches 8; Indels 2; Gaps 1;

QY 1 MAGCCSONEYFDSLHACIPQLRCCSNTPLTCORYCNASVTSVKGT 49
DB 1 MAQCCFSEYFDSLHACKCHLRCSN--PPATCQPCDPSVTSVKGS 47

RESULT 15

US-09-854-864-12
; Sequence 12, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-854-864-12

Query Match 38.4%; Score 109; DB 10; Length 117;

Best Local Similarity 70.5%; Pred. No. 3.3e-05; Mismatches 2; Indels 10; Gaps 6;

QY 6 SONEFYDSLHACIPQLRCCSNTPLTCORYCNASVTSVKGT 49
DB 2 AQCEYFDSLHAC-PC-LRCS---PPTCQ-YC--SVT-SVKGT 35

Search completed: January 7, 2003, 09:54:53
Job time : 3.83459 secs

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OM protein - protein search, using sw model

Run on: January 7, 2003, 09:31:39 ; Search time 18.2782 Seconds
(without alignment)
371.797 Million cell updates/sec

Title: US-09-855-158-6
Perfect score: 284
Sequence: 1 MAGOCSQNEFYDSLHACIP.....ITCRPCNAYSVNKGKTN A 51

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Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 - 3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
 - 4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
 - 5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
 - 6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
 - 7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
 - 8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
 - 9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
 - 10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
 - 11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
 - 12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
 - 13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
 - 14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
 - 15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
 - 16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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 - 19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
 - 20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
 - 21: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
 - 22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
 - 23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
 - 24: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	284	100.0	51	AAE15485	Human B-cell matur
2	284	100.0	181	AAE15484	Human B-cell matur
3	284	100.0	184	AAE15483	Amino acid sequenc
4	284	100.0	184	AAE15482	Human B cell matur
5	284	100.0	184	AAE15481	Human B cell matur
6	284	100.0	184	AAE15480	Human B cell matur
7	284	100.0	184	AAE15479	Human B cell matur
8	284	100.0	184	AAE15478	Human B cell matur
9	284	100.0	184	AAE15477	Human B cell matur
10	284	100.0	184	AAE15476	Human B cell matur

11	270	95.1	302	AAE00507	Human BCMA-Immunog
12	270	95.1	302	AAE00506	Mouse IgG signal/h
13	264	93.0	58	AAE15501	Human B cell matur
14	264	93.0	58	AAE15500	Human B cell matur
15	201.5	71.0	157	AAE15486	Human BAFF recepto
16	186	65.5	185	AAE15485	Human BAFF recepto
17	186	65.5	185	AAE15484	Amino acid sequenc
18	186	65.5	185	AAE15483	Human B cell matur
19	186	65.5	185	AAE15482	Human B cell matur
20	182	64.1	182	AAE15481	Human B cell matur
21	109	38.4	117	AAE15480	Human BCMA-human i
22	90.5	31.9	24	AAE15479	Human-murine BCMA
23	71.5	25.2	249	AAE15478	A murine znrf4, a
24	67.5	23.8	37	AAE15477	Human AGP-3 recept
25	67.5	23.8	37	AAE15476	Human TACI cyto
26	67.5	23.8	59	AAE15500	Human TACI cyto
27	67.5	23.8	166	AAE15498	Human TACI cyto
28	67.5	23.8	166	AAE15497	Human TACI cyto
29	67.5	23.8	166	AAE15496	Human TACI cyto
30	67.5	23.8	166	AAE15495	Human TACI cyto
31	67.5	23.8	166	AAE15494	Human TACI cyto
32	67.5	23.8	166	AAE15493	Human TACI cyto
33	67.5	23.8	166	AAE15492	Human TACI cyto
34	67.5	23.8	166	AAE15491	Human TACI cyto
35	67.5	23.8	166	AAE15490	Human TACI cyto
36	67.5	23.8	166	AAE15489	Human TACI cyto
37	67.5	23.8	166	AAE15488	Human TACI cyto
38	67.5	23.8	166	AAE15487	Human TACI cyto
39	67.5	23.8	166	AAE15486	Human TACI cyto
40	67.5	23.8	166	AAE15485	Human TACI cyto
41	67.5	23.8	166	AAE15484	Human TACI cyto
42	67.5	23.8	166	AAE15483	Human TACI cyto
43	67.5	23.8	166	AAE15482	Human TACI cyto
44	67.5	23.8	166	AAE15481	Human TACI cyto
45	66.5	23.4	33	AAE15480	Human TACI cyto

ALIGNMENTS

RESULT 1
ID AAE15485
AAE15485 standard; peptide: 51 AA.
AC AAE15485;
XX 12-MAR-2002 (first entry)
XX Human B-cell maturation (BCMA) protein extracellular domain.
XX Human, transmembrane activator and intracellular CAML interactor; TACI,
XX cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
XX lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
XX prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
XX drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
XX Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
XX human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
XX rheumatoid arthritis; atherosclerosis.
XX Homo sapiens.
XX WO200187979-A2.
XX 22-NOV-2001.
XX 14-MAY-2001; 2001WO-US15567.
XX 12-MAY-2000; 2000US-204039P.
XX 27-JUN-2000; 2000US-214591P.
XX 14-MAY-2001; 2001US-0214591.
XX (AMGE-) AMGEN INC.

```

PI Theill LE, Yu G;
XX WPI; 2002-066686/09.
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
XX activator and intracellular cyclophilin ligand interactor, by
XX administering a binding partner for APRIL, a tumor necrosis factor
XX family ligand
XX
XX Claim 1; Fig 10A; 94pp; English.
XX
XX The invention relates to a method for inhibiting TAC1 (transmembrane
XX activator and intracellular CAML interactor) and/or B cell maturation
XX protein (BCMA) activity in a mammal. The method comprises administering
XX a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
XX family ligand), having the consensus region of TAC1, BCMA, or the TAC1/
XX BCMA extracellular consensus sequence, but not the extracellular region
XX of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1
XX and/or BCMA in a mammal which is useful for treating B-cell or T-cell
XX lymphoproliferative disorders, one or more solid tumours such as lung,
XX gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1
XX antagonists are useful for treating inflammation and immune function
XX diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
XX dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
XX disease), drug and insect sting allergy, inflammatory bowel disease
XX (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
XX sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
XX bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
XX with leucocyte infiltration of the skin or organs. The present sequence
XX is human BCMA protein extracellular domain.
XX
XX Sequence 51 AA;
XX
XX Query Match 100.0%; Score 284; DB 23; Length 51;
XX Best Local Similarity 100.0%; Pred No. 8.3e-27;
XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MAGQCSQNEYFDSLHACIPQLRCSNTPTPLTCQRYCNASVTSVKGTNA 51
DB 1 MAGQCSQNEYFDSLHACIPQLRCSNTPTPLTCQRYCNASVTSVKGTNA 51
XX
RESULT 2
AAE15484
ID AAE15484 standard; Protein; 181 AA.
XX
XX AAE15484;
XX
XX 12-MAR-2002 (first entry)
XX
XX Human B-cell maturation (BCMA) protein.
XX
XX Human; transmembrane activator and intracellular CAML interactor; TAC1;
XX cytotatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
XX lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
XX prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
XX drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
XX Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
XX human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
XX rheumatoid arthritis; atherosclerosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 5..38
XX /note= "Cysteine-rich consensus region; This is region
XX is specifically claimed as SEQ ID NO: 7 in claim 1 of
XX the specification"
XX
XX Domain 52..72
XX /label= Transmembrane_domain
XX
XX WO200187979-A2.
XX

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PD 22-NOV-2001.
XX
XX 14-MAY-2001; 2001WO-US15567.
XX
XX 12-MAY-2000; 2000US-204039P.
XX 27-JUN-2000; 2000US-214591P.
XX 14-MAY-2001; 2001US-0214591.
XX
XX (AMGE-) AMGEN INC.
XX
XX Theill LE, Yu G;
XX
XX WPI; 2002-066686/09.
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
XX activator and intracellular cyclophilin ligand interactor, by
XX administering a binding partner for APRIL, a tumor necrosis factor
XX family ligand
XX
XX Disclosure; Fig 10A; 94pp; English.
XX
XX The invention relates to a method for inhibiting TAC1 (transmembrane
XX activator and intracellular CAML interactor) and/or B cell maturation
XX protein (BCMA) activity in a mammal. The method comprises administering
XX a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
XX family ligand), having the consensus region of TAC1, BCMA, or the TAC1/
XX BCMA extracellular consensus sequence, but not the extracellular region
XX of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1
XX and/or BCMA in a mammal which is useful for treating B-cell or T-cell
XX lymphoproliferative disorders, one or more solid tumours such as lung,
XX gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1
XX antagonists are useful for treating inflammation and immune function
XX diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
XX dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
XX disease), drug and insect sting allergy, inflammatory bowel disease
XX (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
XX sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
XX bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
XX with leucocyte infiltration of the skin or organs. The present sequence
XX is human BCMA protein.
XX
XX Sequence 181 AA;
XX
XX Query Match 100.0%; Score 284; DB 23; Length 181;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-26;
XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MAGQCSQNEYFDSLHACIPQLRCSNTPTPLTCQRYCNASVTSVKGTNA 51
DB 1 MAGQCSQNEYFDSLHACIPQLRCSNTPTPLTCQRYCNASVTSVKGTNA 51
XX
RESULT 3
AAB08843
ID AAB08843 standard; peptide; 184 AA.
XX
XX AAB08843;
XX
XX 02-JAN-2001 (first entry)
XX
XX Amino acid sequence of human.
XX
XX BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;
XX anti-cell death gene; apoptosis; viral infection; inflammatory response;
XX rheumatoid arthritis; inflammatory bowel disease; septic shock.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 57..77
XX /note= "putative transmembrane domain"
XX
XX WO2000050633-A1.
XX

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XX 31-AUG-2000.
XX
XX 24-FEB-2000; 2000MO-US04925.
XX
XX 24-FEB-1999; 99US-0121485.
XX
XX (GENO) GEN HOSPITAL CORP.
XX
XX Seed B, Ting A;
XX
XX WPI; 2000-558405/51.
XX
XX Identifying a modulator of gene expression for drug designing, by
XX contacting a compound library with a cell expressing an anti-cell death
XX gene and reporter gene, and determining alteration in reporter gene
XX expression
XX
XX Claim 32; Fig 7A; 53pp; English.
XX
XX The present sequence represents a BCMA (not defined) polypeptide. BCMA
XX is a necrosis factor (NF)-kB activator. The method of the invention is
XX used to identify compounds which modulate BCMA activity (and thus NF-kB
XX activity). The specification describes a method of identifying a
XX polypeptide which increases gene expression from a promoter. The method
XX involves contacting a library of with a cell which expresses a
XX recombinant anti-cell death gene and a reporter gene operably linked to
XX the promoter, and then determining whether the expression of the
XX reporter gene is altered as a result of contact with library. The method
XX is useful for identifying polypeptides which increase or decrease gene
XX expression from a promoter. The BCMA polypeptide or nucleic acid are
XX useful for preparing a pharmaceutical composition for treating cancer,
XX apoptosis, viral infections, inflammatory response, such as rheumatoid
XX arthritis, inflammatory bowel disease or septic shock. BCMA is useful for
XX identifying compounds that modulate NF-kB expression and thus for drug
XX designing.
XX
XX Sequence 184 AA:
XX
XX Query Match 100.0%; Score 284; DB 21; Length 184;
XX Best Local Similarity 100.0%; Pred. No. 3.3e-26;
XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MAGCCSONEYFDSLHACIPCOLRCSSTNPPLTCORYCNASVTNSVKGTA 51
XX 4 MAGCCSONEYFDSLHACIPCOLRCSSTNPPLTCORYCNASVTNSVKGTA 54
XX
XX RESULT 4
XX ID AAY94001 standard; Protein; 184 AA.
XX
XX AAY94001;
XX
XX 20-OCT-2000 (first entry)
XX
XX A human BCMA protein, a B cell protein related to TNF.
XX
XX Human, BR43x2; TNF receptor; extracellular domain; BCMA; B cell protein;
XX transmembrane activator and CAML-interactor; tumor necrosis factor; TNF;
XX zntf4 activity; antibody production; autoimmune disease; amyloidosis;
XX systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
XX rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
XX end stage renal failure; glomerulonephritis; vasculitis; nephritis;
XX renal neoplasia; multiple myeloma; lymphoma; light chain neuropathy;
XX immune response; immunosuppression; graft rejection; joint pain;
XX graft versus host disease; inflammation; swelling; anaemia; septic shock;
XX insulin dependent diabetes mellitus; Crohn's disease; hypertension;
XX renal artery stenosis; occlusion; cholesterol; renal emboli.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO200040716-A2.
XX PD

XX 13-JUL-2000.
XX
XX 07-JAN-2000; 2000MO-US00396.
XX
XX 07-JAN-1999; 99US-0226533.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Gross JA, Xu W, Madden K, Yee DP;
XX
XX WPI; 2000-452538/39.
XX
XX N-PSDB; AAA58559.
XX
XX Inhibiting zntf4 activity in a mammal, to treat autoimmune diseases,
XX renal disease, graft versus host disease, and inflammation, comprises
XX administering a BR43x2, TNF or BCMA extracellular domain polypeptide -
XX
XX Disclosure; Page 152; 175pp; English.
XX
XX The present sequence represents a human BCMA protein, a B cell protein
XX related to transmembrane activator and CAML-interactor (TACI) receptor.
XX TACI is a tumour necrosis factor (TNF) receptor. The extracellular
XX domains of BR43x2 (an isoform of TACI), TNF or BCMA (a related B cell
XX protein) receptor contain a cysteine rich domain, and are used for
XX inhibiting zntf4 activity. Zntf4 is a TNF ligand. They may also be used
XX for inhibiting BR43x2, TNF or BCMA receptor-ligand engagement associated
XX with activated or resting B lymphocytes, effector T-cells, or with
XX antibody production. The antibody production is associated with an
XX autoimmune disease selected from systemic lupus erythematosus, myasthenia
XX gravis, multiple sclerosis and rheumatoid arthritis. The zntf4 activity
XX and BR43x2, TNF or BCMA receptor-ligand engagement is associated with
XX asthma, bronchitis, emphysema, end stage renal failure,
XX glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal
XX amyloidosis, multiple myelomas, lymphomas, light chain neuropathy,
XX rejection, graft versus host disease, immunosuppression, graft
XX diabetes mellitus, Crohn's disease, inflammation, insulin dependent
XX septic shock, BR43x2, TNF, and BCMA polypeptides, fusions, antibodies,
XX agonists or antagonists can be used to treat hypertension, renal artery
XX stenosis, or occlusion, and cholesterol or renal emboli.
XX
XX Sequence 184 AA:
XX
XX Query Match 100.0%; Score 284; DB 21; Length 184;
XX Best Local Similarity 100.0%; Pred. No. 3.3e-26;
XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MAGCCSONEYFDSLHACIPCOLRCSSTNPPLTCORYCNASVTNSVKGTA 51
XX 4 MAGCCSONEYFDSLHACIPCOLRCSSTNPPLTCORYCNASVTNSVKGTA 54
XX
XX RESULT 5
XX ID AAE09241 standard; Protein; 184 AA.
XX
XX AAE09241;
XX
XX 19-NOV-2001 (first entry)
XX
XX Human BCMA protein.
XX
XX Human, TNF; tumor necrosis factor; TNF-1; APRIL; TNF receptor;
XX TNFR; TNF; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
XX autoimmune disease; rheumatoid arthritis; multiple sclerosis;
XX psoriasis.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO200160397-A1.
XX XX
XX PD 23-AUG-2001.

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XX PF 28-NOV-2000; 2000WO-US32378.
XX PR 16-FEB-2000; 2000US-0182938.
XX PR 22-AUG-2000; 2000US-0226986.
XX PA (GETH ) GENENTECH INC.
XX PI Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
XX PI Yan M;
XX PR WPI; 2001-541628/60.
XX DR N-PSDB; AAD15902.
XX PT Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
XX PT activity, for treating autoimmune disorders and cancer, comprises
XX PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
XX PT antagonists.
XX PR Example 2; Fig 2; 160pp; English.
XX CC The invention relates to methods of using one or more agonists or
XX CC antagonists to modulate the activity of the members of TNF (tumour
XX CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
XX CC e.g. TACI or BCMA. The method is useful for treating pathological
XX CC conditions or diseases associated with increased TALL-1 and APRIL
XX CC expression or activity. TALL-1 and APRIL antagonists are used to
XX CC block the interaction between APRIL and TALL-1 with TACI or BCMA.
XX CC They are useful for treating a mammal suffering from cancer such
XX CC as leukaemia, lymphoma, myeloma, cancers of lung and colon and
XX CC autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
XX CC psoriasis and lupus erythematosus. The present sequence is human
XX CC BCMA protein.
XX SQ Sequence 184 AA;
XX
Query Match 100.0%; Score 284; DB 22; Length 184;
Best Local Similarity 100.0%; Pred. No. 3,3e-26;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAGQCSNEYFDSLHACIPCOLRCSSTPPLTCQRYCNASVTNSVKGTNA 51
DB 4 MAGQCSNEYFDSLHACIPCOLRCSSTPPLTCQRYCNASVTNSVKGTNA 54
RESULT 6
AAE00506
ID AAE00506 standard; Protein; 184 AA.
XX AC AAE00506;
XX DT 31-JUL-2001 (first entry)
XX DE Human B cell maturation protein (BCMA).
XX KW Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
XX KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
XX KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
XX KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
XX KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
XX KW organ transplantation; HIV; human immunodeficiency virus; TNF;
XX KW tumour necrosis factor; BCMA; B cell maturation protein.
XX OS Homo sapiens.
XX PN WO200124811-A1.
XX PR 12-APR-2001.
XX PF 05-OCT-2000; 2000WO-US27579.
XX PR 06-OCT-1999; 99US-0157933.
XX PR 11-FEB-2000; 2000US-0181807.
PR 30-JUN-2000; 2000US-0215688.
XX FA (BIOJ ) BIOGEN INC.
XX PA (APOT-) APOTECH R & D SA.
XX PI Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
XX PR WPI; 2001-266242/27.
XX DR N-PSDB; AAD03844.
XX PT Treating a mammal for a condition associated with undesired cell
XX PT proliferation such as cancer or carcinoma, comprises administering a
XX PT composition comprising A Proliferation Inducing Ligand Receptor
XX PT (APRIL-R) antagonist.
XX PR Claim 3; Fig 3A; 85pp; English.
XX CC The invention relates to a method of treating a mammal for a condition
XX CC associated with undesired cell proliferation such as cancer or
XX CC carcinoma. The method involves administering a composition comprising
XX CC A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as
XX CC B cell maturation protein (BCM or BCMA) antagonist that antagonises the
XX CC interaction between APRIL and its cognate receptor(s). This method is
XX CC useful for treating undesired cell proliferation such as cancer or
XX CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
XX CC prostate carcinoma, and other carcinomas whose proliferation is modulated
XX CC by APRIL. It is also useful for treating autoimmune diseases (Grave's
XX CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
XX CC diseases, renal disorders, B-cell lympho-proliferative disorders,
XX CC immunosuppressive diseases, organ transplantation, inflammation and
XX CC human immunodeficiency virus (HIV), and for treating, suppressing or
XX CC altering an immune response involving a signalling pathway between
XX CC APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
XX CC The present sequence is human APRIL-R also referred as BCMA or
XX CC BCM protein.
XX SQ Sequence 184 AA;
XX
Query Match 100.0%; Score 284; DB 22; Length 184;
Best Local Similarity 100.0%; Pred. No. 3,3e-26;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAGQCSNEYFDSLHACIPCOLRCSSTPPLTCQRYCNASVTNSVKGTNA 51
DB 4 MAGQCSNEYFDSLHACIPCOLRCSSTPPLTCQRYCNASVTNSVKGTNA 54
RESULT 7
AAB60698
ID AAB60698 standard; Protein; 184 AA.
XX AC AAB60698;
XX DT 22-MAY-2001 (first entry)
XX DE Human BAFF receptor (BAFF-R).
XX KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
XX KW immune-related disorder; B-cell growth inhibitor; BCMA;
XX KW B-cell maturation inhibitor; immunoglobulin production inhibitor;
XX KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
XX KW renal disorder; immunosuppressive disorder; HIV infection;
XX KW organ transplantation; antiinflammatory; systemic lupus erythematosus;
XX KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
XX KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
XX KW lymphoma; gene therapy; cancer; tumour.
XX OS Homo sapiens.
XX PN WO200112812-A2.
XX PR 22-FEB-2001.

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XX 16-AUG-2000; 2000MO-US22507.
XX 17-AUG-1999; 99US-0149378.
PR 11-FEB-2000; 2000US-0181684.
PR 18-FEB-2000; 2000US-0183536.
XX
PA (BIOJ) BIOGEN INC.
PI (APOT) APOTECH R & D SA.
PI Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
PI Thompson J;
DR N-PDOB; AAF93998.
DR WPI; 2001-202866/20.
PT Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
PT lympho-proliferative disorder by administering BAFF-receptor
PT polypeptide, chimeric molecule comprising receptor or anti-BAFF-R
PT antibody homolog -
XX
PS Claim 20; Fig 1; 59pp; English.

CC The invention relates to the use of a BAFF receptor (BAFF-R, also known
CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the
CC treatment of a variety of immune-related disorders. BAFF-R is a member of
CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
CC agent, and also plays a role in the development of hypertension and
CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
CC specific antibodies can be used for inhibiting B-cell growth, dendritic
CC cell-induced B-cell growth and maturation, and immunoglobulin production,
CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
CC disorders, hypertension and renal disorders. The BAFF-R proteins may also
CC be used in the treatment of immunosuppressive disorders and HIV
CC infection, and in patients undergoing organ transplantation. The BAFF-R
CC protein or BAFF-R specific antibodies may be used for treating,
CC suppressing or altering an immune response involving a signalling pathway
CC between BAFF-R and BAFF thereby inhibiting inflammation. Since BAFF-R
CC inhibits B-cell growth and maturation it is useful for treating diseases
CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
CC Grave's disease, multiple myeloma, B-cell carcinoma, leukaemia, rapidly
CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
CC autoimmune disorders and inherited B-cell-associated disorders. The
CC present sequence represents human BAFF-R.

CC
CC
CC Sequence 184 AA;
SQ

Query Match	100.0%	Score 284;	DB 22;	Length 184;
Best Local Similarity	100.0%;	Pred. No. 3.3e-26;		
Matches 51; Conservative 0; Mismatches 0;		Indels 0;	Gaps 0	
Oy	1 MAGGCSQNEVFDSDILHACIFCQLRCSNPPPLTCORYCNASVTNSVKGTNA 51			
Ddb	4 MAGGCSQNEVFDSDILHACIFCQLRCSNPPPLTCORYCNASVTNSVKGTNA 54			

RESULT 8
AAVY71979
ID AAVY1979 standard; Protein; 184 AA.
XX
XX AAY1979;
AC
XX
DT 28-MAR-2001 (first entry)
XX
DE Human B cell maturation factor (BCMA) protein.
XX
KW Human; Tumour Necrosis Factor; TNF; Immunosuppressant; TALL-1;
KW Tumour necrosis factor and Abou-related leukocyte expressed ligand 1;
KW Therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
KW thrombocytopenia purpurina; acute rheumatic fever; Goodpasture's syndrome;
KW haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 10;
KW post-streptococcal glomerulonephritis; polyarthritis nodosa; BCMA;

XX	B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
XX	Homo sapiens.
OS	
XX	
FH	Key
FT	Location/Qualifiers
FT	Domain
XX	1..62
XX	/label= Extracellular_domain
PN	WO200068378-A1.
XX	
ED	16-NOV-2000.
PF	05-MAY-2000; 2000WO-US12266.
PR	06-MAY-1999; 99US-0132892.
XX	01-MAY-2000; 2000US-0201012.
PA	(NAME-) NAT JEWISH MEDICAL & RES CENT.
PI	Shu HS;
DR	WPI; 2001-016094/02.
XX	N-PEDB; AAD02125.
PT	Isolated TALL-1 protein is used to identify compounds that regulate B lymphocyte proliferation, used to treat B lymphocyte associated autoimmune disorders -
PS	Claim 37; Page 104-105; 112pp; English.
XX	The present invention relates to Tumour necrosis factor (TNF) and Apol-related leucocyte expressed ligand 1 (TALL-1) nucleic acid molecules, proteins (including homologues), and their antibodies. The invention in particular relates to methods for regulating the interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to regulate monocyte, macrophage and B lymphocyte mediated immune responses. TALL-1 protein is useful for identifying compounds that regulate B lymphocyte proliferation. It is also useful for treating B lymphocyte associated autoimmune disorders like rheumatoid arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes mellitus, multiple sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic anaemia, pemphigus vulgaris, acute rheumatic fever, Goodpasture's syndrome, polyarteritis nodosa, or polyarthritis nodosa. post streptococcal glomerulonephritis; or polychondritis nodosa. The TALL-1 protein and its corresponding nucleic acid sequence are also useful in diagnostic assays.
CC	The present sequence is a human B cell maturation factor (BCMA)
CC	protein. It is the receptor for TALL-1 protein. BCMA gene is located on chromosome 16, in human tissues, BCMA is expressed by spleen and lymph nodes but not by brain, muscle, heart, lung, kidney, pancreas, testis and placenta. BCMA mRNA is absent in the pro-B lymphocyte stage but its expression increases with B lymphocyte maturation.
CC	
XX	
SO	Sequence 184 AA;
OY	
ID	1 MAGQCSQNEYFDLSLTHACIPCOLRCSSNPPLTCORFCYNASVTNSVKGTNA 51
ABBB1487	
XX	4 MAGQCSQNEYFDLSLTHACIPCOLRCSSNPPLTCORFCYNASVTNSVKGTNA 54
XX	
DT	02-SEP-2002 (first entry)
XX	

DE XX Human BCMA receptor related protein SEQ ID NO:7.

KW Human; Ztnfr12; tumour necrosis factor receptor; cytotostatic; immunosuppressive; dermatological; antiinflammatory; antidiabetic; neuroprotective; antirheumatic; antiarthritis; antiasthmatic; nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour; autoimmune disorder; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; insulin dependent diabetes mellitus; asthma; rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma; glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis; pylonelonephritis; renal neoplasm; multiple myeloma; amyloidosis; light chain neuropathy; hypertension; large vessel disease; graft-versus host disease; graft rejection; Crohn's disease.

KW Homo sapiens.

OS Homo sapiens.

PN WO200238766-A2.

XX 16-MAY-2002.

PF 05-NOV-2001; 2001WO-US47018.

XX 07-NOV-2000; 2000US-246449P.

PR 20-DEC-2000; 2000US-257131P.

PR 28-JUN-2001; 2001US-301715P.

PR 29-AUG-2001; 2001US-315565P.

XX (ZYMO) ZYMOGENETICS INC.

PA Gross JA, Xu W, Henne RM, Grant FJ;

PI WPI; 2002-508212/54.

DR Novel isolated human tumor necrosis factor receptor polypeptide, termed Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage renal failure or renal disease and lymphoma.

XX Disclosure; Page 135-136; 154pp; English.

PS The present invention describes a human tumour necrosis factor receptor designated Ztnfr12 (I) (I) has cytotostatic, immunosuppressive, dermatological, antiinflammatory, neuroprotective, antidiabetic, antirheumatic, antiarthritis, antiasthmatic, nephrotropic and hypotensive activities, and can be used in gene therapy. (I) can be used for inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12 (e.g. Ztnfr4), for treating disorders and diseases associated with B lymphocytes, activated B lymphocytes or resting B lymphocytes, and for inhibiting the proliferation of tumour cells. (I) is useful for treating autoimmune disorders such as systemic lupus erythematosus, myasthenia gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma, rheumatoid arthritis, bronchitis, emphysema and end stage renal failure or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid leukaemia, nephritis, and pylonelonephritis, and for treating renal neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or amyloidosis, hypertension, large vessel diseases, graft-versus host disease, graft rejection and Crohn's disease. (I) is useful for modulating the immune system, for regulating B cell responses and development, for modulating development of other cells, antibody production and cytokine production, and for modulating T and B cell communication. The present sequence represents a protein which is given in the exemplification of the present invention.

XX Sequence 184 AA;

SQ Query Match 100.0%; Score 284; DB 23; Length 184;

Best Local Similarity 100.0%; Pred. No. 3.3e-26;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGCQSQNEYFDSLLHACIFCQLRCSNTPTPLTCQRYCNASVTNSVKGNTA 51

DB 4 MAGCQSQNEYFDSLLHACIFCQLRCSNTPTPLTCQRYCNASVTNSVKGNTA 54

RESULT 10

AAE15488

ID AAE15488 standard; Protein; 283 AA.

XX AAE15488;

AC 12-MAR-2002 (first entry)

XX Human BCMA-immunoglobulin Fc region fusion protein.

DE Human; transmembrane activator and intracellular CAML interactor; TAC1; cytotostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis; fusion protein.

XX Homo sapiens.

OS Homo sapiens.

XX WO200187979-A2.

XX 22-NOV-2001.

XX 14-MAY-2001; 2001WO-US15567.

XX 12-MAY-2000; 2000US-204039P.

PR 27-JUN-2000; 2000US-214591P.

PR 14-MAY-2001; 2001US-0214591.

XX (AMGE-) AMGEN INC.

PA Theill LE, Yu G;

PI WPI; 2002-066686/09.

DR Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumour necrosis factor family ligand.

XX Disclosure; Fig 10B; 94pp; English.

PS The invention relates to a method for inhibiting TAC1 (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TAC1, BCMA, or the TAC1/BCMA extracellular consensus sequence, but not the extracellular region of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1 and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1 antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCMA protein-immunoglobulin Fc region fusion protein.

XX Sequence 283 AA;

SQ Query Match 100.0%; Score 284; DB 23; Length 283;

Best Local Similarity 100.0%; Pred. No. 5.1e-26;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGCQSQNEYFDSLLHACIFCQLRCSNTPTPLTCQRYCNASVTNSVKGNTA 51

DB 1 MAGCQSQNEYFDSLLHACIFCQLRCSNTPTPLTCQRYCNASVTNSVKGNTA 51


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RESULT 11
AAE00507
ID AAE00507 standard; Protein; 302 AA.
XX
XX AAE00507;
XX
XX 31-JUL-2001 (first entry)
XX
XX Human BCMA-Immunoglobulin G Fc region fusion construct.
XX
XX Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
XX gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
XX carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
XX systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
XX B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
XX organ transplantation; HIV; human immunodeficiency virus; TNF; murine;
XX tumour necrosis factor; B cell maturation protein; BCMA; fusion protein;
XX immunoglobulin G; IgG; Fc region.
XX
XX Chimeric - Homo sapiens.
XX
XX Chimeric - Mus sp.
XX
XX Key Location/Qualifiers
XX Protein 1-22
XX /label= Signal peptide
XX /note= "Derived from murine Ig kappa sequence"
XX Protein 23..302
XX /label= Mature_human_BCMA_IgG_Fc_fusion_protein
XX Region 23..75
XX /note= "Derived from human BCMA protein"
XX Region 76..302
XX /note= "Derived from human IgG Fc region"
XX Domain 24..302
XX /label= Cysteine_rich_domain
XX /note= "Derived from human BCMA"
XX
XX WO200124811-A1.
XX
XX 12-APR-2001.
XX
XX 05-OCT-2000; 2000WO-US27579.
XX
XX 06-OCT-1999; 99US-0157933.
XX 11-FEB-2000; 2000US-0181807.
XX 30-JUN-2000; 2000US-0215688.
XX
XX PA (BIOT ) BIOGEN INC.
XX PA (APOT-) APOTEC R & D SA.
XX
XX PI Schneider P, Thompson J, Cachero T, Ambrose C, Rennett P;
XX WIPI; 2001-266242/27.
XX N-PSDB; AAD03847.
XX
XX DR N-PSDB; AAD03847.
XX
XX PT Treating a mammal for a condition associated with undesired cell
XX proliferation such as cancer or carcinoma, comprises administering a
XX composition comprising A Proliferation Inducing Ligand Receptor
XX (APRIL-R) antagonist -
XX
XX PS Example 1; Fig 3B; 85pp; English.
XX
XX The invention relates to a method of treating a mammal for a condition
XX associated with undesired cell proliferation such as cancer or
XX carcinoma. The method involves administering a composition comprising
XX A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as
XX B cell maturation protein (BCM or BCMA) antagonist that antagonises the
XX interaction between APRIL and its cognate receptor(s). This method is
XX useful for treating undesired cell proliferation such as cancer or
XX carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
XX prostate carcinoma, and other carcinomas whose proliferation is modulated
XX by APRIL. It is also useful for treating autoimmune diseases (Grave's

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CC disease, systemic lupus erythematosus (SLE); hypertension, cardiovascular
CC diseases, renal disorders, B-cell lympho-proliferative disorders,
CC immunosuppressive diseases, organ transplantation, inflammation and
CC human immunodeficiency virus (HIV), and for treating, suppressing or
CC altering an immune response involving a signalling pathway between
CC APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
CC The present sequence is a fusion construct containing human APRIL-R
CC also referred as BCM or BCM protein, Fc region of human immunoglobulin
CC G (IgG) and a signal sequence from murine Ig kappa cDNA.
XX
XX SO Sequence 302 AA;
XX
XX Query Match 95.1%; Score 270; DB 22; Length 302;
XX Best Local Similarity 96.0%; Pred. No. 2,6e-24;
XX Matches 48; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX Oy 1 MAGCGSNEYFDSULHACIPCOLRCSNTPPLTCORVCNASTNSVKGTN 50
XX 27 MAGCGSNEYFDSULHACIPCOLRCSNTPPLTCORVCNASTNSVKGVD 76
XX
XX RESULT 12
XX AAB60699
XX ID AAB60699 standard; Protein; 302 AA.
XX
XX AC AAB60699;
XX
XX DT 22-MAY-2001 (first entry)
XX
XX DE Mouse IgG signal/human BAFF-R/human IgG Fc fusion protein, BAFF-R-Fc.
XX
XX XX Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
XX immune-related disorder; B-cell growth inhibitor;
XX B-cell maturation inhibitor; immunoglobulin production inhibitor;
XX autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
XX renal disorder; immunosuppressive disorder; HIV infection;
XX organ transplantation; anti-inflammatory; systemic lupus erythematosus;
XX autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
XX B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
XX lymphoma; gene therapy; cancer; tumour; IgG Fc; fusion construct.
XX
XX OS Chimeric - Homo sapiens.
XX
XX OS Chimeric - Mus sp.
XX
XX FN WO200112812-A2.
XX
XX PD 22-FEB-2001.
XX
XX PF 16-AUG-2000; 2000WO-US22507.
XX PR 17-AUG-1999; 99US-0149378.
XX PR 11-FEB-2000; 2000US-0181684.
XX PR 18-FEB-2000; 2000US-0183536.
XX
XX PA (BIOT ) BIOGEN INC.
XX PA (APOT-) APOTEC R & D SA.
XX
XX PI MacKay F, Browning J, Ambrose C, Tschopp J, Schneider P;
XX Thompson J;
XX WIPI; 2001-202866/20.
XX N-PSDB; AAF59990.
XX
XX DR N-PSDB; AAF59990.
XX
XX PT Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
XX lympho-proliferative disorder by administering BAFF-receptor
XX polypeptide, chimeric molecule comprising receptor or anti-BAFF-R
XX antibody homolog -
XX
XX PS Example 4; Fig 2; 59pp; English.
XX
XX The invention relates to the use of a BAFF receptor (BAFF-R, also known
XX as BCM) protein, or a BAFF-R fusion protein as an agent for the
XX treatment of a variety of immune-related disorders. BAFF-R is a member of

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CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
 CC agent, and also plays a role in the development of hypertension and
 CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,
 CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
 CC disorders, hypertension and renal disorders. The BAFF-R proteins may also
 CC be used in the treatment of immunosuppressive disorders and HIV
 CC infection, and in patients undergoing organ transplantation. The BAFF-R
 CC proteins or BAFF-R specific antibodies may be used for treating,
 CC suppressing or altering an immune response involving a signalling pathway
 CC between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
 CC inhibits B-cell growth and maturation it is useful for treating diseases
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
 CC autoimmune disorders and inherited B-cell-associated disorders. The
 CC present sequence represents the BAFF-R fusion protein BAFF-R-FC,
 CC comprising a mouse IgG-kappa signal sequence, residues 1-153
 CC of human BAFF-R and a human IgG FC sequence.

XX SQ Sequence 302 AA;
 Query Match 95.1%; Score 270; DB 22; Length 302;
 Best Local Similarity 96.0%; Pred. No. 2.6e-24;
 Matches 48; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAGQCSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTSVKGYN 50
 DB 27 MAGQCSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTSVKGVD 76

RESULT 13

AAE15501

ID AAE15501 standard; peptide; 58 AA.

XX AC AAE15501;

XX DT 12-MAR-2002 (first entry)

XX DE Human B cell maturation protein cysteine rich extracellular region.

XX Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.

XX OS Homo sapiens.

XX PN WO200187979-A2.

XX PD 22-NOV-2001.

XX PF 14-MAY-2001; 2001WO-US15567.

XX PR 12-MAY-2000; 2000US-204039P.

XX PR 27-JUN-2000; 2000US-214591P.

XX PR 14-MAY-2001; 2001US-0214591.

XX PA (AMGE-) AMGEN INC.

XX PI Theill LE, Yu G;

XX PI WPI; 2002-066686/09.

XX Inhibiting activity of B cell maturation protein and/or transmembrane
 XX activator and intracellular cyclophilin ligand interactor, by
 XX administering a binding partner for APRIL, a tumor necrosis factor

PT family ligand -

XX PS Disclosure; Fig 13; 94pp; English.

XX CC The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour, APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease (multiple
 CC Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis), systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA cysteine-rich extracellular region.

XX SQ Sequence 58 AA;

Query Match 93.0%; Score 264; DB 23; Length 58;
 Best Local Similarity 100.0%; Pred. No. 2.3e-24;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTSVKGNTA 51

DB 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTSVKGNTA 47

RESULT 14

AAB60700

ID AAB60700 standard; Protein; 157 AA.

XX AC AAB60700;

XX DT 22-MAY-2001 (first entry)

XX DE Human BAFF receptor (BAFF-R) sequence encoded by A plasmid pJST535.

XX Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
 KW immune-related disorder; B-cell growth inhibitor; BCMA;
 KW B-cell maturation inhibitor; immunoglobulin production inhibitor;
 KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
 KW renal disorder; immunosuppressive disorder; HIV infection;
 KW organ transplantation; antiinflammatory; systemic lupus erythematosus;
 KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
 KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
 KW lymphoma; gene therapy; cancer; tumour; plasmid pJST535.

XX OS Homo sapiens.

XX PN WO200112812-A2.

XX PD 22-FEB-2001.

XX PF 16-AUG-2000; 2000WO-US22507.

XX PR 17-AUG-1999; 99US-0149378.

XX PR 11-FEB-2000; 2000US-0181684.

XX PR 18-FEB-2000; 2000US-0183536.

XX PA (BIOJ) BIOGEN INC.

XX PA (APOT-) APOTEC R & D SA.

XX PI Mackay F, Browning J, Ambrose C, Teschopp J, Schneider P;

XX PI Thompson J;

DR WPI: 2001-202866/20.
DR N-PSDB; AAB60000.

XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
XX lympho-proliferative disorder by administering BAF-R-receptor
XX polypeptide, chimeric molecule comprising receptor or anti-BAF-R
XX antibody homolog

PS Example 1; Fig 3; 59pp; English.

XX The invention relates to the use of a BAF-R receptor (BAF-R, also known
XX as BCMA) protein, or a BAF-R fusion protein as an agent for the
XX treatment of a variety of immune-related disorders. BAF-R is a member of
XX the TNF (tumour necrosis factor) family, acting as an immunoregulatory
XX agent, and also plays a role in the development of hypertension and
XX related disorders. BAF-R, fusion proteins containing it, and BAF-R-
XX specific antibodies can be used for inhibiting B-cell growth, dendritic
XX cell-induced B-cell growth and maturation, and immunoglobulin production,
XX and in the treatment of autoimmune disorders, B-cell lymphoproliferative
XX disorders, hypertension and renal disorders. The BAF-R proteins may also
XX be used in the treatment of immunosuppressive disorders and HIV
XX infection, and in patients undergoing organ transplantation. The BAF-R
XX proteins or BAF-R specific antibodies may be used for treating
XX suppressing or altering an immune response involving a signalling pathway
XX between BAF-R and BAF, thereby inhibiting inflammation. Since BAF-R
XX inhibits B-cell growth and maturation it is useful for treating diseases
XX such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
XX Grave's disease, multiple myeloma, B-cell leukaemia, leukaemia, rapidly
XX progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
XX human BAF-R may be used in gene therapy to treat tumours, lymphomas,
XX autoimmune disorders and inherited B-cell-associated disorders. The
XX present sequence represents a human BAF-R protein sequence as encoded
XX by plasmid pJ51535. However, this BAF-R protein sequence is 27 amino
XX acids shorter than that given in AAB60698.

SQ Sequence 157 AA;

Query Match 71.0%; Score 201.5; DB 22; Length 157;
Best Local Similarity 82.4%; Pred. No. 2e-16; Indels 9; Gaps 3;
Matches 42; Conservative 0; Mismatches 0;

OY 1 MAGOCSQNEYFDSLHACIPCOLRCSNTPLTCORVCNASTVNSVKTNA 51
DB 4 MAG---QNEYFDSLHACIPCOLR---NTPLTCORVCNASTVNT---GTNA 45

RESULT 15

AAE15486 standard; peptide: 34 AA.

AAE15486;

12-MAR-2002 (first entry)

Human B-cell maturation (BCMA) protein cysteine-rich consensus region.

XX Human; transmembrane activator and intracellular CAML interactor; TACI;
XX cytoskeletal; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
XX lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
XX prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
XX drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
XX Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
XX human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
XX rheumatoid arthritis; atherosclerosis.

OS Homo sapiens.

PN WO200187979-A2.

22-NOV-2001.

14-MAY-2001; 2001WO-US15567.

PR 12-MAY-2000; 2000US-204039P.
PR 27-JUN-2000; 2000US-214591P.
PR 14-MAY-2001; 2001US-0214591.

PA (AMGE-) AMGEN INC.

PI Thell LE, Yu G;

DR WPI: 2002-066666/09.

XX Inhibiting activity of B cell maturation protein and/or transmembrane
XX activator and intracellular cyclophilin ligand interactor, by
XX administering a binding partner for APRIL, a tumor necrosis factor
XX family ligand

PS Claim 1; Fig 10A; 94pp; English.

XX The invention relates to a method for inhibiting TACI (transmembrane
XX activator and intracellular CAML interactor) and/or B cell maturation
XX protein (BCMA) activity in a mammal. The method comprises administering
XX a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
XX family ligand), having the consensus sequence, but not the extracellular region
XX of TACI or BCMA. The method is useful for inhibiting activity of TACI
XX and/or BCMA in a mammal which is useful for treating B-cell or T-cell
XX lymphoproliferative disorders, one or more solid tumours such as lung,
XX gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
XX antagonists are useful for treating inflammation and immune function
XX diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
XX dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
XX disease), drug and insect sting allergy, inflammatory bowel disease
XX (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
XX sclerosis, rheumatoid arthritis), systemic lupus erythematosus), fungal,
XX bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
XX with leucocyte infiltration of the skin or organs. The present sequence
XX is human BCMA protein cysteine-rich consensus region.

SQ Sequence 34 AA;

Query Match 70.8%; Score 201; DB 23; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.6e-17; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0;

OY 5 CSQNEYFDSLHACIPCOLRCSNTPLTCORVC 38
DB 1 CSQNEYFDSLHACIPCOLRCSNTPLTCORVC 34

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Job time : 19.2782 secs

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OM protein - protein search, using sw model

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Title: US-09-855-158-6

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Searched: 262191 seqs, 70875818 residues

Total number of hits satisfying chosen parameters: 262191

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	284	100.0	184	1	PCT-US02-34376-6
2	284	100.0	184	1	PCT-US02-06001-39
3	284	100.0	184	5	US-09-848-271-2
4	284	100.0	184	6	US-10-281-053-6
5	284	100.0	184	6	US-10-087-080-39
6	201	70.8	34	1	PCT-US02-34376-11
7	201	70.8	34	6	US-10-281-053-11
8	70.5	24.8	1548	6	US-10-180-903-2
9	67.5	23.8	166	6	US-10-293-816-6
10	67.5	23.8	293	6	US-10-268-951-22
11	67.5	23.8	293	6	US-10-258-368-1
12	67.5	23.8	293	6	US-10-293-816-2
13	67.5	23.8	301	6	US-10-258-368-12
14	67.5	23.8	334	6	US-10-258-368-8
15	67.5	23.8	366	6	US-10-258-368-6
16	67.5	23.8	404	6	US-10-258-368-15
17	66.5	23.4	33	1	PCT-US02-34376-13
18	66.5	23.4	133	6	US-10-281-053-13
19	63.5	22.4	133	6	US-10-209-582-950
20	60.5	21.3	3034	6	US-10-120-801-52
21	60.5	21.3	3034	6	US-10-811-70
22	60.5	21.3	3034	6	US-10-131-409-70
23	60.5	21.3	3034	6	US-10-139-854-70
24	60.5	21.3	3034	6	US-10-150-813-70
25	60.5	21.3	3034	6	US-10-150-164-70
26	59	20.8	34	1	PCT-US02-34376-14

27	59	20.8	34	6	US-10-281-053-14	Sequence 14, Appl
28	59	20.8	87	1	PCT-US02-32727-2251	Sequence 2251, Ap
29	59	20.8	87	6	US-10-057-498-2251	Sequence 2251, Ap
30	58	20.4	162	6	US-10-218-102-420	Sequence 420, App
31	58	20.4	277	5	US-09-724-676-75440	Sequence 75440, A
32	58	20.4	277	5	US-09-724-676A-75440	Sequence 75440, A
33	58	20.4	367	5	US-09-724-676-75441	Sequence 75441, A
34	58	20.4	367	5	US-09-724-676A-75441	Sequence 75441, A
35	58	20.4	1485	5	US-08-724-676-75445	Sequence 75445, A
36	58	20.4	1604	5	US-08-724-676A-75445	Sequence 75445, A
37	58	20.4	1604	5	US-09-724-676-75444	Sequence 75444, A
38	58	20.4	1604	5	US-09-724-676A-75444	Sequence 75444, A
39	58	20.4	1659	5	US-09-724-676-75443	Sequence 75443, A
40	58	20.4	1659	5	US-09-724-676A-75443	Sequence 75443, A
41	58	20.4	1685	5	US-09-724-676-75442	Sequence 75442, A
42	58	20.4	1685	5	US-09-724-676A-75442	Sequence 75442, A
43	58	20.4	1816	6	US-10-299-058-2	Sequence 2, Appli
44	58	20.4	1816	6	US-10-299-058-4	Sequence 4, Appli
45	57	20.1	337	6	US-10-270-333-96	Sequence 96, Appl

ALIGNMENTS

RESULT 1
PCT-US02-34376-6
Sequence 6, Application PC/TUS0234376
GENERAL INFORMATION:
APPLICANT: Zhang, Gongyi
APPLICANT: Zhu, Hong-Ring
APPLICANT: Liu, Yingfang
APPLICANT: Xu, Liangguo
TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
TITLE OF INVENTION: Modified Proteins and Methods Related Thereto
FILE REFERENCE: 2879-86-PCT
CURRENT APPLICATION NUMBER: PCT/US02/34376
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 60/345,106
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 60/348,962
PRIOR FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: 60/354,966
PRIOR FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: 60/403,364
PRIOR FILING DATE: 2002-08-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 184
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-34376-6

Query Match 100.0%; Score 284; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 1e-24;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGCQSQNEVDSLHACIPCOLRCSNTPPLTCQRYCNASVTNSVKGTNA 51
Db 4 MAGCQSQNEVDSLHACIPCOLRCSNTPPLTCQRYCNASVTNSVKGTNA 54

RESULT 2
PCT-US02-06001-39
Sequence 39, Application PC/TUS0206001
GENERAL INFORMATION:
APPLICANT: Mack, David H.
APPLICANT: Markowitz, Sanford David
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Novel Methods of Diagnosis of Metastatic Colorectal
TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer

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/ FILE REFERENCE: 018501-000840PC
/ CURRENT APPLICATION NUMBER: PCT/US02/06001
/ CURRENT FILING DATE: 2002-12-20
/ PRIOR APPLICATION NUMBER: US 60/272,206
/ PRIOR FILING DATE: 2001-02-27
/ PRIOR APPLICATION NUMBER: US 60/281,149
/ PRIOR FILING DATE: 2001-04-02
/ PRIOR APPLICATION NUMBER: US 60/284,555
/ PRIOR FILING DATE: 2001-04-17
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 39
/ LENGTH: 184
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: tumor necrosis factor receptor superfamily, member
PCT-US02-06001-39

Query Match          100.0%; Score 284; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 1e-24;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGCCSNEYFDSLHACIPQQLRCSSNTPPLTCORYCNASVTNSVKGNTA 51
Db 4 MAGCCSNEYFDSLHACIPQQLRCSSNTPPLTCORYCNASVTNSVKGNTA 54

RESULT 3
/ Sequence 2, Application US/09848271
/ GENERAL INFORMATION:
/ APPLICANT: Ruben, Steven
/ APPLICANT: Baker, Kevin
/ TITLE OF INVENTION: Human Tumor Necrosis Factor TR18 and Methods Based Thereon
/ FILE REFERENCE: PF526
/ CURRENT APPLICATION NUMBER: US/09/848,271
/ CURRENT FILING DATE: 2001-05-04
/ PRIOR APPLICATION NUMBER: 60/254,931
/ PRIOR FILING DATE: 2000-12-13
/ PRIOR APPLICATION NUMBER: 60/236,038
/ PRIOR FILING DATE: 2000-09-28
/ PRIOR APPLICATION NUMBER: 60/201,852
/ PRIOR FILING DATE: 2000-05-04
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 184
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-848-271-2

Query Match          100.0%; Score 284; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 1e-24;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGCCSNEYFDSLHACIPQQLRCSSNTPPLTCORYCNASVTNSVKGNTA 51
Db 4 MAGCCSNEYFDSLHACIPQQLRCSSNTPPLTCORYCNASVTNSVKGNTA 54

RESULT 4
/ Sequence 6, Application US/10281053
/ GENERAL INFORMATION:
/ APPLICANT: Zhang, Gongyi
/ APPLICANT: Shu, Hong-Bing
/ APPLICANT: Liu, Yingfang
/ APPLICANT: Xu, Liangguo
/ TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
/ TITLE OF INVENTION: Modified Proteins and Methods Related Thereto
/ FILE REFERENCE: 2879-86

/ CURRENT APPLICATION NUMBER: US/10/281,053
/ CURRENT FILING DATE: 2002-10-24
/ PRIOR APPLICATION NUMBER: 60/345,106
/ PRIOR FILING DATE: 2001-10-24
/ PRIOR APPLICATION NUMBER: 60/348,962
/ PRIOR FILING DATE: 2002-01-14
/ PRIOR APPLICATION NUMBER: 60/354,966
/ PRIOR FILING DATE: 2002-02-07
/ PRIOR APPLICATION NUMBER: 60/403,364
/ PRIOR FILING DATE: 2002-08-13
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 6
/ LENGTH: 184
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-281-053-6

Query Match          100.0%; Score 284; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1e-24;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGCCSNEYFDSLHACIPQQLRCSSNTPPLTCORYCNASVTNSVKGNTA 51
Db 4 MAGCCSNEYFDSLHACIPQQLRCSSNTPPLTCORYCNASVTNSVKGNTA 54

RESULT 5
/ Sequence 39, Application US/10087080
/ GENERAL INFORMATION:
/ APPLICANT: Mack, David H.
/ APPLICANT: Markowitz, Sanford David
/ APPLICANT: Ros Biotechnology, Inc.
/ TITLE OF INVENTION: Novel Methods of diagnosis of Metastatic Colorectal
/ TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
/ TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
/ FILE REFERENCE: 018501-000840US
/ CURRENT APPLICATION NUMBER: US/10/087,080
/ CURRENT FILING DATE: 2002-10-25
/ PRIOR APPLICATION NUMBER: US 60/272,206
/ PRIOR FILING DATE: 2001-02-27
/ PRIOR APPLICATION NUMBER: US 60/281,149
/ PRIOR FILING DATE: 2001-04-02
/ PRIOR APPLICATION NUMBER: US 60/284,555
/ PRIOR FILING DATE: 2001-04-17
/ NUMBER OF SEQ ID NOS: 41
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 39
/ LENGTH: 184
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: tumor necrosis factor receptor superfamily, member
/ OTHER INFORMATION: 17 (TNFRSF17)
US-10-087-080-39

Query Match          100.0%; Score 284; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1e-24;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGCCSNEYFDSLHACIPQQLRCSSNTPPLTCORYCNASVTNSVKGNTA 51
Db 4 MAGCCSNEYFDSLHACIPQQLRCSSNTPPLTCORYCNASVTNSVKGNTA 54

RESULT 6
/ Sequence 11, Application PC/TUS0234376
/ GENERAL INFORMATION:
/ APPLICANT: Zhang, Gongyi
/ APPLICANT: Shu, Hong-Bing
PCT-US02-34376-11
```

APPLICANT: Liu, Yingfang
APPLICANT: Xu, Lianguo
TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
TITLE OF INVENTION: Modified Proteins and Methods Related Thereto
FILE REFERENCE: 2879-86-PCT
CURRENT APPLICATION NUMBER: PCT/US02/34376
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 60/345,106
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 60/348,962
PRIOR FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: 60/354,966
PRIOR FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: 60/403,364
PRIOR FILING DATE: 2002-08-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 34
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-34376-11

Query Match 70.8%; Score 201; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.9e-16; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0

Qy 5 CSQNEYFDSLHACIPCOLRCSSTPPLTCQRYC 38
Db 1 CSQNEYFDSLHACIPCOLRCSSTPPLTCQRYC 34

RESULT 7
US-10-281-053-11
Sequence 11, Application US/10281053
GENERAL INFORMATION:
APPLICANT: Zhang, Gongyi
APPLICANT: Shu, Hong-Bing
APPLICANT: Liu, Yingfang
APPLICANT: Xu, Lianguo
TITLE OF INVENTION: Three-Dimensional Structures of TALL-1 and its Cognate Receptors
TITLE OF INVENTION: Modified Proteins and Methods Related Thereto
FILE REFERENCE: 2879-86
CURRENT APPLICATION NUMBER: US/10/281,053
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 60/345,106
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 60/348,962
PRIOR FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: 60/354,966
PRIOR FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: 60/403,364
PRIOR FILING DATE: 2002-08-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 34
TYPE: PRT
ORGANISM: Homo sapiens
US-10-281-053-11

Query Match 70.8%; Score 201; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.9e-16; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0

Qy 5 CSQNEYFDSLHACIPCOLRCSSTPPLTCQRYC 38
Db 1 CSQNEYFDSLHACIPCOLRCSSTPPLTCQRYC 34

RESULT 8
US-10-180-903-2
Sequence 2, Application US/10180903

GENERAL INFORMATION:
APPLICANT: Allen, Keith D.
TITLE OF INVENTION: SPC6 SERINE PROTEASE GENE DISRUPTIONS,
TITLE OF INVENTION: AND COMPOSITIONS AND METHODS RELATED THERETO
FILE REFERENCE: R-720
CURRENT APPLICATION NUMBER: US/10/180,903
CURRENT FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/300,978
PRIOR FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/324,820
PRIOR FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1548
TYPE: PRT
ORGANISM: Mus Musculus
US-10-180-903-2

Query Match 24.8%; Score 70.5; DB 6; Length 1548;
Best Local Similarity 34.7%; Pred. No. 3.4; Indels 5; Gaps 1;
Matches 17; Conservative 5; Mismatches 22

Qy 4 QCSQNEYFDSLHACIPCOLRCSSTPPLTCQRYC 47
Db 1151 ECANVEYDEGSHRCQCHKRCSCGSPEDQCYCTCPRETLNNTCVK 1199

RESULT 9
US-10-293-816-6
Sequence 6, Application US/10293816
GENERAL INFORMATION:
APPLICANT: Von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF
FILE REFERENCE: 44158/254623
CURRENT APPLICATION NUMBER: US/10/293,816
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 09/782,857
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/290,333
PRIOR FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: US 08/810,572
PRIOR FILING DATE: 1997-03-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-816-6

Query Match 23.8%; Score 67.5; DB 6; Length 166;
Best Local Similarity 30.6%; Pred. No. 1.5; Indels 15; Gaps 1;
Matches 11; Conservative 9; Mismatches 15

Qy 5 CSQNEYFDSLHACIPCOLRCSSTPPLTCQRYC 40
Db 34 CPEEQYWDPLLLGTGCMCKTICNHQS-QRTCAAFCS 68

RESULT 10
US-10-268-951-22
Sequence 22, Application US/10268951
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang, et al.
TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
FILE REFERENCE: PF253P2
CURRENT APPLICATION NUMBER: US/10/268,951
CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 10/082,260
PRIOR FILING DATE: 2002-02-26

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; PRIOR APPLICATION NUMBER: 09/879,919
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/328,401
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/293,812
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-268-951-22
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Query Match 23.8%; Score 67.5; DB 6; Length 293;
Best Local Similarity 30.6%; Pred. No. 2.2;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
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QY 5 CSQNEYPDSLHACIPQCLRCSSNTPPLTCORYCNA 40
Db 34 CPEQYWDPLGTGCMSCKTCICNHQS-QRTCAAFCRS 68
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RESULT 11
US-10-258-368-1
; Sequence 1, Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; TITLE OF INVENTION: Tacti As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/10/258,368
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: USSN 60/199,946
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 1
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-1
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Query Match 23.8%; Score 67.5; DB 6; Length 293;
Best Local Similarity 30.6%; Pred. No. 2.2;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
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```
QY 5 CSQNEYPDSLHACIPQCLRCSSNTPPLTCORYCNA 40
Db 34 CPEQYWDPLGTGCMSCKTCICNHQS-QRTCAAFCRS 68
```

```
RESULT 12
US-10-293-816-2
; Sequence 2, Application US/10293816
; GENERAL INFORMATION:
; APPLICANT: Brem, Richard J.
; APPLICANT: Von Bulow, Goltz
```

```
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; FILE REFERENCE: 44158/254623
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US/10/293,816
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-816-2
```

```
Query Match 23.8%; Score 67.5; DB 6; Length 293;
Best Local Similarity 30.6%; Pred. No. 2.2;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
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```
QY 5 CSQNEYPDSLHACIPQCLRCSSNTPPLTCORYCNA 40
Db 34 CPEQYWDPLGTGCMSCKTCICNHQS-QRTCAAFCRS 68
```

```
RESULT 13
US-10-258-368-12
; Sequence 12, Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; TITLE OF INVENTION: Tacti As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/10/258,368
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: USSN 60/199,946
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 12
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-12
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Query Match 23.8%; Score 67.5; DB 6; Length 301;
Best Local Similarity 30.6%; Pred. No. 2.3;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
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```
QY 5 CSQNEYPDSLHACIPQCLRCSSNTPPLTCORYCNA 40
Db 42 CPEQYWDPLGTGCMSCKTCICNHQS-QRTCAAFCRS 76
```

```
RESULT 14
US-10-258-368-8
; Sequence 8, Application US/10258368
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; TITLE OF INVENTION: Tacti As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: USSN 60/199,946
; PRIOR FILING DATE: 2000-04-27
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